

**Methods and Compositions for Reducing Screening in
Oligonucleotide-Directed Nucleic Acid Sequence Alteration**

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. provisional applications nos.
5 60/453,360, filed March 7, 2003, and 60/416,983, filed October 7, 2002, the disclosures of which are
incorporated herein by reference in their entireties.

FIELD OF THE INVENTION

[0002] The technical field of the invention relates to oligonucleotide-directed alteration
10 of nucleic acid sequence.

BACKGROUND OF THE INVENTION

[0003] A number of methods have been developed to alter specific nucleotides within
both isolated DNA molecules and DNA present within intact cells of bacteria, plants, fungi and animals,
15 including humans.

[0004] In one approach, genomic sequences are targeted for alteration by homologous
recombination using duplex fragments. The duplex fragments are large, having several hundred
basepairs. See, e.g., Kunzelmann et al., *Gene Ther.* 3:859-867 (1996).

[0005] In another approach, oligonucleotides are used to effect targeted genetic
20 changes.

[0006] In early experiments, oligonucleotide-directed sequence changes were typically
effected in yeast, Moerschell *et al.*, 1988, *Proc. Natl. Acad. Sci.* 85:524 and Yamamoto *et al.*, *Yeast* 8:935

(1992), which among eukaryotes are known to have high recombinogenic activity, although one series of experiments were attempted in human cells, Campbell et al., *The New Biologist* 1: 223-227 (1989).

[0007] More recently, a number of different types of polynucleotides and oligonucleotides have been described that permit targeted alteration of genetic material in cells of higher eukaryotes, including (i) triplex-forming oligonucleotides; (ii) chimeric RNA-DNA oligonucleotides that are internally duplexed, notably in the region containing the nucleotide that directs the sequence alteration; and (iii) terminally modified single-stranded oligonucleotides having an internally unduplexed DNA domain and modified ends.

[0008] Sequence-altering triplexing oligonucleotides are described, for example, in U.S. Pat. Nos. 6,303,376, 5,962,426, and 5,776,744.

[0009] Triplex-forming oligonucleotides require a structural domain that binds to a DNA helical duplex through Hoogsteen interactions between the major groove of the DNA duplex and the oligonucleotide. The binding domain must typically target polypurine or polypyrimidine tracts. These sequence requirements limit the usefulness of triplex-forming oligonucleotides for targeted sequence alteration, requiring that the target sequence to be modified be situated in proximity to such polypurine or polypyrimidine tract. Triplex-forming oligonucleotides may also require an additional DNA reactive moiety, such as psoralen, to be covalently linked to the oligonucleotide, in order to stabilize the interactions between the triplex-forming domain of the oligonucleotide and the DNA double helix if the Hoogsteen interactions from the oligonucleotide/target base composition are insufficient. See, e.g., U.S. Patent 5,422,251. Such DNA-reactive moieties can, however, be indiscriminately mutagenic.

[0010] In more recent work with sequence-altering triplexing oligonucleotides, the triplex-forming domain is linked or tethered to a domain that effects targeted alteration, Culver et al., *Nat. Biotechnology* 17: 989-93 (1999), relaxing somewhat the permissible distance between target sequence and polypurine/polypyrimidine stretch.

[0011] Internally duplexed, hairpin- and double-hairpin-containing chimeric RNA-DNA oligonucleotides are described, *inter alia*, in U.S. Pat. Nos. 6,573,046; 5,888,983; 5,871,984; 5,795,972; 5,780,296; 5,760,012; 5,756,325; 5,731,181, and 5,565,350. Such chimeric RNA-DNA oligonucleotides are reportedly capable of directing targeted alteration of single base pairs, as well as introducing frameshift alterations, in cells and cell-free extracts from a variety of host organisms, including bacteria, fungi, plants and animals. The oligonucleotides are reportedly able to operate on almost any target sequence.

[0012] Such chimeric molecules have significant structural requirements, however, including a requirement for both ribonucleotides and deoxyribonucleotides, and typically also a requirement that the oligonucleotide adopt a double-hairpin conformation. Even when such double hairpins are not required, however, significant structural constraints remain.

5 [0013] Single-stranded oligonucleotides having modified ends and an internally unduplexed DNA domain that directs sequence alteration are described in copending international patent applications published as WO 03/027265; WO 02/10364; WO 01/92512; WO 01/87914; and WO 01/73002, as well as in U.S. Pat. Nos. 6,479,292 and 6,271,360, the disclosures of which are incorporated herein by reference in their entireties.

10 [0014] These single-stranded oligonucleotides have fewer structural requirements than chimeric oligonucleotides and are capable of directing sequence alteration, including introduction of frameshift mutations, in cells and cell-free extracts from a variety of host organisms, including bacteria, fungi, plants and animals, in episomal and in chromosomal targets, often at alteration efficiencies that exceed those observed with hairpin-containing, internally duplexed, chimeric oligonucleotides.

15 [0015] The usefulness of oligonucleotide-mediated nucleic acid sequence alteration — as a means, for example, for manipulating cloned DNA, for generating agricultural products with enhanced traits, for generating cellular models for laboratory use, or for generating animal models or animals with desired traits — is affected by its frequency. The usefulness of oligonucleotide-mediated nucleic acid sequence alteration as an *ex vivo* or *in vivo* therapeutic method would also be enhanced by increasing its
20 efficiency.

[0016] A need exists, therefore, for methods to enhance the efficiency of targeted alteration of genetic material.

SUMMARY OF THE INVENTION

25 [0017] The invention provides methods, compositions and kits for enhancing oligonucleotide-directed nucleic acid sequence alteration by reducing the number of target nucleic acid molecules required to be screened during oligonucleotide-directed targeted nucleic acid sequence alteration. The methods, compositions and kits involve using at least two oligonucleotides, where at least one of the oligonucleotides directs alteration of a selectable target.

30 [0018] In one aspect, the invention provides methods for reducing the number of target nucleic acid molecules required to be screened during oligonucleotide-directed nucleic acid sequence alteration comprising combining a nucleic acid molecule in the presence of repair proteins with at least two

oligonucleotides capable of directing alteration in at least two nucleic acid targets, where alteration by at least one oligonucleotide confers a selectable phenotype which is selected for, and selecting or screening for a nucleic acid molecule having the alteration directed by the other oligonucleotide in a composition having the selectable phenotype.

5 **[0019]** In other aspects, the invention provides compositions and kits for oligonucleotide-directed nucleic acid sequence alteration comprising at least two oligonucleotides, where at least one of the oligonucleotides directs an alteration which confers a selectable phenotype.

[0020] Other embodiments of the invention are set forth in the following numbered items:

10 **[0021]** 1. A method for reducing the number of target nucleic acid molecules required to be screened during oligonucleotide-directed nucleic acid sequence alteration of a first nucleic acid target in a composition comprising said first nucleic acid target and a second nucleic acid target,

[0022] wherein alteration of said first nucleic acid target is effected by combining, in the presence of cellular repair proteins, a nucleic acid molecule comprising said first nucleic acid target with a first oligonucleotide and a second oligonucleotide,

15 **[0023]** wherein said first oligonucleotide is capable of effecting alteration of said first nucleic acid target and said second oligonucleotide is capable of effecting alteration of said second nucleic acid target, and wherein alteration of said second nucleic acid target confers a selectable phenotype,

20 **[0024]** said method comprising:

[0025] (a) selecting for alteration of said second nucleic acid target and

[0026] (b) screening for a nucleic acid molecule comprising an alteration of said first nucleic acid target.

25 **[0027]** 2. A method for targeted alteration of a first nucleic acid target in a composition comprising said first nucleic acid target and a second nucleic acid target, comprising:

[0028] (a) combining, in the presence of cellular repair proteins, a nucleic acid molecule comprising said first nucleic acid target with a first oligonucleotide and a second oligonucleotide,

30 **[0029]** wherein said first oligonucleotide is capable of effecting alteration of said first nucleic acid target and said second oligonucleotide is capable of effecting alteration of said second nucleic acid target, and wherein alteration of said second nucleic acid target confers a selectable phenotype; and

[0030] (b) identifying a nucleic acid molecule comprising an alteration of said first nucleic acid target in a composition in which alteration of the second nucleic acid target has occurred.

[0031] 3. The method of item 1 or 2, wherein alteration of the selectable phenotype is selected from the group consisting of: antibiotic resistance, prototrophy, expression of a fluorescent protein, presence of an epitope and resistance to an apoptotic signal.

[0032] 4. The method of any one of items 1-3, wherein the alteration of the first nucleic acid target is a substitution, deletion or insertion of at least one base.

[0033] 5. The method of item 4, wherein the alteration of the second nucleic acid target is a substitution, deletion or insertion of at least one base.

[0034] 6. The method of any one of items 1-5, wherein the nucleic acid molecule comprising the first nucleic acid target does not comprise the second nucleic acid target.

[0035] 7. The method of any one of items 1-5, wherein the nucleic acid molecule comprising the first nucleic acid target comprises the second nucleic acid target.

[0036] 8. The method of any one of items 1-7, wherein the nucleic acid molecule comprising the first nucleic acid target is a DNA molecule.

[0037] 9. The method of item 8, wherein the DNA molecule is selected from the group consisting of: a chromosome, a plasmid, a YAC, a BAC, a PLAC, a MAC, and a PAC.

[0038] 10. The method of item 8 or 9, wherein the DNA molecule is present in a cell.

[0039] 11. The method of item 10, wherein the cell is selected from the group consisting of: a prokaryotic cell, a fungal cell, a plant cell, and an animal cell.

[0040] 12. The method of item 11, wherein the cell is prokaryotic cell.

[0041] 13. The method of item 12, wherein the prokaryotic cell is an *Escherichia coli* cell.

5 [0042] 14. The method of item 11, wherein the cell is a fungal cell.

[0043] 15. The method of item 14, wherein the fungal cell is selected from the group consisting of: a *Saccharomyces cerevisiae* cell, an *Ustilago maydis* cell, a *Neurospora crassa* cell and a *Candida albicans* cell.

10 [0044] 16. The method of item 11, wherein the cell is a plant cell.

[0045] 17. The method of item 16, wherein the plant cell is selected from the group consisting of: an angiosperm cell, a gymnosperm cell and a moss cell.

15 [0046] 18. The method of item 16, wherein the cell is a *Chlamydomonas reinhardtii* cell.

20 [0047] 19. The method of item 17, wherein the angiosperm cell is an *Arabidopsis thaliana* cell.

[0048] 20. The method of item 17, wherein the moss cell is a *Physcomitrella patens* cell.

25 [0049] 21. The method of item 11, wherein the cell is an animal cell.

[0050] 22. The method of item 21, wherein the animal cell is a mammalian cell.

30 [0051] 23. The method of item 22, wherein the mammalian cell is selected from the group consisting of: a human cell, a rodent cell, a mouse cell, a hamster cell, a rat cell, and a monkey cell.

[0052] 24. The method of item 23, wherein the human cell is selected from the group consisting of: a liver cell, a lung cell, a colon cell, a cervical cell, a kidney cell, an epithelial cell, a blood cell, a cancer cell, and a stem cell.

5 **[0053]** 25. The method of any one of items 1-24, wherein the first oligonucleotide has a region that is fully complementary in sequence to the first nucleic acid target, but for one or more mismatches as between the sequences of the first oligonucleotide and its complement on the first nucleic acid target, and wherein the first oligonucleotide has at least one terminal modification.

10 **[0054]** 26. The method of item 25, wherein the at least one terminal modification is selected from the group consisting of: at least one terminal locked nucleic acid (LNA), at least one terminal 2'-O-Me base analog, and at least three terminal phosphorothioate linkages.

15 **[0055]** 27. The method of item 26, wherein the first oligonucleotide is a single-stranded oligonucleotide 15 - 121 nucleotides in length, has an internally unduplexed domain of at least 8 contiguous deoxyribonucleotides, and wherein the one or more mismatches are positioned exclusively in the oligonucleotide DNA domain and at least 7 nucleotides from said oligonucleotide's 5' and 3' termini.

20 **[0056]** 28. The method of item 27, wherein the first oligonucleotide has at least one terminal locked nucleic acid (LNA).

[0057] 29. The method of item 1 or 2, wherein the first oligonucleotide is at least 25 nucleotides in length.

25 **[0058]** 30. The method of item 1 or 2, wherein the first oligonucleotide is no more than 121 nucleotides in length.

[0059] 31. The method of item 30, wherein the first oligonucleotide is no more than 74 nucleotides in length.

30 **[0060]** 32. A composition for targeted alteration of a first nucleic acid target, comprising:

[0061] a first oligonucleotide and a second oligonucleotide, wherein the oligonucleotides are capable, in the presence of cellular repair proteins, of effecting targeted alteration of a first nucleic target and a second nucleic acid target, respectively; and

[0062] wherein alteration of the second nucleic acid target confers a selectable phenotype.

[0063] 33. The composition of item 32 further comprising cellular repair proteins.

[0064] 34. The composition of item 33, wherein said cellular proteins are purified.

[0065] 35. The composition of item 33, wherein said cellular proteins are present in a cell-free protein extract.

[0066] 36. The composition of item 33, wherein said cellular proteins are present within an intact cell.

[0067] 37. The composition of any one of items 33 – 36, wherein the cell is selected from the group consisting of: a prokaryotic cell, a fungal cell, a plant cell, and an animal cell.

[0068] 38. The composition of any one of items 33 – 37, further comprising lambda beta protein.

[0069] 39. The composition of any one of items 33 – 37, wherein the cellular proteins are derived from a cell prior-contacted with hydroxyurea.

[0070] 40. The composition of any one of items 33 – 37, wherein the cellular proteins are derived from a cell prior-contacted with a histone deacetylase inhibitor.

[0071] 41. The composition of item 37, wherein the cell is prokaryotic cell.

[0072] 42. The composition of item 41, wherein the prokaryotic cell is an *E. coli* cell.

[0073] 43. The composition of item 37, wherein the cell is a fungal cell.

[0074] 44. The composition of item 43, wherein the fungal cell is selected from the group consisting of: a *Saccharomyces cerevisiae* cell, an *Ustilago maydis* cell, a *Neurospora crassa* cell and a *Candida albicans* cell.

[0075] 45. The composition of item 37, wherein the cell is a plant cell.

[0076] 46. The composition of item 45, wherein the plant cell is selected from the group consisting of: an angiosperm cell, a gymnosperm cell and a moss cell.

[0077] 47. The composition of item 45, wherein the cell is a *Chlamydomonas reinhardtii* cell.

[0078] 48. The composition of item 46, wherein the angiosperm cell is an *Arabidopsis thaliana* cell.

[0079] 49. The composition of item 46, wherein the moss cell is a *Physcomitrella patens* cell.

[0080] 50. The composition of item 37, wherein the cell is an animal cell.

[0081] 51. The composition of item 50, wherein the animal cell is a mammalian cell.

[0082] 52. The composition of item 51, wherein the mammalian cell is selected from the group consisting of: a human cell, a rodent cell, a mouse cell, a hamster cell, a rat cell, and a monkey cell.

[0083] 53. The composition of item 52, wherein the human cell is selected from the group consisting of: a liver cell, a lung cell, a colon cell, a cervical cell, a kidney cell, an epithelial cell, a blood cell, a cancer cell, and a stem cell.

[0084] 54. The composition of any one of items 32 - 53, wherein the first oligonucleotide is fully complementary in sequence to the first nucleic acid target, but for one or more mismatches as between the sequences of the first oligonucleotide and its complement on the first nucleic acid target, and wherein the first oligonucleotide has at least one terminal modification.

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[0085] 55. The composition of item 54, wherein the at least one terminal modification is selected from the group consisting of: at least one terminal locked nucleic acid (LNA), at least one terminal 2'-O-Me base analog, and at least three terminal phosphorothioate linkages.

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[0086] 56. The composition of item 55, wherein the first oligonucleotide is a single-stranded oligonucleotide 15 - 121 nucleotides in length, has an internally unduplexed domain of at least 7 contiguous deoxyribonucleotides, and wherein the one or more mismatches are positioned exclusively in the oligonucleotide DNA domain and at least 8 nucleotides from said oligonucleotide's 5' and 3' termini.

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[0087] 57. The composition of item 55, wherein the first oligonucleotide has at least one terminal locked nucleic acid (LNA).

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[0088] 58. The composition of any one of items 32 - 57, wherein said oligonucleotide is at least 25 nucleotides in length.

[0089] 59. The composition of any one of items 32 - 57, wherein said oligonucleotide is no more than 121 nucleotides in length.

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[0090] 60. The composition of item 59, wherein said oligonucleotide is no more than 74 nucleotides in length.

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[0091] 61. A kit for targeted alteration of nucleic acid sequence comprising:
[0092] a first oligonucleotide and a second oligonucleotide, wherein the oligonucleotides are capable, in the presence of cellular repair proteins, of effecting targeted alteration of a first nucleic target and a second nucleic acid target, respectively; and

[0093] wherein alteration of the second nucleic acid target confers a selectable phenotype.

[0094] 62. The kit of item 61 further comprising a cellular repair protein.

5 [0095] 63. The kit of item 62, wherein the cellular repair protein is from a cell precontacted with an HDAC inhibitor; hydroxyurea or lambda phage beta protein.

[0096] 64. The kit of item 62, wherein the cellular repair protein is selected from the group consisting of: RAD10, RAD51, RAD52, RAD54, RAD55, MRE11, PMS1 and XRS2.

10 [0097] 65. The kit of any one of items 61 - 64 further comprising an HDAC inhibitor; hydroxyurea or lambda phage beta protein.

[0098] 66. The kit of item 65 further comprising a cell.

15 [0099] 67. The kit of item 66, wherein the cell has increased levels or activity of at least one protein selected from the group consisting of: RAD10, RAD51, RAD52, RAD54, RAD55, MRE11, PMS1 and XRS2.

20 [0100] 68. The kit of item 66 or 67, wherein the cell has decreased levels or activity of at least one protein selected from the group consisting of: RAD10, RAD51, RAD52, RAD54, RAD55, MRE11, PMS1 and XRS2.

25 [0101] 69. The kit of any one of items 66 – 68, wherein the cell comprises a target nucleic acid sequence, wherein alteration of said target nucleic acid sequence by said second oligonucleotide confers a selectable phenotype.

[0102] 70. The kit of any one of items 61-69, wherein the kit further comprises instructions for performing the method of item 1 or item 2.

30 BRIEF DESCRIPTION OF THE DRAWINGS

[0103] Figure 1. *Diagram of pAURHYG(x)eGFP target plasmids.* Sequences are shown for the normal hygromycin resistance allele (SEQ ID NO:) and the mutant alleles present in

pAURHYG(rep)eGFP (SEQ ID NO: __), pAURHYG(ins)eGFP (SEQ ID NO: __) and pAURHYG(Δ)eGFP (SEQ ID NO: __).

[0104] FIG. 2. *Dual targeting protocol*. (A) Schematic diagram of the generalized strategy for dual targeting. (B) Sequences of the hygromycin-resistance gene and its mutation. (C) Schematic of the YAC containing the human β -globin locus and the β Thal1 and β Thal2 sequences that are changed by the corresponding oligonucleotides.

[0105] FIG. 3. *Dual targeting results*. (A) Efficiency of gene editing of hygromycin mutation using the dual targeting protocol. For these experiments, YAC-containing LSY678IntHyg(rep) β cells are grown in the presence of HU, electroporated with the selectable and nonselectable oligonucleotides, and allowed to recover in the presence of TSA. (B) Gene editing of the human β -globin gene directed by the β Thal1 oligonucleotide, including the sequence of the altered segment before (SEQ ID NO: __) and after (SEQ ID NO: __) the conversion.

[0106] FIG. 4. *Dual targeting and Rad51*. (A) Efficiency of gene editing of hygromycin mutation using the dual targeting protocol in combination with overexpression of yeast Rad51. For these experiments, YAC-containing LSY678IntHyg(rep) β cells are grown in the presence of HU, electroporated with the selectable and nonselectable oligonucleotides, and allowed to recover in the presence of TSA. (B) Gene editing of the human β -globin gene directed by the β Thal2 oligonucleotide, including the sequence of the altered segment before (SEQ ID NO: __) and after (SEQ ID NO: __) the conversion.

DETAILED DESCRIPTION

[0107] We have discovered, surprisingly, that the frequency of oligonucleotide-directed sequence alterations at a first nucleic acid target site is higher in a population of cells that has been selected for concurrent alteration at a second nucleic acid target site, as compared to a population of cells that has not been selected for concurrent alteration at a second nucleic acid target site.

[0108] Accordingly, in a first aspect the invention provides a method for identifying cells having a desired oligonucleotide-directed sequence alteration at a first nucleic acid target site within the cell. The method comprises identifying the desired sequence alteration in cells that have been selected for the presence of a selectable phenotype conferred upon the cell by a concurrent oligonucleotide-directed sequence alteration at a second nucleic acid target site within the cell.

[0109] In a second aspect, the invention provides a method for effecting a desired sequence alteration at a first nucleic acid target site within a cell, the method comprising concurrently targeting first and second nucleic acid sites within the cell for sequence alteration with respective first and

second sequence-altering oligonucleotides, the second alteration conferring a selectable phenotype upon the cell; selecting cells having the selectable phenotype; and then identifying among the selected cells those having the desired sequence alteration at the first nucleic acid target site.

[0110] The methods of the present invention increase the efficiency with which
5 bacteria, plant, fungi and animal cells having a desired genotypic change at the first target site may be identified. In related aspects, the invention provides compositions and kits for effecting or facilitating practice of the methods of the present invention.

[0111] Either or both of the first and second nucleic acid target sites within the cell may be in genomic double-stranded DNA.

[0112] The targeted genomic DNA can be normal, cellular chromosomal DNA;
10 organellar DNA, such as mitochondrial or plastid DNA; or extrachromosomal DNA present in cells in different forms including, e.g., mammalian artificial chromosomes (MACs), PACs from P-1 vectors, yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), plant artificial chromosomes (PLACs), BiBACS, as well as episomal DNA, including episomal DNA from an exogenous source such as
15 a plasmid or recombinant vector. Many of these artificial chromosome constructs containing human DNA can be obtained from a variety of sources, including, e.g., the Whitehead Institute, and are described, e.g., in Cohen et al., *Nature* 336: 698-701 (1993) and Chumakov, et al., *Nature* 377: 175-297 (1995).

[0113] The first targeted nucleic acid site may be in a part of the DNA that is transcriptionally silent or transcriptionally active; typically, the second targeted nucleic acid site will be in a
20 part of the DNA that is transcriptionally active so as to confer a selectable phenotype upon the cell. The first and second targeted sites may be in any part of a gene including, for example, an exon, an intron, a promoter, an enhancer or a 3'- or 5'- untranslated region, and may be in intergenic regions, with the second targeted site typically being in an exon so as to confer a selectable phenotype upon the cell.

[0114] In some embodiments, the first and/or second sequence-altering oligonucleotide
25 is designed to direct alteration of the transcribed strand of the target sequence; in other embodiments, the first and/or second oligonucleotide is designed to direct alteration of nucleic acid sequence targeting the non-transcribed strand of the target sequence. The targeted strand may differ as between first and second target sites.

[0115] The first and second oligonucleotides may independently be selected from any
30 type of sequence-altering oligonucleotide known in the art, including (i) triplex-forming oligonucleotides; (ii) chimeric RNA-DNA oligonucleotides that are internally duplexed, notably in the region containing the

nucleotide that directs the sequence alteration; and (iii) terminally modified single-stranded oligonucleotides having an internally unduplexed DNA domain and modified ends.

[0116] Sequence-altering triplexing oligonucleotides useful in the methods, compositions, and kits of the present invention are described, for example, in U.S. Pat. Nos. 6,303,376, 5,962,426, and 5,776,744, the disclosures of which are incorporated herein by reference in their entireties. Bifunctional oligonucleotides having a triplex-forming domain linked or tethered to a domain that effects targeted alteration, useful in the methods, compositions, and kits of the present invention, are described in Culver et al., *Nat. Biotechnology* 17: 989-93 (1999), the disclosure of which is incorporated herein by reference in its entirety.

[0117] Internally duplexed, hairpin- and double-hairpin-containing chimeric RNA-DNA oligonucleotides useful in the methods, compositions, and kits of the present invention are described, *inter alia*, in U.S. Pat. Nos. 6,573,046; 5,888,983; 5,871,984; 5,795,972; 5,780,296; 5,760,012; 5,756,325; 5,731,181, and 5,565,350, the disclosures of which are incorporated herein by reference in their entireties.

[0118] In preferred embodiments, at least one of the first and second oligonucleotides is a single-stranded oligonucleotide having modified ends and an internally unduplexed DNA domain that directs sequence alteration.

[0119] Such oligonucleotides are further described in copending international patent applications published as WO 03/027265; WO 02/10364; WO 01/92512; WO 01/87914; and WO 01/73002, as well as in U.S. Pat. Nos. 6,479,292 and 6,271,360, the disclosures of which are incorporated herein by reference in their entireties.

[0120] In typical embodiments, the oligonucleotide is 17 - 121 nucleotides in length and has an internally unduplexed domain (that is, a nonhairpin domain) of at least 8 contiguous deoxyribonucleotides. The oligonucleotide is fully complementary in sequence to the sequence of a first strand of the respective nucleic acid target, but for one or more mismatches as between the sequences of the oligonucleotide internally unduplexed deoxyribonucleotide domain and its complement on the target nucleic acid first strand. Each of the mismatches is positioned at least 8 nucleotides from each of the oligonucleotide's 5' and 3' termini. The oligonucleotide has at least one terminal modification.

[0121] In some embodiments, the at least one terminal modification may be selected from the group consisting of 2'-O-alkyl, such as 2'-O-methyl, residue; phosphorothioate internucleoside linkage; and locked nucleic acid (LNA) residue. The basic structural and functional characteristics of LNAs and related analogues are disclosed in various publications and patents, including WO 99/14226, WO 00/56748, WO 00/66604, WO 98/39352, United States Patent No. 6,043,060, and United States

Patent No. 6,268,490, the disclosures of which are incorporated herein by reference in their entireties. In some embodiments, the terminal modification comprises a plurality of adjacent phosphorothioate internucleoside linkages, such as three phosphorothioate linkages at the 3' terminus of the oligonucleotide.

5 **[0122]** In certain preferred embodiments, both of the first and second sequence-altering oligonucleotides are single-stranded oligonucleotides having modified ends and an internally unduplexed DNA domain that directs sequence alteration.

[0123] In some embodiments, a plurality of single-stranded oligonucleotides having modified ends and an internally unduplexed DNA domain that directs sequence alteration can be used to effect either or both of the first and second sequence alterations. Use of such plural oligonucleotides is described in copending U.S. patent application no. 10/623,107, filed July 18, 2003 ("Targeted Nucleic Acid Sequence Alteration Using Plural Oligonucleotides"), the disclosure of which is incorporated herein by reference in its entirety.

10 **[0124]** In the methods, compositions, and kits of the present invention, at least the second oligonucleotide directs a sequence alteration that produces a selectable phenotype. Although the first oligonucleotide may also direct an alteration that produces a selectable phenotype, generally the first oligonucleotide directs an alteration that must be identified by screening, *e.g.*, by determining the corresponding nucleic acid sequence or by assaying a non-selectable phenotype that is generated by the alteration event.

15 **[0125]** The selectable phenotype chosen will depend on the host cell chosen and whether the selection is effected *in vitro* or *in vivo*. As is well known in the art, exemplary selectable phenotypes include, *e.g.*, antibiotic or other chemical resistance, ability to use a nutrient source, expression of a fluorescent protein, presence of an epitope or resistance to an apoptotic signal. The selectable phenotype chosen may be selectable based on preferential growth of a cell with the desired sequence alteration. Examples of such selectable phenotypes include, *e.g.*, the ability to grow in the presence of a compound that either kills or prevents the growth of the cell such as an apoptotic signal or an antibiotic, the ability to grow in the absence of a nutrient that is required prior to the sequence alteration, or the ability to utilize a particular resource that is not usable prior to the sequence alteration. The selectable phenotype may also be selected mechanically. Examples of phenotypes that may be selected mechanically include, *e.g.*, expression of a fluorescent protein or a particular epitope. Mechanical selection may be by any means known to one of skill in the art including, *e.g.*, FACS (directly in the case of a fluorescent protein or using a labeled antibody for an epitope), column chromatography,

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or using paramagnetic beads produced by, e.g., Miltenyi Biotec. Selection also does not require intact cells. For example, a single nucleotide change (SNP) in a nucleic acid molecule may be detected and isolated *in vitro* using methods such as are described in WO 03/027640. In such cases, the first oligonucleotide effects a change in the selected molecule.

5 **[0126]** The methods, compositions and kits of the invention typically reduce the number of cells required to be screened by at least about two-fold relative to the number that must be screened in a population of targeted cells that has not previously been selected for an oligonucleotide-directed nucleic acid sequence alteration that confers a selectable phenotype. The reduction can be by at least about two, three, four, five, six, seven, eight, nine, ten, twelve, fifteen, twenty, thirty, and fifty or more fold.

10 **[0127]** The methods, compositions and kits of the invention may be used with any oligonucleotide that directs targeted alteration of nucleic acid sequence. In the examples and in Tables 5 to 42 herein, correcting oligonucleotides of defined sequence are provided for alteration of human genes, including correction of genes mutated in human diseases, and for directing specific alterations in plant genes. Each of these oligonucleotides may be a first sequence-altering oligonucleotide as defined herein.

15 Certain of these oligonucleotides may also be a second sequence-altering oligonucleotide as defined herein, e.g., where the oligonucleotide effects a nucleic acid sequence alteration that confers a selectable phenotype such as herbicide resistance. In the tables of these examples, the oligonucleotides are not limited to the particular sequences disclosed. The oligonucleotides include extensions of the appropriate sequence of the longer 121 base oligonucleotides which can be added base by base to the smallest disclosed oligonucleotides of 17 bases. Some oligonucleotides may be 15 or 16 bases which can be obtained by subtraction or one or two bases from the smallest disclosed oligonucleotides of 17 bases.

20 Thus the representative oligonucleotides include for each correcting change, oligonucleotides of length 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, or 120 with further single-nucleotide additions up to the longest sequence disclosed. These

25 oligonucleotide sequences can be used to design first oligonucleotides, or, where the oligonucleotide directs an alteration that confers a selectable phenotype, first and/or second oligonucleotides. Moreover, 30 the oligonucleotides of the invention do not require a symmetrical extension on either side of the central DNA domain. Similarly, the oligonucleotides designed using the sequences of oligonucleotides disclosed in the various tables for correction of human diseases or for directing specific alterations in plant genes

comprise structures or modifications that enable them to effect oligonucleotide-directed nucleic acid sequence alteration, such as, e.g., phosphorothioate linkages, LNA residues or chimeric RNA-DNA internally duplexed structure.

[0128] Efficiency of conversion is defined herein as the percentage of recovered
5 substrate target molecules that have undergone a conversion event. Depending on the nature of the target genetic material, e.g. an extrachromosomal element in a cell, efficiency could be represented as the proportion of cells or clones containing an extrachromosomal element that exhibit a particular phenotype. Alternatively, representative samples of the target genetic material can be analyzed, e.g. by sequencing, allele-specific PCR or comparable techniques, to determine the percentage that have acquired the
10 desired change. This latter method of determining efficiency is most frequently applied where the phenotype conferred by the alteration is a non-selectable phenotype.

[0129] Each of the first and second oligonucleotides can direct any kind of alteration, including, for example, deletion, insertion or replacement of 1, 2 or 3 nucleotides in the target sequence. These altered nucleotides may be contiguous or non-contiguous to each other. Multiple alterations can
15 be directed to each of the first and second target sites by a single oligonucleotide or by 1, 2 or 3 separate oligonucleotides. In some embodiments, the multiple alterations are directed by a single oligonucleotide. In some embodiments, the multiple alterations are within 1 to 10 nucleotides of each other.

[0130] The methods, compositions and kits of the invention can be combined with one or more other methods of enhancing the efficiency of oligonucleotide-directed alteration of nucleic acid
20 sequence known in the art.

[0131] Such methods are described, e.g., in copending International patent applications published as WO 02/10364 ("Methods for Enhancing Targeted Gene Alteration Using Oligonucleotides,"); WO 03/027265 ("Composition and Methods for Enhancing Oligonucleotide-Directed Sequence
25 Alteration"); and WO 03/075856 ("Methods, Compositions, and Kits for Enhancing Oligonucleotide-Mediated Nucleic Acid Sequence Alteration Using Compositions Comprising a Histone Deacetylase Inhibitor, Lambda Phage Beta Protein, or Hydroxyurea"), the disclosures of which are incorporated herein by reference in their entireties.

[0132] For example, in typical embodiments of this aspect of the invention, the methods
30 comprise treating a cell or tissue from a bacterium, a fungus, a plant, or an animal with a histone deacetylase (HDAC) inhibitor or hydroxyurea (HU), and then administering to the treated cell or tissue at least first and second oligonucleotides having nucleic acid sequence alteration activity. In other

embodiments, the HDAC inhibitor or hydroxyurea, respectively, may be added contemporaneously with oligonucleotide addition or even following oligonucleotide addition.

[0133] The HDAC inhibitor can be trichostatin A.

[0134] One of skill in the art will appreciate, however, that other HDAC inhibitors may be suitable for these purposes. For example, U.S. Patent Application Publication No. 2002/0143052, which is hereby incorporated by reference in its entirety, discloses compounds having HDAC inhibitor activity due to the presence of a zinc-binding moiety. Other examples of HDAC inhibitors suitable for purposes of the invention include butyric acid, MS-27-275, suberoylanilide hydroxamic acid (SAHA), oxamflatin, trapoxin A, depudecin, FR901228 (also known as depsipeptide), apicidin, *m*-carboxy-cinnamic acid bishydroxamic acid (CBHA), suberic bishydroxamic acid (SBHA), and pyroxamide. See Marks *et al.*, *J. Natl. Canc. Inst.* 92(15):1210-1216 (2000), which is hereby incorporated by reference in its entirety. Yet other examples of suitable HDAC inhibitors are chlamydocin, HC-toxin, Cyl-2, WF-3161, and radicicol, as disclosed in WO 00/23567, which is hereby incorporated by reference in its entirety.

[0135] When administering an HDAC inhibitor or HU to cells or cell extracts, the dosage to be administered and the timing of administration will depend on various factors, including cell type.

[0136] In the case of TSA, the dosage may be 10 nM, 100 nM, 1 μ M, 10 μ M, 100 μ M, 1 mM, 10 mM, or even higher, or as little as 1 nM, 100 μ M, 10 μ M, 1 μ M, 100 nM, 10 nM, 1 nM, or even lower. In the case of HU, the dosage may be 100 nM, 1 μ M, 10 μ M, 100 μ M, 1 mM, 10 mM, 100 mM, 1 M or even higher, or as little as 100 mM, 10 mM, 1 mM, 100 μ M, 10 μ M, 1 μ M, 100 nM, 10 nM, or even lower.

[0137] In the case of HU, treatment may be with 100 mM, 75 mM, 50 mM, 40 mM, 20 mM, 10 mM, 2 mM, 1 mM, 100 microM, 10 microM, 1 microM, 100 nM, 10 nM or lower. The dosage is preferably from about 4 to 100 mM for yeast cells and from about 0.05 mM to 3 mM for mammalian cells. The dosage may be at least 0.05 mM, 0.10 mM, 0.15 mM, 0.20 mM, 0.25 mM, 0.30 mM, 0.35 mM, 0.40 mM, 0.50 mM or more, including at least 0.55 mM, 0.60 mM, 0.65 mM, 0.70 mM, 0.75 mM, 0.80 mM, 0.85 mM, 0.90 mM, 0.95 mM or even 1 mM, 1.1 mM, 1.2 mM, 1.3 mM, 1.4 mM, 1.4 mM, 1.5 mM, 1.6 mM, 1.7 mM, 1.8 mM, 1.9 mM, 2.0 mM, 2.5 mM, 3 mM, or more. Typically, the dosage for mammalian cells is less than about 3.0 mM, and can be less than 2.5 mM, 2.0 mM, 1.5 mM, 1.0 mM, even less than 0.90, 0.85, 0.80, 0.75, 0.70, 0.65, 0.60, 0.55, 0.50, 0.45, 0.40, and even less than about 0.35 or 0.30 mM.

[0138] Cells may be grown in the presence of an HDAC inhibitor or HU, and cell extracts may be treated with the HDAC inhibitor or HU, for various times prior to combination with a sequence-altering oligonucleotide. Growth or treatment may be as long as 1 h, 2 h, 3 h, 4 h, 6 h, 8 h, 12

h, 20 h, or even longer, including up to 28 days, 14 days, 7 days, or shorter, or as short as 12 h, 8 h, 6 h, 4 h, 3 h, 2 h, 1 h, or even shorter. Alternatively, treatment of cells or cell extracts with HDAC inhibitor or HU and the sequence-altering oligonucleotide may occur simultaneously, or the HDAC inhibitor or HU, respectively, may be added after oligonucleotide addition.

5 **[0139]** Cells may further be allowed to recover from treatment with an HDAC inhibitor or HU by growth in the absence of the HDAC inhibitor or HU for various times prior to treatment with a sequence-altering oligonucleotide. Recovery may be as long as 10 min, 20 min, 40 min, 60 min, 90 min, 2 h, 4 h, or even longer, or as short as 90 min, 60 min, 40 min, 20 min, 10 min, or even shorter. Cells may also be allowed to recover following their treatment with a sequence-altering oligonucleotide. This
10 recovery period may be as long as 1 h, 2 h, 4 h, 6 h, 8 h, 12 h, or even longer, or as short as 8 h, 6 h, 4 h, 2 h, 1 h, or even shorter. The HDAC inhibitor or HU may either be present in or absent from the cell medium during the recovery period.

[0140] Optimum dosages and the timing and duration of administration of HDAC inhibitors and HU to cells or cell extracts can be determined by routine experimentation. For example,
15 optimized dosage and timing of treatment with an HDAC inhibitor, such as TSA, can be determined using the assay system described in WO 03/075856.

[0141] Cultured cells (such as yeast cells) are treated with varying concentrations of HDAC inhibitor for a varying number of hours prior to electroporation with the sequence altering oligonucleotide. After recovery for varying periods, the cells are plated and tested for efficiency of
20 sequence alteration. Parameters are then selected that provide the highest efficiency of correction. The method may then be repeated, as necessary, further to optimize dosage, duration of pretreatment, duration of recovery period, if any, and the like.

[0142] A similar approach for HU can be determined using the assay system set forth in WO 03/075856.

25 **[0143]** The methods, compositions, and kits of the instant invention comprising either an HDAC inhibitor, such as trichostatin A, or HU typically increase nucleic acid sequence alteration efficiency by at least two fold relative to the same method respectively lacking the HDAC inhibitor or HU. The increase in nucleic acid sequence alteration efficiency can also be about three, four, five, six, seven, eight, nine, ten, twelve, fifteen, twenty, thirty, and fifty or more fold. The methods, compositions, and kits
30 of the instant invention comprising beta protein increase the efficiency of altering a DNA sequence, as compared to the same method lacking beta protein, typically at least 2 fold, and can increase the efficiency 5 fold, 10 fold, 15 fold, 20 fold, 25 fold, 30 fold, 40 fold, 50 fold, 60 fold, 70 fold, 80 fold, 90 fold,

100 fold, 250 fold, 500 fold, 1000 fold, or more; in certain embodiments, the methods, compositions, and kits of the instant invention that comprise beta protein increase efficiency less than two-fold as compared to comparable methods lacking beta protein, such as 1.9 fold, 1.5 fold, or even by 10%, 20%, 30%, 40%.

[0144] The cells in which targeted nucleic acid sequence alterations may usefully be made according to the methods of the present invention include mammalian cells, including human cells, such as liver, lung, colon, cervix, kidney, and epithelium cells.

[0145] Cultured mammalian cells that usefully may be targeted for desired sequence alteration according to the methods of the present invention include HT1080 cells (human epithelial fibrosarcoma), COS-1 and COS-7 cells (African green monkey), CHO-K1 cells (Chinese hamster ovary), H1299 cells (human epithelial carcinoma, non-small cell lung cancer), C127I (immortal murine mammary epithelial cells), MEF (mouse embryonic fibroblasts), HEC-1-A (human uterine carcinoma), HCT15 (human colon cancer), HCT116 (human colon carcinoma), LoVo (human colon adenocarcinoma), and HeLa (human cervical carcinoma) cancer cells as well as PC12 cells (rat pheochromocytoma).

[0146] Alterations in cultured mammalian cells may usefully be made to create coisogenic cell collections, as described in copending international patent application published as WO 03/027264 and U.S. patent application no. 10/260,638, the disclosures of which are incorporated herein by reference in their entireties. Genes usefully targeted in such coisogenic collections include loci affecting drug resistance (equivalently, drug sensitivity) or drug metabolism, including: CYP1A2, CYP2C17, CYP2D6, CYP2E, CYP3A4, CYP4A11, CYP1B1, CYP1A1, CYP2A6, CYP2A13, CYP2B6, CYP2C8, CYP2C9, CYP11A, CYP2C19, CYP2F1, CYP2J2, CYP3A5, CYP3A7, CYP4B1, CYP4F2, CYP4F3, CYP6D1, CYP6F1, CYP7A1, CYP8, CYP11A, CYP11B1, CYP11B2, CYP17, CYP19, CYP21A2, CYP24, CYP27A1, CYP51, ABCB1, ABCB4, ABCC1, ABCC2, ABCC3, ABCC4, ABCC5, ABCC6, MRP7, ABCC8, ABCC9, ABCC10, ABCC11, ABCC12, EPHX1, EPHX2, LTA4H, TRAG3, GUSB, TMPT, BCRP, HERG, hKCNE2, UDP glucuronosyl transferase (UGT), sulfotransferase, sulfatase, glutathione S-transferase (GST) -alpha, glutathione S-transferase -mu, glutathione S-transferase -pi, ACE, and KCHN2.

[0147] In other embodiments, cells within which targeted alterations may usefully be effected according to the methods of the present invention include progenitor and stem cells — both embryonic (ES) stem cells and non-ES cells such as hematopoietic progenitor or stem cells, including CD34⁺CD38⁻ hematopoietic progenitor and stem cells and muscle-derived stem cells.

[0148] ES cells can be mammalian ES cells, either non-human mammalian ES cells or human ES cells; human ES cells may, e.g., be from a cell line approved for use in the jurisdiction in which

the methods, compositions and kits of the present invention are to be used. For example, for use in the United States, any human stem cell line that does not violate state or federal law may be used, such as those cell lines that meet United States federal funding criteria; the National Institutes of Health is currently compiling a list of these existing stem cell lines (<http://escr.nih.gov>) which includes those held by the following: BresaGen, Inc., Athens, Georgia (4 lines); CyThera, Inc., San Diego, California (9 lines); Karolinska Institute, Stockholm, Sweden (5 lines); Monash University, Melbourne, Australia (6 lines); National Center for Biological Sciences, Bangalore, India (3 lines); Reliance Life Sciences, Mumbai, India (7 lines); Technion-Israel Institute of Technology, Haifa, Israel (4 lines); University of California, San Francisco, California (2 lines); Göteborg University, Göteborg, Sweden (19 lines); Wisconsin Alumni Research Foundation, Madison, Wisconsin (5 lines).

[0149] In yet other embodiments, the cells within which targeted alterations are made are plant cells.

[0150] Particularly useful plants from which the cells to be used may be drawn include, for example, experimental model plants such as *Chlamydomonas reinhardtii*, *Physcomitrella patens*, and *Arabidopsis thaliana* in addition to crop plants such as cauliflower (*Brassica oleracea*), artichoke (*Cynara scolymus*), fruits such as apples (*Malus*, e.g. *domesticus*), mangoes (*Mangifera*, e.g. *indica*), banana (*Musa*, e.g. *acuminata*), berries (such as currant, *Ribes*, e.g. *rubrum*), kiwifruit (*Actinidia*, e.g. *chinensis*), grapes (*Vitis*, e.g. *vinifera*), bell peppers (*Capsicum*, e.g. *annuum*), cherries (such as the sweet cherry, *Prunus*, e.g. *avium*), cucumber (*Cucumis*, e.g. *sativus*), melons (*Cucumis*, e.g. *melo*), nuts (such as walnut, *Juglans*, e.g. *regia*; peanut, *Arachis hypogaeae*), orange (*Citrus*, e.g. *maxima*), peach (*Prunus*, e.g. *persica*), pear (*Pyrus*, e.g. *communis*), plum (*Prunus*, e.g. *domestica*), strawberry (*Fragaria*, e.g. *moschata* or *vesca*), tomato (*Lycopersicon*, e.g. *esculentum*); leaves and forage, such as alfalfa (*Medicago*, e.g. *sativa* or *truncatula*), cabbage (e.g. *Brassica oleracea*), endive (*Cichorium*, e.g. *endivia*), leek (*Allium*, e.g. *porrum*), lettuce (*Lactuca*, e.g. *sativa*), spinach (*Spinacia*, e.g. *oleraceae*), tobacco (*Nicotiana*, e.g. *tabacum*); roots, such as arrowroot (*Maranta*, e.g. *arundinacea*), beet (*Beta*, e.g. *vulgaris*), carrot (*Daucus*, e.g. *carota*), cassava (*Manihot*, e.g. *esculenta*), turnip (*Brassica*, e.g. *rapa*), radish (*Raphanus*, e.g. *sativus*), yam (*Dioscorea*, e.g. *esculenta*), sweet potato (*Ipomoea batatas*); seeds, including oilseeds, such as beans (*Phaseolus*, e.g. *vulgaris*), pea (*Pisum*, e.g. *sativum*), soybean (*Glycine*, e.g. *max*), cowpea (*Vigna unguiculata*), mothbean (*Vigna aconitifolia*), wheat (*Triticum*, e.g. *aestivum*), sorghum (*Sorghum* e.g. *bicolor*), barley (*Hordeum*, e.g. *vulgare*), corn (*Zea*, e.g. *mays*), rice (*Oryza*, e.g. *sativa*), rapeseed (*Brassica napus*), millet (*Panicum* sp.), sunflower (*Helianthus annuus*), oats (*Avena sativa*), chickpea (*Cicer*, e.g. *arietinum*); tubers, such as kohlrabi (*Brassica*, e.g. *oleraceae*), potato (*Solanum*, e.g.

tuberosum) and the like; fiber and wood plants, such as flax (*Linum* e.g. *usitatissimum*), cotton (*Gossypium* e.g. *hirsutum*), pine (*Pinus* sp.), oak (*Quercus* sp.), eucalyptus (*Eucalyptus* sp.), and the like and ornamental plants such as turfgrass (*Lolium*, e.g. *rigidum*), petunia (*Petunia*, e.g. *x hybrida*), hyacinth (*Hyacinthus orientalis*), carnation (*Dianthus* e.g. *caryophyllus*), delphinium (*Delphinium*, e.g. *ajacis*), Job's tears (*Coix lacryma-jobi*), snapdragon (*Antirrhinum majus*), poppy (*Papaver*, e.g. *nudicaule*), lilac (*Syringa*, e.g. *vulgaris*), hydrangea (*Hydrangea* e.g. *macrophylla*), roses (including Gallicas, Albas, Damasks, Damask Perpetuals, Centifolias, Chinas, Teas and Hybrid Teas) and ornamental goldenrods (e.g. *Solidago* spp.).

[0151] Generally, the oligonucleotides are administered to isolated plant cells or protoplasts according to a method of the present invention and the resulting cells are used to regenerate whole plants according to any method known in the art.

[0152] Relatively few specific plant mutations that produce desirable phenotypes have been described for plant species or cultivars.

[0153] However, the methods, compositions and kits of the instant invention may be used to identify a desirable mutation in one species, for example an experimental model plant, and the desirable mutation can then be introduced in the homologous genes of other species using the kits, compositions and methods of the invention. Further, the methods, compositions and kits of the invention can be used to produce "knock out" mutations by modification of specific amino acid codons to produce stop codons (e.g., a CAA codon specifying glutamine can be modified at a specific site to TAA; a AAG codon specifying lysine can be modified to TAG at a specific site; and a CGA codon for arginine can be modified to a TGA codon at a specific site). Such base pair changes will terminate the reading frame and produce a truncated protein shortened at the site of the stop codon, which truncated protein may be defective or have an altered function. Alternatively, frameshift additions or deletions can be directed at a specific sequence to interrupt the reading frame and produce a garbled downstream protein. Such stop or frameshift mutations can be introduced to determine the effect of knocking out the protein in either plant or animal cells.

[0154] Desirable phenotypes that may be obtained in plants by known nucleic acid sequence alterations include, for example, herbicide resistance; male- or female-sterility; salt, drought, lead, freezing and other stress tolerances; altered amino acid content; altered levels or composition of starch; altered levels or composition of oils; and elimination of epitopes in gluten that are known to instigate autoimmune responses in individuals with celiac disease.

[0155] The cells within which targeted alterations are effected according to the methods of the present invention can be primary isolated cells, selectively enriched cells, cultured cells, or tissue explants.

[0156] In certain *ex vivo* embodiments of the methods of the present invention, in which
5 targeted sequence alterations are made in non-human cells, such as non-human mammalian ES cells or plant cells, the sequence-altered cells can be used to generate intact organisms, which can thereafter be propagated.

[0157] For example, the methods of the present invention can be used to create
10 genetically altered animals, including livestock — such as cattle, bison, horses, goats, sheep, pigs, chickens, geese, ducks, turkeys, pheasant, ostrich and pigeon — to enhance expression of desirable traits, and/or decrease expression of undesirable traits, by first creating genetically altered cells. In other embodiments, the methods of the present invention can be used to create genetically altered animals useful as laboratory models, such as rodents, including mice, rats, guinea pigs; lagomorphs, such as rabbits; monkeys; apes; dogs; and cats. Methods for producing transgenic animals comprising genetically
15 modified cells are known in the art, and are disclosed, for example, in WO 00/51424, "Genetic Modification of Somatic Cells and Uses Thereof," the disclosure of which is hereby incorporated herein by reference in its entirety.

[0158] Further aspects of the present invention are the non-human animals produced
thereby.

[0159] In other *ex vivo* embodiments of the methods of the present invention, the
20 targeted sequence alterations are made in human ES cells, which are thereafter used, where legally permissible, to generate tissue or, where permitted, a viable embryo.

[0160] In other *ex vivo* embodiments of the methods of the present invention, in which
25 targeted sequence alterations are made in human non-ES cells, such as hematopoietic progenitor or stem cells, such as CD34⁺CD38⁻ hematopoietic stem cells, the sequence-altered cells can be reintroduced into a human subject for *ex vivo* gene therapies.

[0161] In certain particularly useful embodiments of the methods of the present
invention, the first and second oligonucleotides are designed to alter the nucleic acid sequence of an expressed human gene or a plant gene.

[0162] The oligonucleotides used in the methods, compositions and kits of the invention
30 can be introduced into cells or tissues by any technique known to one of skill in the art. Such techniques include, for example: electroporation; carrier-mediated delivery using, e.g., liposomes, aqueous-cored

lipid vesicles, lipid nanospheres or polycations; naked nucleic acid insertion; particle bombardment and calcium phosphate precipitation. In some embodiments, the oligonucleotides are introduced using electroporation, for example using a BTX ECM® 830 Square Wave electroporator. In other embodiments the transfection is performed with a liposomal transfer compound, for example, DOTAP (N-1-(2,3-
5 Dioleoyloxy)propyl-N,N,N-trimethylammonium methylsulfate, Boehringer-Mannheim) or an equivalent, such as LIPOFECTIN®. In other embodiments, the transfection technique uses cationic lipids. In some embodiments, transfection is performed with Lipofectamine™ 2000 (Invitrogen Corporation, Carlsbad, CA).

[0163] The methods of the invention can be used with a wide range of concentrations
10 of oligonucleotides. For example, good results can be achieved with 10 nM/10⁵ cells. A ratio of about 500 ng of oligonucleotide in 3 µg of DOTAP per 10⁵ cells can be used. The transfected cells may be cultured in different media, including, for example, in serum-free media, media supplemented with fetal calf serum, human serum albumin, or human serum. The first and second oligonucleotides are typically used in a 1:1 stoichiometric ratio, but other ratios including, e.g., 1:2, 1:3, 1:4 and 1:5, may be used in the methods,
15 composition and kits of the invention. In some embodiments, the first and second oligonucleotides used in the methods and compositions of the invention are administered simultaneously; in other embodiments the oligonucleotides are adjunctively administered.

[0164] Further embodiments of the invention are compositions and kits comprising a cell, cell-free extract, or cellular repair protein and at least one oligonucleotide which is capable of
20 effecting a desired sequence alteration at a nucleic acid target site, which sequence alteration confers a selectable phenotype. In some embodiments, the compositions and kits also comprise a second oligonucleotide that is capable of effecting a desired sequence alteration, typically a sequence alteration that is frequently desired and/or is not selectable. In some embodiments the compositions or kits comprise a nucleic acid molecule comprising a nucleic acid sequence which is the target for the at least
25 one oligonucleotide which capable of effecting a desired sequence alteration at a nucleic acid target site, which sequence alteration confers a selectable phenotype.

[0165] A cell, cell-free extract, or cellular repair protein for a composition or kit of the invention may be derived from any organism. Compositions and kits of the invention and may comprise any combination of cells, cell-free extracts, or cellular repairs proteins and the cells, cell-free extracts, or
30 cellular repair proteins may be from the same organism or from different organisms. Cellular repair proteins that may be used include, for example, proteins from the RAD52 epistasis group, the mismatch repair group, or the nucleotide excision repair group. In some embodiments, the cell, cell-free extract, or

cellular repair protein is or is from a eukaryotic cell or tissue. In some embodiments, the eukaryotic cell is a fungal cell, e.g. a yeast cell. In other embodiments, the cell is a plant cell, e.g., a maize, rice, wheat, barley, soybean, cotton, potato or tomato cell. Other exemplary plant cells include those described elsewhere herein. In some embodiments, the kits comprise a chemical compound selected from the group consisting of: a trichostatin, a histone deacetylase inhibitor and the lambda beta protein. In some
5 embodiments such kits also include instructions for use.

[0166] Other embodiments of the invention relate to kits comprising a nucleic acid molecule the nucleic acid sequence of which has been altered according to a method of the invention or using a composition or kit of the invention. In some embodiments, the invention relates to kits comprising
10 a cell comprising a nucleic acid molecule the nucleic acid sequence of which has been altered according to the methods of the invention or using a composition or kit of the invention. In some embodiments, the nucleic acid molecule is selected from the group consisting of: mammalian artificial chromosomes (MACs), PACs from P-1 vectors, yeast artificial chromosomes (YACs), bacterial artificial chromosomes (BACs), plant artificial chromosomes (PLACs), plasmids, viruses or other recombinant vectors.

[0167] The purified oligonucleotides compositions may be formulated in accordance with routine procedures as a pharmaceutical composition adapted for bathing cells in culture, for microinjection into cells in culture, and for intravenous administration to human beings or animals. Typically, compositions for cellular administration or for intravenous administration into animals, including humans, are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also
20 include a solubilizing agent and a local anaesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients will be supplied either separately or mixed together in unit dosage form, for example, as a dry, lyophilized powder or water-free concentrate. The composition may be stored in a hermetically sealed container such as an ampule or sachette indicating the quantity of active agent in activity units. Where the composition is administered by infusion, it can be dispensed with an infusion
25 bottle containing sterile pharmaceutical grade "water for injection" or saline. Where the composition is to be administered by injection, an ampule of sterile water for injection or saline may be provided so that the ingredients may be mixed prior to administration.

[0168] Pharmaceutical compositions of this invention comprise the oligonucleotides used in the methods of the present invention and pharmaceutically acceptable salts thereof, with any
30 pharmaceutically acceptable ingredient, excipient, carrier, adjuvant or vehicle.

[0169] The oligonucleotides of the invention are preferably administered to the subject in the form of an injectable composition. The composition is preferably administered parenterally,

meaning intravenously, intraarterially, intrathecally, interstitially or intracavitarily. Pharmaceutical compositions of this invention can be administered to mammals including humans in a manner similar to other diagnostic or therapeutic agents. The dosage to be administered, and the mode of administration will depend on a variety of factors including age, weight, sex, condition of the subject and genetic factors, and will ultimately be decided by medical personnel subsequent to experimental determinations of varying dosage as described herein. In general, dosage required for targeted nucleic acid sequence alteration and therapeutic efficacy will range from about 0.001 to 50,000 µg/kg, e.g. between 1 to 250 µg/kg of host cell or body mass or a concentration of between 30 and 60 micromolar.

[0170] For cell administration, direct injection into the nucleus, biolistic bombardment, electroporation, liposome transfer and calcium phosphate precipitation may be used. In yeast, lithium acetate or spheroplast transformation may also be used. In one method, the administration is performed with a liposomal transfer compound, e.g., DOTAP (Boehringer-Mannheim), Lipofectamine™ 2000 (Invitrogen™) or an equivalent such as lipofectin. The amount of the oligonucleotide pair used, for example, is about 500 nanograms in 3 micrograms of DOTAP per 100,000 cells or about 1 microgram with 1 microliter Lipofectamine™ 2000 per 1,000,000 cells. For electroporation, between 20 nanograms and 30 micrograms of oligonucleotide per million cells to be electroporated is an appropriate range of dosages which can be increased to improve efficiency of genetic alteration upon review of the appropriate sequence according to the methods described herein.

[0171] In order that this invention may be better understood, the following examples are set forth. These examples are for purposes of illustration only, and are not to be construed as limiting the scope of the invention in any manner.

EXAMPLE 1

Yeast Cell Targeting Assay Method for Nucleic Acid Sequence Alteration and Preferred Oligonucleotide Selection

[0172] In this example, we use single-stranded oligonucleotides to measure oligonucleotide-directed nucleic acid sequence alteration using a Mata wild-type yeast strain with an integrated plasmid with a fusion between a hygromycin resistance gene and eGFP as a target for gene repair (Mata+IntHYG(x)eGFP). Modifications to the oligonucleotides and construction of target vectors are disclosed in WO 01/73002, the disclosure of which is hereby incorporated by reference.

[0173] *In vivo* assay systems. We monitor targeted alteration of genetic material in yeast using both episomal and chromosomal targets. To monitor gene alteration of episomal targets, we

employ a yeast system using the plasmids pAURHYG(rep)eGFP, which contains a point mutation in the hygromycin resistance gene, pAURHYG(ins)eGFP, which contains a single-base insertion in the hygromycin resistance gene and pAURHYG(Δ)eGFP which has a single base deletion (shown in Figure 1). We also use the same plasmid containing a functional copy of the hygromycin-eGFP fusion gene, designated pAURHYG(wt)eGFP, as a control. These plasmids are collectively designated pAURHYG(x)eGFP. These plasmids also contain an aureobasidinA resistance gene. In pAURHYG(rep)eGFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when a G at position 137, in codon 46 of the hygromycin B coding sequence, is converted to a C thus removing a premature stop codon in the hygromycin resistance gene coding region. In pAURHYG(ins)eGFP, hygromycin resistance gene function and green fluorescence from the eGFP protein are restored when an A inserted between nucleotide positions 136 and 137, in codon 46 of the hygromycin B coding sequence, is deleted and a C is substituted for the T at position 137, thus correcting a frameshift mutation and restoring the reading frame of the hygromycin-eGFP fusion gene. In pAURHYG(Δ)eGFP, hygromycin resistance gene function and green fluorescence from eGFP are restored when a C is inserted at the site of the single nucleotide deletion.

[0174] We synthesize the set of three yeast expression constructs pAURHYG(rep)eGFP, pAURHYG(Δ)eGFP, pAURHYG(ins)eGFP, that contain a point mutation at nucleotide 137 of the hygromycin-B coding sequence as follows: (rep) indicates a T137G replacement, (Δ) represents a deletion of G137 and (ins) represents an A insertion between nucleotides 136 and 137. We construct this set of plasmids by excising the respective expression cassettes by restriction digest from pHyg(x)eGFP and ligation into pAUR123 (Panvera, CA). We digest 10 μ g pAUR123 vector DNA as well as 10 μ g of each pHyg(x)eGFP construct with KpnI and Sall (NEB). We gel purify each of the DNA fragments and prepare them for enzymatic ligation. We ligate each mutated insert into pAUR123 vector at a 3:1 molar ratio using T4 DNA ligase (Roche). We screen clones by restriction digest, confirm by Sanger dideoxy chain termination sequencing and purify plasmid DNA using a Qiagen maxiprep kit.

[0175] To monitor oligonucleotide-directed alteration of chromosomal nucleic acid sequence targets, we typically employ a yeast system in which we monitor chromosomal genes or we use integrational plasmids such as those designated pAUR101-HYG(x)eGFP. These plasmids do not replicate in yeast. These plasmids comprise the HYG(x)eGFP fusion proteins used in the pAURHYG(x)eGFP episomal plasmid system (shown in Figure 1) and an aureobasidinA resistance gene. Therefore, like pAURHYG(x)eGFP, these constructs can also be used to monitor all types of gene alterations, i.e. replacements, insertions and deletions. We designate yeast strains into which the

pAUR101-HYG(x)eGFP plasmid integrates as "+IntHYG(x)eGFP." In addition to this construct, we monitor gene alteration of specific yeast genes including, for example, CYC1.

[0176] *Oligonucleotide synthesis and cells.* We synthesize and purify the chimeric, RNA-DNA oligonucleotides with internally duplexed conformation and single-stranded oligonucleotides (including those with the indicated modifications) using available phosphoramidites on controlled pore glass supports. After deprotection and detachment from the solid support, the oligonucleotides are gel-purified using, for example, procedures such as those described in Gamper et al., *Biochem.* 39, 5808-5816 (2000), or the oligonucleotides are ion-exchange HPLC-purified. We determine the concentration of the oligonucleotides spectrophotometrically (33 or 40 µg/ml per A₂₆₀ unit of single-stranded or hairpin oligonucleotide, respectively). We introduce the oligonucleotides into yeast cells by electroporation as follows: we prepare electrocompetent yeast cells by inoculating 10 ml of YPD media supplemented with 250 µg/ml aureobasidin from a single colony and grow the cultures overnight with shaking at 300 rpm at 30°C. We pellet the cells from the overnight culture by centrifuging at 3000 rpm for 5 minutes, resuspend the cells in 40 ml YPD media (OD₆₀₀ approximately 0.2). We incubate the cells with shaking at 30°C until the OD₆₀₀ is between 0.5 and 1.0 (3-5 hours). We wash the cells by centrifuging at 4°C at 3000 rpm for 5 minutes and twice resuspending the cells in 25 ml ice-cold distilled water. We centrifuge at 4°C at 3000 rpm for 5 minutes and resuspend in 1 ml ice-cold 1M sorbitol and then finally centrifuge the cells at 4°C at 5000 rpm for 5 minutes and resuspend the cells in 120 µl 1M sorbitol. To transform electrocompetent cells with plasmids or oligonucleotides, we mix 40 µl of cells with oligonucleotide (typically 5 µg or amounts as indicated) and incubate on ice for 5 minutes. We transfer the mixture to a 0.2 cm electroporation cuvette and electroporate with a BIO-RAD Gene Pulser apparatus at 1.5 kV, 25 µF, 200 Ω for one five-second pulse. We then immediately resuspend the cells in 3 ml YPD media supplemented with 2M sorbitol and incubate the cultures at 30°C with shaking at 300 rpm for 6 hours. We spread 200 µl of this culture on selective plates containing 300 µg/ml hygromycin and spread 200 µl of a 10⁵ dilution of this culture on selective plates containing 500 ng/ml aureobasidinA and/or and incubate at 30°C for 3 days to allow individual yeast colonies to grow. We count the colonies on the plates and calculate the gene conversion efficiency by determining the number of hygromycin resistance colonies per 10⁵ aureobasidinA resistant colonies.

[0177] *Oligonucleotides direct gene alteration.* We use this system to assay the ability of various oligonucleotides (sequences shown in Table 1) to support correction under a variety of conditions. The oligonucleotides are designed so that they can direct correction of the replacement, insertion and deletion mutations in Mata+IntHYG(x)eGFP. The oligonucleotides generally are centered

around the base targeted for alteration. In this example, we test the ability of these oligonucleotides to direct alteration of nucleic acid sequence in Mata+IntHYG(rep)eGFP (see Table 2).

[0178] We also use additional oligonucleotides to assay the ability of individual oligonucleotides to correct multiple mutations in both the pAURHYG(x)eGFP plasmid and in yeast strains with integrated copies of pAUR101-HYG(x)eGFP. These include, for example, an oligonucleotide that alters two basepairs that are 3 nucleotides apart with the sequence 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG GGT ACG TCC TGC GGG TAA ATA GCT GCG CCG ATG GTT TCT AC-3' (SEQ ID NO: _); a 74-mer that alters two basepairs that are 15 nucleotides apart with the sequence 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG GAT ACG TCC TGC GGG TAA ACA GCT GCG CCG ATG GTT TCT AC-3' (SEQ ID NO: _); and a 74-mer that alters two basepairs that are 27 nucleotides apart with the sequence 5'-CTC GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG CCG ACG GTT TCT AC (SEQ ID NO: _). The nucleotides in these oligonucleotides that direct alteration of the target sequence are in boldface. These oligonucleotides are chemically modified to enable them to effect oligonucleotide-directed nucleic acid sequence alteration.

Table 1: Oligonucleotides used in Examples 1 and 2

| Name | Size | Sequence | SEQ ID NO: |
|------------|-------|--|------------|
| Hyg3S/74T | 74mer | 5'-C*T*C* GTG CTT TCA GCT TCG ATG TAG GAG GGC GTG GAT ACG TCC TGC GGG TAA ATA GCT GCG CCG ATG GTT TC *T*A*C-3' | |
| Hyg3S/74NT | 74mer | 5'-G*T*A* GAA ACC ATC GGC GCA GCT ATT TAC CCG CAG GAC GTA TCC ACG CCC TCC TAC ATC GAA GCT GAA AGC AC*G *A*G-3' | |

Phosphorothioate linkages are indicated as "*" between the bases. The base corresponding to the location of the replacement mutation in the Hyg(rep) target is in bold.

Table 2: Gene alteration in Mata+IntHYG(rep)eGFP

| Oligonucleotide assayed | Alteration per 10 ⁵ Aureobasidin ^R colonies ¹ | Fold correction (relative to Hyg3S/74T) |
|-------------------------|--|---|
| Hyg3S/74T | 0.22 ± 0.3 | 1x |
| Hyg3S/74NT | 0.89 ± 1.3 | 4.0x |

¹These numbers represent an average of four experiments with the standard deviation indicated for alteration efficiency.

EXAMPLE 2

Selection for a First Alteration Reduces Screening Required to Identify a Second Alteration in the Same Cell

[0179] In this example we demonstrate that the efficiency of alteration of nucleic acid
5 sequence at a second site is enhanced in a population of nucleic acid molecules that have been
previously selected for alteration at a first target site. We use yeast strains having an integrated copy of
the pAUR101-HYG(rep)eGFP plasmid described in Example 1 that also contain the β S YAC (230 kb YAC
comprising the human β -globin gene). In some experiments, the yeast strains also contain a plasmid that
overexpresses yeast Rad51, designated pYNARad51. We use several oligonucleotides: Hyg3S/74NT,
10 which, as described in Example 1, is capable of directing alteration of the mutated Hyg(x)eGFP target to
confer hygromycin resistance; and β S-386m and β S-378m, each of which is a 71-mer oligonucleotide
with 3 phosphorothioate linkages on each end, which is capable of directing a mutation in the human β -
globin gene. The sequence of β S-386m is 5' – G*C*C* TCA CCA CCA ACT TCA TCC ACG TTC ACC
TTG CCT CAC AGG GCA GTA ACG GCA GAC TTC TCC ACA GG*A *G*T – 3' (SEQ ID NO: _) and the
15 sequence of β S-378m is 5' – T*A*A* CGG CAG ACT TCT CCA CAG GAG TCA GGT GCA CCG TGG
TGT CTG TTT GAG GTT GCT AGT GAA CAC AG*T *T*G – 3' (SEQ ID NO: _). β S-386m and β S-378m
both hybridize to the non-transcribed sequence of the human β -globin gene and direct a nucleic acid
sequence alteration that creates a β -thalassemia mutation: β S-386m converts a TGG codon to a stop
codon (TGA) and β S-378m converts the ATG start codon to ACG.

20 [0180] We introduce the oligonucleotides into the yeast cells by electroporation as
follows: we prepare electrocompetent yeast cells by inoculating a single colony into 10 ml of appropriate
media supplemented with 250 μ g/ml aureobasidin and grow the cultures overnight with shaking at 300
rpm at 30°C. In this Example, we use YPD media unless the cells contain a plasmid to overexpress a
repair protein when we use SC-ade media. We dilute the cells into 40 ml media to an initial OD₆₀₀ of
25 approximately 0.15. We incubate the cells with shaking at 30°C until the OD₆₀₀ is approximately 0.25 and,
in some experiments, we add 100 mM hydroxyurea (HU). We continue to incubate the cells with shaking
at 30°C until the OD₆₀₀ is approximately 0.6. We spin down the cells at 3000 rpm for 5 minutes and
resuspend in 1 ml YPD supplemented with 25 μ l 1M DTT and incubate the culture with shaking at 30°C
for 20 minutes. We wash the cells four times by centrifuging at 4°C at 3000 rpm for 5 minutes and
30 resuspending the cells twice in 25 ml ice-cold distilled water; once in 25 ml ice-cold 1M sorbitol; and once
in 1 ml ice-cold 1M sorbitol. We centrifuge the cells at 4°C at 5000 rpm for 5 minutes and resuspend the
cells in 120 μ l 1M sorbitol. We transform the electrocompetent cells with Hyg3S/74NT and either β S-

386m or β S-378m by mixing 40 μ l of cells with 30 μ g oligonucleotide (or 30 μ g of each oligonucleotide) and incubate on ice for 5 minutes. We transfer the mixture to a 0.2 cm electroporation cuvette and electroporate with a BIO-RAD® Gene Pulser® apparatus at 1.5 kV, 25 μ F, 200 Ω for one approximately five-second pulse. We then resuspend the cells in 3 ml YPD media supplemented with Aureobasidin and allow the cells to recover by incubating them overnight at 30°C with shaking at 300 rpm. In some experiments, we supplement the culture with 50 mg/ml Trichostatin A (TSA) during this recovery phase. We spin down the cells, resuspend in 1 ml YPD and spread 100 μ l of this culture (and/or 100 μ l of 10^1 or 10^2 dilutions) on selective plates containing 300 μ g/ml hygromycin and spread 200 μ l of a 10^5 dilution of this culture on selective plates containing 500 ng/ml aureobasidinA and incubate at 30°C for 3 days to allow individual yeast colonies to grow. We count the colonies on the plates and calculate the conversion efficiency for the hygromycin target by determining the number of hygromycin resistance colonies per 10^5 aureobasidinA resistant colonies. We pick individual colonies from YPD-hygromycin plates into 96-well plates with 150 μ l YPD/well and allow the cells to grow overnight at 30°C. We screen individual wells for alteration of the β -globin target in the β S YAC as follows: we PCR amplify a 345 bp fragment of the β -globin gene using forward primer PCO2; 5'- TCC TAA GCC AGT GCC AGA AGA -3' (SEQ ID NO:) and reverse primer PCO5; 5'- CTA TTG GTC TCC TTA AAC CTG -3' (SEQ ID NO:) and purify the PCR product. We analyze the sequence at the target nucleotide in the PCR products by SNaPshot™ analysis on an ABI3100 (Applied Biosystems™) using primers corresponding to the different alterations directed by β S-386m and β S-378m as follows: 386RC; 5'- CCC CCC CCC CCC CCC CCA AGT CTG CCG TTA CTG CCC TGT G -3' (SEQ ID NO:) and 378MF; 5'- TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TGC AAC CTC AAA CAG ACA CCA -3' (SEQ ID NO:).

[0181] As shown in Tables 3 and 4, we observe that the alteration efficiency of the β -globin gene is approximately 10-fold higher than for alteration of the hygromycin target. We observe this result with both β S-386m and β S-378m as well as in the presence or absence of additional factors that enhance oligonucleotide-directed nucleic acid sequence alteration such as, e.g., overexpression of Rad51.

[0182] In other experiments, we do the experiments in yeast strains overexpressing other repair protein(s) in place of or in addition to Rad51 and/or yeast strains with one or more mutations in repair proteins. We also do experiments where we add other compounds that enhance oligonucleotide-directed nucleic acid sequence alteration such as histone deacetylase inhibitors and the bacteriophage lambda beta protein.

Table 3: β S-386m Experiment

| Yeast Strain and treatment | Oligonucleotide(s) | Hygromycin Alteration Efficiency (/10 ⁵) | β -globin Alteration Efficiency |
|--|-----------------------------|--|---------------------------------------|
| Mata-intHyg(rep)eGFP/ β YAC (HU + TSA) | Hyg3S/74NT | 12.35 | NA |
| Mata-intHyg(rep)eGFP/ β YAC (HU + TSA) | Hyg3S/74NT + β S-386m | 30.51 | 0.0031 |
| Mata-intHyg(rep)eGFP/ β YAC | Hyg3S/74NT | 3.22 | NA |
| Mata-intHyg(rep)eGFP/ β YAC | Hyg3S/74NT + β S-386m | 5.07 | ND |

NA = not applicable; ND = not determined

5

Table 4: β S-378m Experiment

| Yeast Strain and treatment | Oligonucleotide(s) | Hygromycin Alteration Efficiency (/10 ⁵) | β -globin Alteration Efficiency |
|--|-----------------------------|--|---------------------------------------|
| Mata-intHyg(rep)eGFP/ β YAC (HU + TSA) | Hyg3S/74NT + β S-378m | 44.58 | ND |
| Mata-intHyg(rep)eGFP/ β YAC (HU + TSA) | Hyg3S/74NT | 12.79 | NA |
| Mata-intHyg(rep)eGFP/ β YAC (HU + TSA) | KanUD3/71 | 0.00 | NA |
| Mata-intHyg(rep)eGFP/ β YAC + pYNARad51 (HU + TSA) | Hyg3S/74NT + β S-378m | 123.73 | 0.15 |
| Mata-intHyg(rep)eGFP/ β YAC + pYNARad51 (HU + TSA) | Hyg3S/74NT | 96.96 | NA |
| Mata-intHyg(rep)eGFP/ β YAC + pYNARad51 (HU + TSA) | KanUD3/71 | 0.01 | NA |

NA = not applicable; ND = not determined; KanUD3/71 is a negative control oligonucleotide

EXAMPLE 3

Selection for a First Alteration Reduces Screening Required to Identify a Second Alteration in Human Blood Cells

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[0183] *Assay system.* We monitor targeted alteration of genetic material in human blood cells using the chromosomal gene encoding the beta subunit of hemoglobin as the target. We coinroduce two oligonucleotides with a plasmid comprising a mutant copy of the green fluorescent protein (GFP) gene. The second oligonucleotide is designed to direct an alteration which repairs the mutant GFP resulting in fluorescence. The first oligonucleotide is designed to convert the wild-type allele to the sickle

allele. We use first oligonucleotides that correspond in sequence to the wild-type allele at all positions except the single nucleotide position designed to introduce the sickle mutation into the gene. Therefore, these oligonucleotides are identical to the oligonucleotides described in Example 6 and shown in Table 7 except for a single base. For example, we use first oligonucleotides selected from: 5'- C*A*A* CCT CAA
 5 ACA GAC ACC ATG GTG CAC CTG ACT CCT GtG GAG AAG TCT GCC GTT ACT GCC CTG TGG
 GGC AA*G *G*T -3'; SEQ ID NO: _; 5'- A*C*C* TTG CCC CAC AGG GCA GTA ACG GCA GAC TTC
 TCC aCA GGA GTC AGG TGC ACC ATG GTG TCT GTT TGA GG*T *T*G-3'; SEQ ID NO: _; 5'-ACC
 TCA AAC AGA CAC CAT GGT GCA CCT GAC TCC TGt GGA GAA GTC TGC CGT TAC TGC CCT GTG
 GGG CAA GG -3'; SEQ ID NO: _; 5'- G*A*C* ACC ATG GTG CAC CTG ACT CCT GtG GAG AAG TCT
 10 GCC GTT ACT GCC *C*T*G -3'; SEQ ID NO: _; and 5'- A*C*C* TCA AAC AGA CAC CAT GGT GCA
 CCT GAC TCC TGt GGA GAA GTC TGC CGT TAC TGC CCT GTG GGG CA*A *G*G -3'. The bases in
 the oligonucleotides which are mismatched to the wild-type allele are shown in lowercase. The
 oligonucleotides are synthesized with three phosphorothioate linkages on each end (represented with
 asterisks) or with a single LNA base at each end (bold).

15 **[0184]** *Preparation and treatment of cells.* We thaw and electroporate cells as follows.
 We warm QBSF-60 medium (Quality Bio) containing 10% FCS (StemCell Technologies) to 37°C. We
 quickly thaw frozen G-CSF mobilized peripheral blood CD-34⁺ cells (BioWhittaker) in a 37°C water bath,
 wipe the outside of the tube with 70% ethanol and aseptically transfer about 2 ml (approximately 1 x 10⁶
 cells) of cell suspension to a 15 ml or 50 ml conical tube. We rinse the vial in 1 ml of medium and add it
 20 dropwise to the cells, gently swirling the conical tube every few drops. We slowly add medium dropwise
 until the volume is about 5 ml, still gently swirling the conical tube every few drops, and then slowly bring
 the volume up to fill the tube by adding 1-2 ml of medium dropwise, swirling after every addition. We
 centrifuge the cell suspension at 200 x g (1500 rpm) for 15 minutes at room temperature. We use a pipet
 to remove most of the wash to a second tube, leaving a few ml behind to avoid disturbing the cell pellet.
 25 We resuspend the pellet in the remaining medium and transfer to a 15 ml conical tube. We rinse the
 original tube with 5 ml medium and add the wash to the cells dropwise, swirling gently after each addition,
 and recentrifuge at 200 x g for 15 minutes. We pipet off all but 2 ml of the wash and gently resuspend the
 cells in the remaining medium and count them. We rest the cells at 37°C and 5% CO₂ for 1 hour and then
 recount the cells. We add 5 ml QBSF-60 medium without FCS containing the cytokines flt-3, SCF and
 30 TPO at 100 ng/ml final concentration (Stem Cell Technologies), repellet the cells at 200 x g (1500 rpm for
 15 min), and gently remove as much liquid volume as possible without disturbing the pellet. We
 resuspend the cells at about 5 x 10⁵ - 1 x 10⁶ cells/ml and transfer them to 6-well tissue culture treated

dishes. We stimulate the cells for three days with cytokines (QBSF-60 medium without FCS containing the cytokines flt-3, SCF and TPO at 100 ng/ml final concentration) and perform a cell count using trypan blue exclusion staining. We centrifuge the cells at 200 x g (1500 rpm) for 15 minutes. We remove the excess volume by pipet and resuspend the cells in the same medium at 2×10^6 cells/ml.

5 **[0185]** We electroporate the oligonucleotides and the GFP plasmid into the cells under square wave conditions as follows. We add 250 μ l cell suspension, 5 μ g GFP plasmid and 30 μ g each oligonucleotide to a 2 mm gap cuvette and electroporate for one 19 msec pulse at 220 V. We then add 750 μ l Iscove's Medium (Invitrogen™), 10% FCS (StemCell Technologies) and the cytokines flt-3, SCF, TPO at 100 ng/ml final concentration, glutamine and penicillin/streptomycin. Alternatively, we add 250 μ l
10 cell suspension, 250 μ l QBSF-60 medium supplemented with flt-3, SCF and TPO and 30 μ g oligonucleotide to a 4 mm gap cuvette and electroporate for five 19 msec pulse at 220 V with a pulse interval of 1 sec. We then add 500 μ l Iscove's Medium (Invitrogen™), 10% FCS (StemCell Technologies) and the cytokines flt-3, SCF and TPO at 100 ng/ml final concentration. We select for the repair of the mutant GFP protein using by FACS and analyze the sequence of the hemoglobin target by PCR
15 amplification and analysis on the SNaPShot™ device using two oligonucleotides: 5'- TTT TTT TTT TTT TTT GAC ACC ATG GTG CAC CTG ACT CCT G -3'; SEQ ID NO _; and 5'- TTT TTT TTT TTT TTT TTT TTC AGT AAC GGC AGA CTT CTC C -3'; SEQ ID NO _. As we see in other cells, these oligonucleotides direct targeted alteration in human blood cells.

20 **EXAMPLE 4**

Use of HU and TSA in Dual Targeting Experiments

25 **[0186]** The efficiency of targeted alteration can be increased and the cost decreased by using at least two unrelated oligonucleotides simultaneously in dual targeting experiments. In this approach, alteration by a first oligonucleotide confers a selectable phenotype that is selected for. Alterations directed by a second oligonucleotide are then screened for from within this selected population. Because the population identified by selective pressure is enriched for cells that bear an edited base at the non-selective site, the approach is useful as a method, termed gene editing, for rapidly and efficiently introducing a single nucleotide polymorphism of choice into virtually any gene at any
30 desired location using modified single-stranded oligonucleotides.

[0187] The dual targeting strategy is illustrated in FIG. 2A. The LSY678IntHyg(rep) β strain (Table 5) contains a 240 kb human β^S -globin YAC and a cassette containing a chromosomal

hygromycin-resistance gene inactivated by a single base mutation and a functional aureobasidin-resistance gene. See Liu et al., *Nucleic Acids Res.* 31:2742-2750 (2002); Parekh-Olmedo et al., *Chem. Biol.* 9:1073-1084 (2002); and Liu et al., *Mol. Cell Biol.* 22:3852-3863 (2002). FIG. 2B shows the oligonucleotide that is used to direct editing of the chromosomal hygromycin mutant gene. Hyg3S/74NT (SEQ ID NO: __) is a 74-mer that is specific for binding to the nontranscribed strand and contains three terminal phosphorothioate linkages. *Id.* Also shown is the target sequence of the mutant, which contains a TAG stop codon. FIG. 2C illustrates the structure of the β -globin YAC and nucleotides targeted for editing are specified. The two nonselectable changes are directed by different oligonucleotides, β Thal1 (SEQ ID NO: __) and β Thal2 (SEQ ID NO: __), in separate experiments. The YAC contains approximately 230 kb of genomic DNA from human chromosome 11, indicated by the shaded region. The unshaded regions represent the yeast sequences that are on either end of the YAC (not drawn to scale). Yu et al., *Proc. Natl. Acad. Sci. USA* 97:5978-5983 (2000). A portion of the β -globin sequence is shown, beginning with the start codon. β Thal1 directs a change from a G to an A while β Thal2 directs a change from a T to a C. The sequences of the oligonucleotides having nucleic acid sequence alteration activity are shown and are designed to bind to the non-transcribed strand, relative to human transcription of the β -globin locus. Both changes result in single-base substitutions that have been documented to result in β -thalassemia in humans.

[0188] For editing experiments, YAC-containing LSY678IntHyg(rep) β cells (Table 5) are grown in the presence of HU, electroporated with the selectable and nonselectable oligonucleotides, and allowed to recover in the presence of TSA (FIG. 2A). Because the human β -globin gene is likely to be transcriptionally inactive in yeast, HU and TSA are especially important in increasing target accessibility. The results of dual targeting experiments are presented in FIG. 3A. Hygromycin-resistant colonies are observed when the oligonucleotide, Hyg3S/74NT, is used. The ratio of hygromycin-resistant colonies to aureobasidin-resistant colonies is referred to as the correction efficiency (C.E.). The presence of HU and TSA leads to an increase in the C.E. of the hygromycin mutation, here about 4- to 6-fold. In this experiment, hygromycin-resistant colonies are found at roughly 1 per 3000 aureobasidin-resistant colonies. Hygromycin-resistant colonies are then analyzed for second-site editing in the YAC β -globin gene. The β Thal1 oligonucleotide is designed to direct the replacement of a G in TGG codon 16 of exon 1 with an A, giving the stop codon TGA (FIG. 2C). FIG. 3B shows an ABI SNaPshot (middle panels) and direct DNA sequence (bottom panel) of a region of the β -globin gene in a corrected colony from this experiment; in both, the G to A change is evident. Of those colonies that are corrected in the hygromycin

mutation, 1 in 325 also contain the second change in the YAC β -globin sequence. Thus, approximately 10% of the cells with the corrected hygromycin-resistance gene also contain the edited β -globin gene.

[0189] As shown in various experiments above, overexpression of RAD51 consistently increases the frequency of chromosomal gene editing. Accordingly, we introduce an expression plasmid containing the yeast RAD51 gene into LSY678IntHyg(rep) β cells (Table 5). FIG. 4 shows results of dual targeting in this strain and, as expected, expression of RAD51 increases the hygromycin correction efficiency of oligonucleotide Hyg3S/74NT (compare with FIG. 3). For these editing experiments, YAC-containing LSY678IntHyg(rep) β cells (Table 5) are grown in the presence of HU, electroporated with the selectable and nonselectable oligonucleotides, and allowed to recover in the presence of TSA (FIG. 2A). Here too, addition of a second oligonucleotide, β Thal2, increases the correction efficiency further, to roughly 1 hygromycin-resistant colony per 800 aureobasidin-resistant colonies.

[0190] The β Thal2 oligonucleotide is designed to direct the replacement of a T in the initiator ATG codon of exon 1 with a C, giving the non-initiator codon ACG (FIG. 2). FIG. 4B shows an ABI SNaPshot (middle panels) and direct DNA sequence (bottom panel) of the β -globin gene from a corrected Hyg^r colony; the T to C change is evident in both analytical panels. Importantly, of those colonies that are corrected in the hygromycin mutation, 1 in 70 also contain the second single-base change in the YAC β -globin sequence. Thus, the dual targeting approach is again successful; approximately 10% of the cells bearing the corrected hygromycin also contain the edited β -globin gene. In addition, in the presence of high levels of Rad51, gene editing occurs at a higher level, indicating that the presence of HU, TSA, and RAD51 overexpression exhibit synergistic effects on the overall process.

Table 5
Genotype of yeast strains

| Strain | Genotype/Description |
|---------------------------------------|--|
| AB1380 | MATa <i>ura3 trp1 ade2-1 can1-100 lys2-1 his5</i> ψ^+ |
| LSY678 | MATa <i>ura3 trp1-1 ade2-1 leu2-3,112 can1 his3-11,15</i> |
| LSY678IntHyg(rep) | LSY678 with mutant hygromycin gene and functional aureobasidin-resistance gene integrated into the <i>AUR-1</i> locus on chromosome XI |
| LSY678IntHyg(rep) β | LSY678IntHyg(rep) with 250 kb YAC containing the human β -globin locus |
| LSY678IntHyg(rep) β + pYNARAD51 | The above strain containing an episomal expression plasmid overexpressing <i>RAD51</i> |

[0191] Strains. The genotypes of the yeast strains used in these studies are listed in Table 5. Details of the LSY678IntHyg(rep) strain are published in Liu et al., *Mol. Cell Biol.* 22:3852-3863 (2002).

[0192] YAC Manipulations. The β -globin YAC is isolated from a preparative pulsed-field gel as described in Gnirke et al., *Genomics* 15:659-667 (1993). Briefly, concentrated chromosomal DNA from the β S-YAC strain (AB1380 background, see Chang et al., *Proc. Natl. Acad. Sci. USA* 95:14886-14890 (1998)) is prepared and resolved on a 1% low-melt agarose pulsed-field gel at 200V, 14°C, 20-50s, 33 hours. The YAC is isolated, equilibrated with a modified agarase buffer (10mM BisTris-HCl pH6.5, 1mM EDTA, 100mM NaCl), treated with β -agarase I (New England Biolabs), and concentrated to a final volume of ~200 μ l. Thirty μ l of the purified YAC are introduced into competent LSY678IntHyg(rep) cells by spheroplast transformation and selection on agar/sorbitol plates lacking tryptophan. Transformants are restreaked and confirmed by pulsed-field gel electrophoresis, PCR, and sequence analysis for a fragment of the human β -globin gene.

[0193] The pYNARad51 episomal expression plasmid is constructed by replacing the *TRP1* gene of pYNRad51 (see Liu et al., *Nucleic Acids Res.* 31, 2742-2750 (2002)) with the *ADE2* gene. pYNARad51 is introduced into LSY678IntHyg(rep) β by electroporation and selection on agar plates lacking adenine.

[0194] Oligonucleotides. Hyg3S/74NT (SEQ ID NO: __), β Thal1 (SEQ ID NO: __), and β Thal2 (SEQ ID NO: __) are ordered from IDT with HPLC purification. Hyg3S/74NT is a 74mer and both β Thal1 and β Thal2 are 71mers; all three oligonucleotides have three phosphorothioate linkages at the 5' and 3' ends (FIG. 2).

[0195] Dual Targeting. The dual targeting protocol is outlined in FIG. 2A. LSY678IntHyg(rep) β cells are grown overnight in 10 ml YPD media at 30°C. The culture is diluted to OD₆₀₀ ~0.15-0.20 in 40 ml YPD media and grown for one doubling time to OD₆₀₀ ~0.3-0.4. 100mM HU is added to the culture and the cells are grown for one doubling time to OD₆₀₀ ~0.6-0.8. Cells are harvested and resuspended in 1 ml YPD containing 25 μ l 1M DTT and grown for an additional 20 minutes at 30°C. The cells are washed twice with 25 ml cold dH₂O and once with 25 ml cold 1M sorbitol. The cells are resuspended gently in 1 ml cold 1M sorbitol, spun for 5 minutes at 5000 rpm in a microcentrifuge, and resuspended in 120 μ l 1M sorbitol. Forty microliters of cells are electroporated with 30 μ g of each oligonucleotide in a 2 mm gap cuvette using a Bio-Rad Gene Pulser apparatus (Richmond, CA) with 1.5 kV, 25 μ F, 200 Ω , 1 pulse, 5s/pulsed length. The cells are immediately resuspended in 3 ml YPD with 0.8 μ g/ml aureobasidin A and 50 μ g/ml TSA and recovered overnight at 30°C. The cells are spun down and

resuspended in 1 ml fresh YPD. Dilutions are plated on YPD agar plates containing either hygromycin (300 µg/ml) or aureobasidin A (0.5 µg/ml). Correction efficiencies (C.E.s) are determined based on the number of hygromycin-resistant colonies per aureobasidin-resistant colonies.

[0196] Individual colonies are picked from the hygromycin agar plates into 96-well plates (Corning) containing 150 µl YPD and grown overnight at 30°C with shaking. A 345 bp PCR product specific for the human β -globin locus is amplified from each of the 96 wells using the primers PCO2 (5'-TCCTAAGCCAGTGCCAGAAG-3' (SEQ ID NO.: __)) and PCO5 (5'-CTATTGGTCTCCTTAAACCTG-3' (SEQ ID NO.: __)) in order to screen for the β Thal1 or β Thal2 conversion. The PCR reactions are performed by adding 8 pmoles of each primer and 2.5 µl yeast cell culture into pre-aliquoted PCR reaction mixes (Marsh/Abgene). The PCR reactions use an annealing temperature of 45.8°C and an extension time of 1 min for 35 cycles. The PCR reactions are purified using a QiaQuick PCR 96-well purification kit (Qiagen) and eluted in a volume of 80 µl. One microliter of the purified PCR product is used as a template for the ABI SNaPshot reaction. The sequence of the SNaPshot primer used to screen for the β Thal1 conversion is: 5'-CCCCCCCCCCCCCCCCCAAGTCTGCCGTTACTGCCCTGTG-3' (SEQ ID NO: __).

15 The sequence of the SNaPshot primer used to screen for the β Thal2 conversion is: 5'-TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCCACAGGAGTCAGGTGCACC-3' (SEQ ID NO: __). The SNaPshot reactions are performed using an ABI Prism SNaPshot Multiplex Kit, as specified by the manufacturer, and analyzed on an ABI 3100 Genetic Analyzer.

[0197] *Sequence Analysis.* Any potential converted clones from the SNaPshot reactions are confirmed by sequence analysis. Both strands of the PCR products are sequenced using primers PCO2 and PCO5 by Sanger dideoxy sequencing using an ABI Prism kit, as specified by the manufacturer, on an automated ABI 3100 Genetic Analyzer.

20

EXAMPLE 5

Adenosine Deaminase (ADA)

[0198] Adenosine deaminase (ADA, EC 3.5.4.4) catalyses the deamination of adenosine and 2'-deoxyadenosine to inosine or 2'-deoxyinosine respectively. ADA deficiency has been identified as the metabolic basis for 20-30% of cases with recessively inherited severe combined immunodeficiency (SCID). Affected infants are subject to recurrent chronic viral, fungal, protozoal, and bacterial infections and frequently present with persistent diarrhea, failure to thrive and candidiasis. In patients homozygous for ADA deficiency, 2'-deoxyadenosine accumulating during the rapid turnover of cells rich in DNA is converted back to dATP, either by adenosine kinase or deoxycytidine kinase. Many hypotheses have been advanced to explain the specific toxicity to the immune system in ADA deficiency. The apparently selective accumulation of dATP in thymocytes and peripheral blood B cells, with resultant inhibition of ribonucleotide reductase and DNA synthesis is probably the principal mechanism.

[0199] The structural gene for ADA is encoded as a single 32 kb locus containing 12 exons. Studies of the molecular defect in ADA-deficient patients have shown that mRNA is usually detectable in normal or supranormal amounts. Specific base substitution mutations have been detected in the majority of cases with the complete deficiency. A C-to-T base substitution mutation in exon 11 accounts for a high proportion of these, whilst a few patients are homozygous for large deletions encompassing exon I. A common point mutation resulting in a heat-labile ADA has been characterised in some patients with partial ADA deficiency, a disorder with an apparently increased prevalence in the Caribbean.

[0200] As yet no totally effective therapy for ADA deficiency has been reported, except in those few cases where bone marrow from an HLA/MLR compatible sibling donor was available.

[0201] Two therapeutic approaches have provided long-term benefit in specific instances. First, reconstitution using T cell depleted mismatched sibling marrow has been encouraging, particularly in early presenters completely deficient in ADA. Secondly, therapy with polyethylene glycol-modified adenosine deaminase (PEG-ADA) for more than 5 years has produced a sustained increase in lymphocyte numbers and mitogen responses together with evidence of in vivo B cell function. Success has generally been achieved in late presenters with residual ADA activity in mononuclear cells.

[0202] ADA deficiency has been chosen as the candidate disease for gene replacement therapy and the first human experiment commenced in 1990. The clinical consequences of overexpression of ADA activity - one of the potential hazards of gene implant - are known and take the form of an hereditary haemolytic anaemia associated with a tissue-specific increase in ADA activity. The

genetic basis for the latter autosomal dominant disorder seemingly relates to markedly increased levels of structurally normal ADA mRNA.

Table 6

ADA Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Adenosine deaminase deficiency GLN3TERM CAG to TAG | AGAGACCCACCGAGCGGCGGCGGAGGGAGCAGCGCCGGGG CGCACGAGGGGCACCATGGCC <u>C</u> AGACGCCCGCCTTCGACAAG CCCAAAGTGAGCGCGCGCGGGGGCTCCGGGGACGGGGGTC | 1 |
| | GACCCCGTCCCCGGAGCCCCCGCGCGCGCTCACTTTGGGC TTGTCTGAAGGCGGGCGTCT <u>G</u> GGCCATGGTGCCCTCGTGCGC CCCGGCGCTGCTCCCTCCGCCCGCGCTCGGTGGGTCTCT | 2 |
| | CCATGGCC <u>C</u> AGACGCCC | 3 |
| | GGGCGTCT <u>G</u> GGCCATGG | 4 |
| Adenosine deaminase deficiency HIS15ASP CAT to GAT | TATTTGTTCTCTCTCTCCCTTTCTCTCTCTTCCCCCTGCCCC CTTGCAAGTAGAACTG <u>C</u> ATGTCCACCTAGACGGATCCATCAA GCCTGAAACCATCTTATACTATGGCAGGTAAGTCC | 5 |
| | GGAATTACCTGCCATAGTATAAGATGGTTTCAGGCTTGATGGA TCCGTCTAGGTGGACAT <u>G</u> CAGTTCTACCTGCAAGGGGGCAG GGGGAAGAGAGAGAGAAAGGGAGAGAGAGAAACAAATA | 6 |
| | TAGAACTG <u>C</u> ATGTCCAC | 7 |
| | GTGGACAT <u>G</u> CAGTTCTA | 8 |
| Adenosine deaminase deficiency GLY20ARG GGA to AGA | TCCCTTTCTCTCTCTTCCCCCTGCCCCCTTGCAAGGTAGAAC TGCATGTCCACCTAGAC <u>G</u> GATCCATCAAGCCTGAAACCATCTT ATACTATGGCAGGTAAGTCCATACAGAAGAGCCCT | 9 |
| | AGGGCTCTTCTGTATGGACTTACCTGCCATAGTATAAGATGGT TTCAGGCTTGATGGATC <u>C</u> GTCTAGGTGGACATGCAGTTCTAC CTGCAAGGGGGCAGGGGGAAGAGAGAGAGAAAGGGA | 10 |
| | ACCTAGAC <u>G</u> GATCCATC | 11 |
| | GATGGATC <u>C</u> GTCTAGGT | 12 |
| Adenosine deaminase deficiency GLY74CYS GGC to TGC | CCTGGAGCTCCCAAGGGACTTGGGGAAGGTTGTTCCCAACC CCTTTCTTCCCTTCCAGG <u>G</u> GCTGCCGGGAGGCTATCAAAAG GATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGG | 13 |
| | CCTCTTTGGCCTTCATCTCTACAAACTCATAGGCGATCCTTTT GATAGCCTCCCGGCAGCC <u>C</u> CTGGGAAGGGAAGAAAGGGGTT GGGAACAACCTTCCCAAGTCCCTTGGGAGCTCCAGG | 14 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | CTATCGCG <u>G</u> GCTGCCGG | 15 |
| | CCGGCAGC <u>C</u> CGCGATAG | 16 |
| Adenosine Deaminase Deficiency ARG76TRP CGG to TGG | GCTCCCAAGGGACTTGGGGAAGGTTGTTCCCAACCCCTTTCT TCCCTTCCCAGGGGCTGCC <u>G</u> GGGAGGCTATCAAAAGGATCGC CTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCGTGG | 17 |
| | CCACGCCCTCTTTGGCCTTCATCTCTACAACTCATAGGCGAT CCTTTTGATAGCCTCCC <u>G</u> GCAGCCCCTGGGAAGGGAAGAAA GGGGTTGGGAACAACCTTCCCCAAGTCCCTTGGGAGC | 18 |
| | GGGGCTGCC <u>G</u> GGGAGGCT | 19 |
| | AGCCTCCC <u>G</u> GCAGCCCC | 20 |
| Adenosine Deaminase Deficiency LYS80ARG AAA to AGA | TTGGGGAAGGTTGTTCCCAACCCCTTTCTTCCCTTCCCAGGG GCTGCCGGGAGGCTATCA <u>A</u> AAGGATCGCCTATGAGTTTGTAG AGATGAAGGCCAAAGAGGGCGTGGTGTATGTGGAGGT | 21 |
| | ACCTCCACATACACCACGCCCTCTTTGGCCTTCATCTCTACAA ACTCATAGGCGATCCTTT <u>T</u> GATAGCCTCCCGGCAGCCCCTGG GAAGGGAAGAAAGGGGTTGGGAACAACCTTCCCCAA | 22 |
| | GGCTATCA <u>A</u> AAGGATCG | 23 |
| | CGATCCTTTT <u>T</u> GATAGCC | 24 |
| Adenosine deaminase deficiency ALA83ASP GCC to GAC | GTTGTTCCCAACCCCTTTCTTCCCTTCCCAGGGGCTGCCGGG AGGCTATCAAAAGGATCG <u>C</u> CTATGAGTTTGTAGAGATGAAGG CCAAAGAGGGCGTGGTGTATGTGGAGGTGCGGTACAG | 25 |
| | CTGTACCGCACCTCCACATACACCACGCCCTCTTTGGCCTTC ATCTCTACAACTCATAG <u>G</u> CGATCCTTTTGATAGCCTCCCGGC AGCCCCTGGGAAGGGAAGAAAGGGGTTGGGAACAAC | 26 |
| | AAGGATCG <u>C</u> CTATGAGT | 27 |
| | ACTCATAG <u>G</u> CGATCCTT | 28 |
| Adenosine deaminase deficiency TYR97CYS TAT to TGT | AGGCTATCAAAAGGATCGCCTATGAGTTTGTAGAGATGAAGG CCAAAGAGGGCGTGGTGT <u>A</u> TGTGGAGGTGCGGTACAGTCCG CACCTGCTGGCCAACCTCCAAAGTGAGCCAATCCCCTG | 29 |
| | CAGGGGATTGGCTCCACTTTGGAGTTGGCCAGCAGGTGCGG ACTGTACCGCACCTCCACA <u>T</u> ACACCACGCCCTCTTTGGCCTT CATCTCTACAACTCATAGGCGATCCTTTTGATAGCCT | 30 |
| | CGTGGTGT <u>A</u> TGTGGAGG | 31 |
| | CCTCCACATACACCAG | 32 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Adenosine deaminase deficiency ARG101GLN CGG to CAG | GGATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCG TGGTGTATGTGGAGGTGCGGTACAGTCCGCACCTGCTGGCC AACTCCAAAGTGGAGCCAATCCCCTGGAACCAGGCTGA | 33 |
| | TCAGCCTGGTTCCAGGGGATTGGCTCCACTTTGGAGTTGGCC AGCAGGTGCGGACTGTACCGCACCTCCACATACACCACGCC CTCTTTGGCCTTCATCTCTACAAACTCATAGGCGATCC | 34 |
| | GGAGGTGCGGTACAGTC | 35 |
| | GACTGTACCGCACCTCC | 36 |
| Adenosine deaminase deficiency ARG101LEU CGG to CTG | GGATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCG TGGTGTATGTGGAGGTGCGGTACAGTCCGCACCTGCTGGCC AACTCCAAAGTGGAGCCAATCCCCTGGAACCAGGCTGA | 37 |
| | TCAGCCTGGTTCCAGGGGATTGGCTCCACTTTGGAGTTGGCC AGCAGGTGCGGACTGTACCGCACCTCCACATACACCACGCC CTCTTTGGCCTTCATCTCTACAAACTCATAGGCGATCC | 38 |
| | GGAGGTGCGGTACAGTC | 39 |
| | GACTGTACCGCACCTCC | 40 |
| Adenosine deaminase deficiency ARG101TRP CGG to TGG | AGGATCGCCTATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCG GTGGTGTATGTGGAGGTGCGGTACAGTCCGCACCTGCTGGC CAACTCCAAAGTGGAGCCAATCCCCTGGAACCAGGCTG | 41 |
| | CAGCCTGGTTCCAGGGGATTGGCTCCACTTTGGAGTTGGCCA GCAGGTGCGGACTGTACCGCACCTCCACATACACCACGCCCT CTTTGGCCTTCATCTCTACAAACTCATAGGCGATCCT | 42 |
| | TGGAGGTGCGGTACAGT | 43 |
| | ACTGTACCGCACCTCCA | 44 |
| Adenosine deaminase deficiency PRO104LEU CCG to CTG | ATGAGTTTGTAGAGATGAAGGCCAAAGAGGGCGTGGTGTATG TGGAGGTGCGGTACAGTCCGCACCTGCTGGCCAACTCCAAA GTGGAGCCAATCCCCTGGAACCAGGCTGAGTGAGTGAT | 45 |
| | ATCACTCACTCAGCCTGGTTCCAGGGGATTGGCTCCACTTTG GAGTTGGCCAGCAGGTGCGGACTGTACCGCACCTCCACATA CACCACGCCCTCTTTGGCCTTCATCTCTACAAACTCAT | 46 |
| | GTACAGTCCGCACCTGC | 47 |
| | GCAGGTGCGGACTGTAC | 48 |
| Adenosine deaminase deficiency LEU106VAL | TTTGTAGAGATGAAGGCCAAAGAGGGCGTGGTGTATGTGGAG GTGCGGTACAGTCCGCACCTGCTGGCCAACTCCAAAGTGGGA GCCAATCCCCTGGAACCAGGCTGAGTGAGTGATGGGCC | 49 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| CTG to GTG | GGCCCATCACTCACTCAGCCTGGTTCCAGGGGATTGGCTCCA CTTTGGAGTTGGCCAGCAGGTGCGGACTGTACCGCACCTCCA CATACACCACGCCCTCTTTGGCCTTCATCTCTACAAA | 50 |
| | GTCCGCACCTGCTGGCC | 51 |
| | GGCCAGCAGGTGCGGAC | 52 |
| Adenosine deaminase deficiency LEU107PRO CTG to CCG | TAGAGATGAAGGCCAAAGAGGGCGTGGTGTATGTGGAGGTG CGGTACAGTCCGCACCTGCTGGCCAACTCCAAAGTGGAGCC AATCCCCTGGAACCAGGCTGAGTGAGTGATGGGCCTGGA | 53 |
| | TCCAGGCCCATCACTCACTCAGCCTGGTTCCAGGGGATTGGC TCCACTTTGGAGTTGGCCAGCAGGTGCGGACTGTACCGCAC CTCCACATACACCACGCCCTCTTTGGCCTTCATCTCTA | 54 |
| | GCACCTGCTGGCCAACT | 55 |
| | AGTTGGCCAGCAGGTGC | 56 |
| Adenosine deaminase deficiency PRO126GLN CCA to CAA | GCCTTCCTTTTGCCTCAGGCCCATCCCTACTCCTCTCCTCACA CAGAGGGGACCTCACCCAGACGAGGTGGTGGCCCTAGTGG GCCAGGGCCTGCAGGAGGGGGAGCGAGACTTCGGGGT | 57 |
| | ACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCCCTGGCCAC TAGGGCCACCACCTCGTCTGGGGTGAGGTCCCCTCTGTGTG AGGAGAGGAGTAGGGATGGGCCTGAGGCAAAGGAAGGC | 58 |
| | CCTCACCCAGACGAGG | 59 |
| | CCTCGTCTGGGGTGAGG | 60 |
| Adenosine deaminase deficiency VAL129MET GTG to ATG | TTTGCCTCAGGCCCATCCCTACTCCTCTCCTCACACAGAGGG GACCTCACCCAGACGAGGTGGTGGCCCTAGTGGGCCAGGG CCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCC | 61 |
| | GGGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCC TGGCCCACTAGGGCCACCCTCGTCTGGGGTGAGGTCCCC TCTGTGTGAGGAGAGGAGTAGGGATGGGCCTGAGGCAA | 62 |
| | CAGACGAGGTGGTGGCC | 63 |
| | GGCCACCACTCGTCTG | 64 |
| Adenosine deaminase deficiency GLY140GLU GGG to GAG | ACAGAGGGGACCTCACCCAGACGAGGTGGTGGCCCTAGTG GGCCAGGGCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCA AGGCCCGGTCCATCCTGTGCTGCATGCGCCACCAGCCCAG | 65 |
| | CTGGGCTGGTGGCGCATGCAGCACAGGATGGACCGGGCCTT GACCCCGAAGTCTCGCTCCCCTCCTGCAGGCCCTGGCCCA CTAGGGCCACCACCTCGTCTGGGGTGAGGTCCCCTCTGT | 66 |
| | GCAGGAGGGGGAGCGAG | 67 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | CTCGCTCCC <u>C</u> CCTCCTGC | 68 |
| Adenosine deaminase deficiency ARG142GLN CGA to CAA | GGGACCTCACCCCAGACGAGGTGGTGGCCCTAGTGGGCCAG GGCCTGCAGGAGGGGGAGC <u>G</u> AGACTTCGGGGTCAAGGCC GGTCCATCCTGTGCTGCATGCGCCACCAGCCCAGTGAGTA | 69 |
| | TACTCACTGGGCTGGTGGCGCATGCAGCACAGGATGGACCG GGCCTTGACCCCGAAGTCT <u>C</u> GCTCCCCCTCCTGCAGGCCCT GGCCCACTAGGGCCACCACCTCGTCTGGGGTGAGGTCCC | 70 |
| | GGGGGAGC <u>G</u> AGACTTCG | 71 |
| | CGAAGTCT <u>C</u> GCTCCCC | 72 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Adenosine deaminase deficiency ARG142TERM CGA to TGA | GGGGACCTCACCCCAGACGAGGTGGTGGCCCTAGTGGGCCA GGGCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCC CGGTCCATCCTGTGCTGCATGCGCCACCAGCCCAGTGAGT | 73 |
| | ACTCACTGGGCTGGTGGCGCATGCAGCACAGGATGGACCGG GCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCCCTG GCCACTAGGGCCACCACCTCGTCTGGGGTGAGGTCCCC | 74 |
| | AGGGGGAGCGAGACTTC | 75 |
| | GAAGTCTCGCTCCCCCT | 76 |
| Adenosine deaminase deficiency ARG149GLN CGG to CAG | TGGTGGCCCTAGTGGGCCAGGGCCTGCAGGAGGGGGAGCG AGACTTCGGGGTCAAGGCCCCGGTCCATCCTGTGCTGCATGC GCCACCAGCCCAGTGAGTAGGATCACCGCCCTGCCAGGG | 77 |
| | CCCTGGGCAGGGCGGTGATCCTACTCACTGGGCTGGTGGCG CATGCAGCACAGGATGGACCGGGCCTTGACCCCGAAGTCTC GCTCCCCCTCCTGCAGGCCCTGGCCCACTAGGGCCACCA | 78 |
| | CAAGGCCCCGGTCCATCC | 79 |
| | GGATGGACCGGGCCTTG | 80 |
| Adenosine deaminase deficiency ARG149TRP CGG to TGG | GTGGTGGCCCTAGTGGGCCAGGGCCTGCAGGAGGGGGAGC GAGACTTCGGGGTCAAGGCCCGGTCCATCCTGTGCTGCATG CGCCACCAGCCCAGTGAGTAGGATCACCGCCCTGCCAGG | 81 |
| | CCTGGGCAGGGCGGTGATCCTACTCACTGGGCTGGTGGCGC ATGCAGCACAGGATGGACCGGGCCTTGACCCCGAAGTCTCG CTCCCCCTCCTGCAGGCCCTGGCCCACTAGGGCCACCAC | 82 |
| | TCAAGGCCCGGTCCATC | 83 |
| | GATGGACCGGGCCTTGA | 84 |
| Adenosine deaminase deficiency LEU152MET CTG to ATG | CTAGTGGGCCAGGGCCTGCAGGAGGGGGAGCGAGACTTCG GGGTCAAGGCCCCGTCCATCCTGTGCTGCATGCGCCACCAG CCCAGTGAGTAGGATCACCGCCCTGCCAGGGCCGCCCGT | 85 |
| | ACGGGCGGCCCTGGGCAGGGCGGTGATCCTACTCACTGGGC TGGTGGCGCATGCAGCACAGGATGGACCGGGCCTTGACCCC GAAGTCTCGTCCCCCTCCTGCAGGCCCTGGCCCACTAG | 86 |
| | GGTCCATCCTGTGCTGC | 87 |
| | GCAGCACAGGATGGACC | 88 |
| Adenosine deaminase deficiency ARG156CYS | GGCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCCC GGTCCATCCTGTGCTGCATGCGCCACCAGCCCAGTGAGTAG GATCACCGCCCTGCCAGGGCCGCCCGTCTCACCCCTGGCC | 89 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| CGC to TGC | GGCCAGGGTGAGACGGGCGGCCCTGGGCAGGGCGGTGATC CTACTCACTGGGCTGGTGGC <u>G</u> CATGCAGCACAGGATGGACC GGGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGCC | 90 |
| | GCTGCATG <u>C</u> GCCACCAG | 91 |
| | CTGGTGGC <u>G</u> CATGCAGC | 92 |
| Adenosine deaminase deficiency ARG156HIS CGC to CAC | GCCTGCAGGAGGGGGAGCGAGACTTCGGGGTCAAGGCCCG GTCCATCCTGTGCTGCATGC <u>G</u> CCACCAGCCCAGTGAGTAGGA TCACCGCCCTGCCAGGGCCGCCCGTCTCACCTGGCCC | 93 |
| | GGGCCAGGGTGAGACGGGCGGCCCTGGGCAGGGCGGTGAT CCTACTCACTGGGCTGGTGG <u>C</u> GCATGCAGCACAGGATGGAC CGGGCCTTGACCCCGAAGTCTCGCTCCCCCTCCTGCAGGC | 94 |
| | CTGCATGC <u>G</u> CCACCAGC | 95 |
| | GCTGGTGG <u>C</u> GCATGCAG | 96 |
| Adenosine deaminase deficiency VAL177MET GTG to ATG | CTGCCCACAGACTGGTCCCCCAAGGTGGTGGAGCTGTGTAA GAAGTACCAGCAGCAGACC <u>G</u> TGGTAGCCATTGACCTGGCTG GAGATGAGACCATCCCAGGAAGCAGCCTCTTGCCTGGAC | 97 |
| | GTCCAGGCAAGAGGCTGCTTCCTGGGATGGTCTCATCTCCAG CCAGGTCAATGGCTACCAC <u>G</u> GTCTGCTGCTGGTACTTCTTAC ACAGCTCCACCACCTTGGGGGACCAGTCTGTGGGCAG | 98 |
| | AGCAGACC <u>G</u> TGGTAGCC | 99 |
| | GGCTACCAC <u>G</u> GTCTGCT | 100 |
| Adenosine deaminase deficiency ALA179ASP GCC to GAC | CAGACTGGTCCCCCAAGGTGGTGGAGCTGTGTAAGAAGTACC AGCAGCAGACCGTGGTAGC <u>C</u> ATTGACCTGGCTGGAGATGAG ACCATCCCAGGAAGCAGCCTCTTGCCTGGACATGTCCA | 101 |
| | TGGACATGTCCAGGCAAGAGGCTGCTTCCTGGGATGGTCTCA TCTCCAGCCAGGTCAATG <u>G</u> CTACCACGGTCTGCTGCTGGTAC TTCTTACACAGCTCCACCACCTTGGGGGACCAGTCTG | 102 |
| | CGTGGTAGC <u>C</u> ATTGACC | 103 |
| | GGTCAATG <u>G</u> CTACCAG | 104 |
| Adenosine deaminase deficiency GLN199PRO CAG to CCG | CCATTGACCTGGCTGGAGATGAGACCATCCCAGGAAGCAGC CTCTTGCCTGGACATGTCC <u>A</u> GGCCTACCAGGTGGGTCTCTGTG AGAAGGAATGGAGAGGCTGGCCCTGGGTGAGCTTGTCT | 105 |
| | AGACAAGCTCACCCAGGGCCAGCCTCTCCATTCTTCTCACA GGACCCACCTGGTAGGCC <u>T</u> GGACATGTCCAGGCAAGAGGCT GCTTCTGGGATGGTCTCATCTCCAGCCAGGTCAATGG | 106 |
| | ACATGTCC <u>A</u> GGCCTACC | 107 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | GGTAGGCCTGGACATGT | 108 |
| Adenosine deaminase deficiency ARG211CYS CGT to TGT | GCTAGGGCACCCATGACCTGGCTCTCCCCCTTCCAGGAGGC TGTGAAGAGCGGCATTACCGTACTGTCCACGCCGGGGAGG TGGGCTCGGCCGAAGTAGTAAAAGAGGTGAGGGCCTGGG | 109 |
| | CCCAGGCCCTCACCTCTTTTACTACTTCGGCCGAGCCACCT CCCCGGCGTGGACAGTACGGTGAATGCCGCTCTTCACAGCC TCCTGGAAGGGGGAGAGCCAGGTCATGGGTGCCCTAGC | 110 |
| | GCATTACCGTACTGTC | 111 |
| | GACAGTACGGTGAATGC | 112 |
| Adenosine deaminase deficiency ARG211HIS CGT to CAT | CTAGGGCACCCATGACCTGGCTCTCCCCCTTCCAGGAGGCT GTGAAGAGCGGCATTACCGTACTGTCCACGCCGGGGAGGT GGGCTCGGCCGAAGTAGTAAAAGAGGTGAGGGCCTGGGC | 113 |
| | GCCCAGGCCCTCACCTCTTTTACTACTTCGGCCGAGCCACC TCCCCGGCGTGGACAGTACGGTGAATGCCGCTCTTCACAGC CTCCTGGAAGGGGGAGAGCCAGGTCATGGGTGCCCTAG | 114 |
| | CATTACCGTACTGTCC | 115 |
| | GGACAGTACGGTGAATG | 116 |
| Adenosine deaminase deficiency ALA215THR GCC to ACC | ATGACCTGGCTCTCCCCCTTCCAGGAGGCTGTGAAGAGCGG CATTACCGTACTGTCCACGCCGGGGAGGTGGGCTCGGCCG AAGTAGTAAAAGAGGTGAGGGCCTGGGCTGGCCATGGGG | 117 |
| | CCCCATGGCCAGCCAGGCCCTCACCTCTTTTACTACTTCGG CCGAGCCACCTCCCCGGCGTGGACAGTACGGTGAATGCCG CTCTTCACAGCCTCCTGGAAGGGGGAGAGCCAGGTCAT | 118 |
| | CTGTCCACGCCGGGGAG | 119 |
| | CTCCCCGGCGTGGACAG | 120 |
| Adenosine deaminase deficiency GLY216ARG GGG to AGG | ACCTGGCTCTCCCCCTTCCAGGAGGCTGTGAAGAGCGGCATT CACCGTACTGTCCACGCCGGGGAGGTGGGCTCGGCCGAAGT AGTAAAAGAGGTGAGGGCCTGGGCTGGCCATGGGGTCC | 121 |
| | GGACCCCATGGCCAGCCAGGCCCTCACCTCTTTTACTACTT CGGCCGAGCCACCTCCCCGGCGTGGACAGTACGGTGAATG CCGCTCTTCACAGCCTCCTGGAAGGGGGAGAGCCAGGT | 122 |
| | TCCACGCCGGGGAGGTG | 123 |
| | CACCTCCCCGGCGTGA | 124 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Adenosine deaminase deficiency GLU217LYS GAG to AAG | TGGCTCTCCCCCTTCCAGGAGGCTGTGAAGAGCGGCATTACAC CGTACTGTCCACGCCGGG <u>G</u> AGGTGGGCTCGGCCGAAGTAGT AAAAGAGGTGAGGGCCTGGGCTGGCCATGGGGTCCCTC | 125 |
| | GAGGGACCCCATGGCCAGCCCAGGCCCTCACCTCTTTTACTA CTTCGGCCGAGCCACCT <u>C</u> CCCGGCGTGGACAGTACGGTGA ATGCCGCTCTTCACAGCCTCCTGGAAGGGGGAGAGCCA | 126 |
| | ACGCCGGG <u>G</u> AGGTGGGC | 127 |
| | GCCACCT <u>C</u> CCCGGCGT | 128 |
| Adenosine deaminase deficiency THR233ILE ACA to ATA | CTGCCTCCTCCCATACTTGGCTCTATTCTGCTTCTCTACAGGC TGTGGACATACTCAAGA <u>C</u> AGAGCGGCTGGGACACGGCTACC ACACCCTGGAAGACCAGGCCCTTTATAACAGGCTGCG | 129 |
| | CGCAGCCTGTTATAAAGGGCCTGGTCTTCCAGGGTGTGGTAG CCGTGTCCAGCCGCTCT <u>G</u> TCTTGAGTATGTCCACAGCCTGT AGAGAAGCAGAATAGAGCCAAGTATGGGAGGAGGCAG | 130 |
| | ACTCAAGA <u>C</u> AGAGCGGC | 131 |
| | GCCGCTCT <u>G</u> TCTTGAGT | 132 |
| Adenosine deaminase deficiency ARG253PRO CGG to CCG | CAGAGCGGCTGGGACACGGCTACCACACCCTGGAAGACCAG GCCCTTTATAACAGGCTG <u>C</u> GCAGGAAAACATGCACTTCGAG GTAAGCGGGCCAGGGAGTGGGGAGGAACCATCCCCGGC | 133 |
| | GCCGGGGATGGTTCCTCCCCACTCCCTGGCCCGCTTACCTC GAAGTGCATGTTTTCTG <u>C</u> GCAGCCTGTTATAAAGGGCCTG GTCTTCCAGGGTGTGGTAGCCGTGTCCAGCCGCTCTG | 134 |
| | CAGGCTG <u>C</u> GCAGGAAA | 135 |
| | TTTCCTG <u>C</u> GCAGCCTG | 136 |
| Adenosine deaminase deficiency GLN254TERM CAG to TAG | GAGCGGCTGGGACACGGCTACCACACCCTGGAAGACCAGGC CCTTTATAACAGGCTGCGG <u>C</u> AGGAAAACATGCACTTCGAGGT AAGCGGGCCAGGGAGTGGGGAGGAACCATCCCCGGCTG | 137 |
| | CAGCCGGGGATGGTTCCTCCCCACTCCCTGGCCCGCTTACCT CGAAGTGCATGTTTTCTG <u>C</u> CGCAGCCTGTTATAAAGGGCCT GGTCTTCCAGGGTGTGGTAGCCGTGTCCAGCCGCTC | 138 |
| | GGCTGCGG <u>C</u> AGGAAAAC | 139 |
| | GTTTTCTG <u>C</u> CGCAGCC | 140 |
| Adenosine deaminase deficiency PRO274LEU | CCACACACCTGCTCTTCCAGATCTGCCCTGGTCCAGCTACC TCACTGGTGCCTGGAAGC <u>C</u> GGACACGGAGCATGCAGTCATTC GGTGAGCTCTGTTCCCTGGGCCTGTTCAATTTTGT | 141 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| CCG to CTG | AACAAAATTGAACAGGCCCCAGGGGAACAGAGCTCACCGAATG ACTGCATGCTCCGTGTCCGGCTTCCAGGCACCAGTGAGGTAG CTGGACCAGGGGCAGATCTGGAAGAGCAGGTGTGTGG | 142 |
| | CTGGAAGCCGGACACGG | 143 |
| | CCGTGTCCGGCTTCCAG | 144 |
| Adenosine deaminase deficiency SER291LEU TCG to TTG | GGAGGCTGATTCTCTCCTCCTCCCTCTTCTGCAGGCTCAAAA ATGACCAGGCTAACTACTCGCTCAACACAGATGACCCGCTCA TCTTCAAGTCCACCCTGGACACTGATTACCAGATGAC | 145 |
| | GTCATCTGGTAATCAGTGTCCAGGGTGGACTTGAAGATGAGC GGGTCATCTGTGTTGAGCGAGTAGTTAGCCTGGTCATTTTTGA GCCTGCAGAAGAGGGAGGAGGAGAGAATCAGCCTCC | 146 |
| | TAACTACTCGCTCAACA | 147 |
| | TGTTGAGCGAGTAGTTA | 148 |
| Adenosine deaminase deficiency PRO297GLN CCG to CAG | CCTCCCTCTTCTGCAGGCTCAAAAATGACCAGGCTAACTACTC GCTCAACACAGATGACCCGCTCATCTTCAAGTCCACCCTGGA CACTGATTACCAGATGACCAAACGGGACATGGGCTT | 149 |
| | AAGCCCATGTCCCGTTTGGTCATCTGGTAATCAGTGTCCAGG GTGGACTTGAAGATGAGCGGGTCATCTGTGTTGAGCGAGTAG TTAGCCTGGTCATTTTTGAGCCTGCAGAAGAGGGAGG | 150 |
| | AGATGACCCGCTCATCT | 151 |
| | AGATGAGCGGGTCATCT | 152 |
| Adenosine deaminase deficiency LEU304ARG CTG to CGG | AAAATGACCAGGCTAACTACTCGCTCAACACAGATGACCCGC TCATCTTCAAGTCCACCCTGGACACTGATTACCAGATGACCAA ACGGGACATGGGCTTTACTGAAGAGGAGTTTAAAAG | 153 |
| | CTTTTAACTCCTCTTCAGTAAAGCCCATGTCCCGTTTGGTCA TCTGGTAATCAGTGTCCAGGGTGGACTTGAAGATGAGCGGGT CATCTGTGTTGAGCGAGTAGTTAGCCTGGTCATTTT | 154 |
| | GTCCACCCCTGGACACTG | 155 |
| | CAGTGTCCAGGGTGGAC | 156 |
| Adenosine deaminase deficiency ALA329VAL C-to-T at base 1081 | GCCTTCTTTGTTCTCTGGTTCCATGTTGTCTGCCATTCTGGCC TTTCCAGAACATCAATGCGGCCAAATCTAGTTTCTCCAGAA GATGAAAAGAGGGAGCTTCTCGACCTGCTCTATAA | 157 |
| | TTATAGAGCAGGTCGAGAAGCTCCCTCTTTTCATCTTCTGGGA GGAACTAGATTTGGCCGCATTGATGTTCTGGAAAGGCCAGA ATGGCAGACAACATGGAACCAGAGAACAAGAAGGC | 158 |
| | CATCAATGCGGCCAAAT | 159 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|-------------------------------|----------------------------|------------|
| | ATTTGGCC <u>G</u> CATTGATG | 160 |

EXAMPLE 6

P53 Mutations

[0203] The p53 gene codes for a protein that acts as a transcription factor and serves as a key regulator of the cell cycle. Mutation in this gene is probably the most significant genetic change characterizing the transformation of cells from normalcy to malignancy.

[0204] Inactivation of p53 by mutation disrupts the cell cycle which, in turn, sets the stage for tumor formation. Mutations in the p53 gene are among the most commonly diagnosed genetic disorders, occurring in as many as 50% of cancer patients. For some types of cancer, most notably of the breast, lung and colon, p53 mutations are the predominant genetic alternations found thus far. These mutations are associated with genomic instability and thus an increased susceptibility to cancer. Some p53 lesions result in malignancies that are resistant to the most widely used therapeutic regimens and therefore demand more aggressive treatment.

[0205] That p53 is associated with different malignant tumors is illustrated in the Li-Fraumeni autosomal dominant hereditary disorder characterized by familial multiple tumors due to mutation in the p53 gene. Affected individuals can develop one or more tumors, including: brain (12%); soft-tissue sarcoma (12%); breast cancer (25%); adrenal tumors (1%); bone cancer (osteosarcoma) (6%); cancer of the lung, prostate, pancreas, and colon as well as lymphoma and melanoma can also occur.

[0206] Certain of the most frequently mutated codons are codons 175, 248 and 273, however a variety of oligonucleotides are described below in the attached table.

Table 7

p53 Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| In 2 families with Li-Fraumeni syndrome, there was a C-to-T mutation at the first nucleotide of | GACTGTACCACCATCCACTACAACCTACATGTGTAACAGTTCCTGCATGGGCGGCATGAAC <u>C</u> GGAGGCCCATCCTCACCATCATCACACTGGAAGACTCCAGGTCAGGAGCCACTTGCCACC | 161 |
| | GGTGGCAAGTGGCTCCTGACCTGGAGTCTTCCAGTGTGATGATGGTGAGGATGGGCCTCC <u>G</u> GTTTCATGCCGCCCATGCAGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGTC | 162 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| codon 248 which changed arginine to tryptophan. | GCATGAAC <u>C</u> GGAGGCC | 163 |
| | GGGCCTCC <u>G</u> GTTTCATGC | 164 |
| In a family with the Li-Fraumeni syndrome, a G-to-A mutation at the first nucleotide of codon 258 resulting in the substitution of lysine for glutamic acid. | TGTAACAGTTCCTGCATGGGCGGCATGAACCGGAGGCCCAT CCTCACCATCATCACACTG <u>G</u> AAGACTCCAGGTCAGGAGCCAC TTGCCACCCTGCACACTGGCCTGCTGTGCCCCAGCCTC | 165 |
| | GAGGCTGGGGCACAGCAGGCCAGTGTGCAGGGTGGCAAGT GGCTCCTGACCTGGAGTCTT <u>C</u> CAGTGTGATGATGGTGAGGAT GGGCCTCCGGTTCATGCCGCCCATGCAGGAAGTGTACA | 166 |
| | TCACACTG <u>G</u> AAGACTCC | 167 |
| | GGAGTCTT <u>C</u> CAGTGTGA | 168 |
| In a family with the Li-Fraumeni syndrome, a G-to-T mutation at the first nucleotide of codon 245 resulting in the substitution of cysteine for glycine. | GTTGGCTCTGACTGTACCACCATCCACTACAACCTACATGTGTA ACAGTTCCTGCATGGGC <u>G</u> GCATGAACCGGAGGCCCATCCTC ACCATCATCACACTGGAAGACTCCAGGTCAGGAGCCA | 169 |
| A gly245-to-ser, GGC-to-AGC, mutation was found in a patient in whom osteosarcoma was diagnosed at the age of 18 years. | TGGCTCCTGACCTGGAGTCTTCCAGTGTGATGATGGTGAGGA TGGGCCTCCGGTTCATGCC <u>G</u> CCCCATGCAGGAAGTGTACACA TGTAGTTGTAGTGGATGGTGGTACAGTCAGAGCCAAC | 170 |
| | GCATGGGC <u>G</u> GCATGAAC | 171 |
| | GTTCATGCC <u>G</u> CCCCATGC | 172 |
| In a family with the Li-Fraumeni syndrome, a germline mutation at codon 252: a T-to-C change at the second position resulted in substitution of proline for leucine. | TCCACTACAACCTACATGTGTAACAGTTCCTGCATGGGCGGCA TGAACCGGAGGCCCATCCT <u>T</u> CACCATCATCACACTGGAAGACT CCAGGTCAGGAGCCACTTGCCACCCTGCACACTGGCC | 173 |
| | GGCCAGTGTGCAGGGTGGCAAGTGGCTCCTGACCTGGAGTC TTCCAGTGTGATGATGGTG <u>A</u> GGATGGGCCTCCGGTTCATGCC GCCCATGCAGGAAGTGTACACATGTAGTTGTAGTGA | 174 |
| | GCCCATCCT <u>T</u> CACCATCA | 175 |
| | TGATGGTG <u>A</u> GGATGGGC | 176 |
| Researchers analyzed for mutations in p53 hepatocellular | TACCACCATCCACTACAACCTACATGTGTAACAGTTCCTGCATG GGCGGCATGAACCGGAG <u>G</u> CCCCATCCTCACCATCATCACACT GGAAGACTCCAGGTCAGGAGCCACTTGCCACCCTGCA | 177 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| hepatocellular carcinomas from patients in Qidong, an area of high incidence | TGCAGGGTGGCAAGTGGCTCCTGACCTGGAGTCTTCCAGTGT GATGATGGTGAGGATGGG <u>C</u> CTCCGGTTCATGCCGCCCATGC AGGAACTGTTACACATGTAGTTGTAGTGGATGGTGGTA | 178 |
| in China, in which both hepatitis B virus and aflatoxin B1 are risk factors. Eight of 16 tumors had a point mutation at the third base position of codon 249. The G-to-T mutation at codon 249 led to a change from arginine to serine (AGG to AGT). | AACCGGAG <u>G</u> CCCATCCT | 179 |
| | AGGATGGG <u>C</u> CTCCGGTT | 180 |
| In cases of hepatocellular carcinoma in southern Africa, a G-to-T substitution in codon 157 resulting in a change from valine to phenylalanine. | CTGGCCAAGACCTGCCCTGTGCAGCTGTGGGTTGATTCCACA CCCCCGCCCGGCACCCG <u>G</u> TCCGCGCCATGGCCATCTACAA GCAGTCACAGCACATGACGGAGGTTGTGAGGCGCTGCC | 181 |
| | GGCAGCGCCTCACAACCTCCGTCATGTGCTGTGACTGCTTGT AGATGGCCATGGCGCGGA <u>C</u> GCGGGTGCCGGGCGGGGGTGT GGAATCAACCCACAGCTGCACAGGGCAGGTCTTGCCAG | 182 |
| | GCACCCG <u>C</u> GTCGCGCC | 183 |
| | GGCGCGGA <u>C</u> GCGGGTGC | 184 |
| In a family with Li-Fraumeni in which noncancerous skin fibroblasts from affected individuals showed an unusual radiation-resistant phenotype, a point mutation in codon 245 of the P53 gene. A change from GGC to GAC predicted substitution of aspartic acid for glycine. | TTGGCTCTGACTGTACCACCATCCACTACAACCTACATGTGTAA CAGTTCCTGCATGGGCG <u>G</u> CATGAACCGGAGGCCCATCCTCA CCATCATCACACTGGAAGACTCCAGGTCAGGAGCCAC | 185 |
| | GTGGCTCCTGACCTGGAGTCTTCCAGTGTGATGATGGTGAGG ATGGGCCTCCGGTTCATG <u>C</u> CGCCCATGCAGGAACTGTTACAC ATGTAGTTGTAGTGGATGGTGGTACAGTCAGAGCCAA | 186 |
| | CATGGGCG <u>G</u> CATGAACC | 187 |
| | GGTTCATG <u>C</u> CGCCCATG | 188 |
| In 2 of 8 families with Li-Fraumeni syndrome, a mutation | ACTGTACCACCATCCACTACAACCTACATGTGTAAACAGTTCCTG CATGGGCGGCATGAAC <u>C</u> GAGGCCCATCCTCACCATCATCA CACTGGAAGACTCCAGGTCAGGAGCCACTTGCCACCC | 189 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| syndrome, a mutation in codon 248: a CCG-to-CAG change resulting in substitution | GGGTGGCAAGTGGCTCCTGACCTGGAGTCTTCCAGTGTGAT GATGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGG AACTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGT | 190 |
| of glutamine for arginine. | CATGAACCCGGAGGCCCA | 191 |
| | TGGGCCTCCGGTTCATG | 192 |
| In 9 members of an extended family with Li-Fraumeni syndrome, a germline mutation at codon 133 (ATG-to-ACG), resulted in the substitution of threonine for methionine (M133T), and completely cosegregated with the cancer syndrome. | CCCTGACTTTCAACTCTGTCTCCTTCCTCTTCTACAGTACTC CCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACCTG CCCTGTGCAGCTGTGGTTGATTCCACACCCCCGCC | 193 |
| | GGCGGGGGTGTGGAATCAACCCACAGCTGCACAGGGCAGGT CTTGCCAGTTGGCAAACATCTTGTTGAGGGCAGGGGAGTA CTGTAGGAAGAGGAAGGAGACAGAGTTGAAAGTCAGGG | 194 |
| | CAACAAGATGTTTTGCC | 195 |
| | GGCAAACATCTTGTTG | 196 |
| In 1 pedigree consistent with the Li-Fraumeni syndrome, a germline G-to-T transversion at codon 272 (valine to leucine) was found. | TCTTGCTTCTCTTTTCTATCCTGAGTAGTGGTAATCTACTGG GACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGA GAGACCGGCGCACAGAGGAAGAGAATCTCCGCAAGA | 197 |
| | TCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCCAG GACAGGCACAAACACGCACTCAAAGCTGTTCCGTCCCAGTA GATTACCACTACTCAGGATAGGAAAAGAGAAGCAAGA | 198 |
| | GCTTTGAGGTGCGTGTT | 199 |
| | AACACGCACTCAAAGC | 200 |
| A ser241-to-phe mutation due to a TCC-to-TTC change was found in a patient with hepatoblastoma and multiple foci of osteosarcoma. | TTATCTCCTAGGTTGGCTCTGACTGTACCACCATCCACTACAA CTACATGTGTAACAGTTCTGTCATGGGCGGCATGAACCGGAG GCCCATCCTCACCATCATCACACTGGAAGACTCCAG | 201 |
| | CTGGAGTCTTCCAGTGTGATGATGGTGAGGATGGGCCTCCG GTTTCATGCCGCCCATGCAGGAAGTGTACACATGTAGTTGTA GTGGATGGTGGTACAGTCAGAGCCAACCTAGGAGATAA | 202 |
| | TAACAGTTCTGTCATGG | 203 |
| | CCATGCAGGAAGTGTTA | 204 |
| An AAG-to-TAG change of codon 120, resulting in conversion | CAGAAAACCTACCAGGGCAGCTACGGTTTCCGTCTGGGCTTC TTGCATTCTGGGACAGCCAAAGTCTGTGACTTGACGGTCAGT TGCCCTGAGGGGCTGGCTTCCATGAGACTTCAATGCC | 205 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| resulting in conversion from lysine to a stop codon, was found in a patient with osteosarcoma and adenocarcinoma of the lung at age 18 and brain tumor (glioma) at the age of 27. | GGCATTGAAGTCTCATGGAAGCCAGCCCCTCAGGGCAACTGACCGTGCAAGTCACAGACTTGGCTGTCCCAGAATGCAAGAAGCCAGACGGAAACCGTAGCTGCCCTGGTAGGTTTTCTG | 206 |
| | GGACAGCCAAAGTCTGTG | 207 |
| | CACAGACTTGGCTGTCC | 208 |
| A CGG-to-TGG change at codon 282, resulting in the substitution of tryptophan for arginine, was found in a patient who developed osteosarcoma at the age of 10 years. | GGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCTGGGAGAGACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACACGAGCTGCCCCCAG | 209 |
| | CTGGGGGCAGCTCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTCCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATTACC | 210 |
| | GGAGAGACCGGCGCACAA | 211 |
| | TGTGCGCCGGTCTCTCC | 212 |
| In 5 of 6 anaplastic carcinomas of the thyroid and in an anaplastic carcinoma thyroid cell line ARO, a CGT-to-CAT mutation converted arginine-273 to histidine. | GCTTCTCTTTTCTATCCTGAGTAGTGGAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGG | 213 |
| | CCTTTCTTGCGGAGATTCTCTTCTCTGTGCGCCGGTCTCTCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATTACCACTACTCAGGATAGGAAAAGAGAAGC | 214 |
| | TGAGGTGCGTGTTTGTG | 215 |
| | CACAAACACGCACCTCA | 216 |
| A germline GGA-to-GTA mutation resulting in a change of glycine-325 to valine was found in a patient who had non-Hodgkin lymphoma diagnosed at age 17 and colon carcinoma at age 26. | TCCTAGCACTGCCCAACAACACCAGCTCCTCTCCCCAGCCAAAGAAGAAACCACTGGATGGAGAGAATATTTACCCTTCAGGTACTAAGTCTTGGGACCTCTTATCAAGTGGAAGTTTCCA | 217 |
| | TGGAACTTTCCACTTGATAAGAGGTCCCAAGACTTAGTACCTGAAGGGTGAAATATTCTCCATCCAGTGTTTCTTCTTTGGCTGGGAGAGGAGCTGGTGTTGTTGGGCAGTGCTAGGA | 218 |
| | ACTGGATGGAGAATATT | 219 |
| | AATATTCTCCATCCAGT | 220 |
| CGC-CCC Arg-72 to Pro | AATGGTTCACTGAAGACCCAGGTCCAGATGAAGCTCCCAGAA TGCCAGAGGCTGCTCCCCCGGTGGCCCCTGCACCAGCAGCT CCTACACCGGCGGCCCTGCACCAGCCCCCTCCTGGCC | 221 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| association with Lung cancer | GGCCAGGAGGGGGCTGGTGCAGGGGCCCGCGGTGTAGGAGCTGCTGGTGCAGGGGCCACGCGGGGAGCAGCCTCTGGCATTCTGGGAGCTTCATCTGGACCTGGGTCTTCAGTGAACCATT | 222 |
| | TGCTCCCCGCGTGGCCC | 223 |
| | GGGCCACGCGGGGAGCA | 224 |
| CCG-CTG Pro-82 to Leu Breast cancer | AAGCTCCCAGAATGCCAGAGGCTGCTCCCCGCGTGGCCCCTGCACCAGCAGCTCCTACACCGGGCGGCCCTGCACCAGCCCCCTCCTGGCCCCGTGCATCTTCTGTCCCTTCCCAGAAAAC | 225 |
| | GTTTTCTGGGAAGGGACAGAAGATGACAGGGGGCCAGGAGGGGGCTGGTGCAGGGGCCCGCGGTGTAGGAGCTGCTGGTGCAGGGGCCACGCGGGGAGCAGCCTCTGGCATTCTGGGAGCTT | 226 |
| | TCCTACACCGGGCGGCC | 227 |
| | GGGCGGCCGGTGTAGGA | 228 |
| cCAA-TAA Gln-136 to Term Li-Fraumeni syndrome | TTCAACTCTGTCTCCTTCCTCTTCTACAGTACTCCCCTGCCCCAACAAGATGTTTTGCCAACTGGCCAAGACCTGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCCGGCACCC | 229 |
| | GGGTGCCGGGCGGGGGTGTGGAATCAACCCACAGCTGCACAGGGCAGGTCTTGCCAGTTGGCAAACATCTTGTTGAGGGCAGGGAGTACTGTAGGAAGAGGAAGGAGACAGAGTTGAA | 230 |
| | TGTTTTGCCAACTGGCC | 231 |
| | GGCCAGTTGGCAAACA | 232 |
| TGC-TAC Cys-141 to Tyr Li-Fraumeni syndrome | TCCTCTTCTACAGTACTCCCCTGCCCTCAACAAGATGTTTTGCCAACTGGCCAAGACCTGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCCGGCACCCGCGTCCGCGCCATGGC | 233 |
| | GCCATGGCGCGGACGCGGGTGCCGGGCGGGGGTGTGGAATCAACCCACAGCTGCACAGGGCAGGTCTTGCCAGTTGGCAAACATCTTGTTGAGGGCAGGGGAGTACTGTAGGAAGAGGA | 234 |
| | CAAGACCTGCCCTGTGC | 235 |
| | GCACAGGGCAGGTCTTG | 236 |
| aCCC-TCC Pro-151 to Ser Li-Fraumeni syndrome | AACAAGATGTTTTGCCAACTGGCCAAGACCTGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCCCGGCACCCGCGTCCGCGCCATGGCCATCTACAAGCAGTCACAGCACATGACGG | 237 |
| | CCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGGTGCCGGGCGGGGGTGTGGAATCAACCCACAGCTGCACAGGGCAGGTCTTGCCAGTTGGCAAACATCTTGTT | 238 |
| | ATTCCACACCCCCGCCC | 239 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | GGGCGGGG <u>G</u> TGTGGAAT | 240 |
| CCG-CTG Pro-152 to Leu Adrenocortical carcinoma | AGATGTTTTGCCAACTGGCCAAGACCTGCCCTGTGCAGCTGT GGGTTGATTCCACACCCC <u>C</u> GCCCGGCACCCGCGTCCGCGCC ATGGCCATCTACAAGCAGTCACAGCACATGACGGAGGT | 241 |
| | ACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCATGGCG CGGACGCGGGTGCCGGGC <u>G</u> GGGGTGTGGAATCAACCCACA GCTGCACAGGGCAGGTCTTGGCCAGTTGGCAAAACATCT | 242 |
| | CACACCCC <u>C</u> GCCCGGCA | 243 |
| | TGCCGGGC <u>G</u> GGGGTGTG | 244 |
| GGC-GTC Gly-154 to Val Glioblastoma | TTTGCCAAGTGGCCAAGACCTGCCCTGTGCAGCTGTGGGTTG ATTCCACACCCCCGCCCC <u>G</u> CACCCGCGTCCGCGCCATGGCC ATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAG | 245 |
| | CTCACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCC ATGGCGCGGACGCGGGTG <u>C</u> CGGGCGGGGGTGTGGAATCAA CCCACAGCTGCACAGGGCAGGTCTTGGCCAGTTGGCAAA | 246 |
| | CCCGCCCG <u>G</u> CACCCGCG | 247 |
| | CGCGGGTG <u>C</u> CGGGCGGG | 248 |
| CGC-CAC Arg-175 to His Li-Fraumeni syndrome | CCCGCGTCCGCGCCATGGCCATCTACAAGCAGTCACAGCAC ATGACGGAGGTTGTGAGGC <u>G</u> CTGCCCCACCATGAGCGCTG CTCAGATAGCGATGGTGAGCAGCTGGGGCTGGAGAGACG | 249 |
| | CGTCTCTCCAGCCCCAGCTGCTCACCATCGCTATCTGAGCAG CGCTCATGGTGGGGGCAG <u>C</u> GCCTCACAACCTCCGTCATGTG CTGTGACTGCTTGTAGATGGCCATGGCGCGGACGCGGG | 250 |
| | TGTGAGGC <u>G</u> CTGCCCCC | 251 |
| | GGGGGCAG <u>C</u> GCCTCACA | 252 |
| tGAG-AAG Glu-180 to Lys Li-Fraumeni syndrome | ATGGCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTG AGGCGCTGCCCCACCAT <u>G</u> AGCGCTGCTCAGATAGCGATGG TGAGCAGCTGGGGCTGGAGAGACGACAGGGCTGGTTGC | 253 |
| | GCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGCTCACCAT CGCTATCTGAGCAGCGCT <u>C</u> ATGGTGGGGGCAGCGCCTCACA ACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGCCAT | 254 |
| | CCCACCAT <u>G</u> AGCGCTGC | 255 |
| | GCAGCGCT <u>C</u> ATGGTGGG | 256 |
| gCGC-TGC Arg-181 to Cys Breast cancer | GCCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGG CGTGCCCCACCATGAG <u>C</u> GCTGCTCAGATAGCGATGGTGA GCAGCTGGGGCTGGAGAGACGACAGGGCTGGTTGCCCA | 257 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | TGGGCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGCTCAC CATCGCTATCTGAGCAGC <u>G</u> CTCATGGTGGGGGCAGCGCCTC ACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGGC | 258 |
| | ACCATGAGC <u>G</u> CTGCTCA | 259 |
| | TGAGCAGC <u>G</u> CTCATGGT | 260 |
| CGC-CAC Arg-81 to His Breast cancer | CCATCTACAAGCAGTCACAGCACATGACGGAGGTTGTGAGGC GCTGCCCCCACCATGAGC <u>G</u> CTGCTCAGATAGCGATGGTGAG CAGCTGGGGCTGGAGAGACGACAGGGCTGGTTGCCAG | 261 |
| | CTGGGCAACCAGCCCTGTCGTCTCTCCAGCCCCAGCTGCTCA CCATCGCTATCTGAGCAGC <u>G</u> CTCATGGTGGGGGCAGCGCCT CACAACCTCCGTCATGTGCTGTGACTGCTTGTAGATGG | 262 |
| | CCATGAGC <u>G</u> CTGCTCAG | 263 |
| | CTGAGCAGC <u>G</u> CTCATGG | 264 |
| CAT-CGT His-193 to Arg Li-Fraumeni syndrome | CCAGGGTCCCCAGGCCTCTGATTCCTCACTGATTGCTCTTAG GTCTGGCCCCTCCTCAGC <u>A</u> TCTTATCCGAGTGGAAGGAAATT TGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCG | 265 |
| | CGAAAAGTGTTTCTGTCATCCAAATACTCCACACGCAAATTTTC CTTCCACTCGGATAAGAT <u>G</u> CTGAGGAGGGGCCAGACCTAAGA GCAATCAGTGAGGAATCAGAGGCCTGGGGACCCTGG | 266 |
| | TCCTCAGC <u>A</u> TCTTATCC | 267 |
| | GGATAAGAT <u>G</u> CTGAGGA | 268 |
| cCGA-TGA Arg-196 to Term Adrenocortical carcinoma | CCCAGGCCTCTGATTCCTCACTGATTGCTCTTAGGTCTGGCC CCTCCTCAGCATCTTATC <u>G</u> GAGTGGAAGGAAATTTGCGTGTG GAGTATTTGGATGACAGAAACACTTTTCGACATAGTG | 269 |
| | CACTATGTCGAAAAGTGTTTCTGTCATCCAAATACTCCACACG CAAATTTCTTCCACTC <u>G</u> GATAAGATGCTGAGGAGGGGCCAG ACCTAAGAGCAATCAGTGAGGAATCAGAGGCCTGGG | 270 |
| | ATCTTATC <u>G</u> GAGTGGAA | 271 |
| | TTCCACTC <u>G</u> GATAAGAT | 272 |
| cAGA-TGA Arg-209 to Term Li-Fraumeni syndrome | GCCCCTCCTCAGCATCTTATCCGAGTGGAAGGAAATTTGCGT GTGGAGTATTTGGATGAC <u>A</u> GAAACACTTTTCGACATAGTGTG GTGGTGCCCTATGAGCCGCCTGAGGTCTGGTTTGCAA | 273 |
| | TTGCAAACCAGACCTCAGGCGGCTCATAGGGCACCACCACAC TATGTCGAAAAGTGTTTCT <u>G</u> TGCATCCAAATACTCCACACGCAA ATTTCTTCCACTCGGATAAGATGCTGAGGAGGGGC | 274 |
| | TGGATGAC <u>A</u> GAAACACT | 275 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | AGTGTTTCTGTCATCCA | 276 |
| tCGA-TGA Arg-213 to Term Li-Fraumeni syndrome | CATCTTATCCGAGTGGAAGGAAATTTGCGTGTGGAGTATTTG GATGACAGAAACACTTTT <u>C</u> GACATAGTGTGGTGGTGCCCTAT GAGCCGCCTGAGGTCTGTTTTGCAACTGGGGTCTCTG | 277 |
| | CAGAGACCCCAGTTGCAAACCAGACCTCAGGCGGCTCATAG GGCACCACCACACTATGTCGAAAAGTGTCTGTGCATCCAAAT ACTCCACACGCAAATTTCTTCCACTCGGATAAGATG | 278 |
| | ACACTTTT <u>C</u> GACATAGT | 279 |
| | ACTATGTCCAAAAGTGT | 280 |
| gCCC-TCC Pro-219 to Ser Adrenocortical carcinoma | GGAAATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTC GACATAGTGTGGTGGTGCCCTATGAGCCGCCTGAGGTCTGG TTTGCAACTGGGGTCTCTGGGAGGAGGGTTAAGGGT | 281 |
| | ACCCTTAACCCCTCCTCCCAGAGACCCCAGTTGCAAACCAGA CCTCAGGCGGCTCATAGGGCACCACCACACTATGTGCGAAAAG TGTTTCTGTGCATCCAAATACTCCACACGCAAATTTCC | 282 |
| | TGGTGGTGCCCTATGAG | 283 |
| | CTCATAGGGCACCACCA | 284 |
| TAT-TGT Tyr-220 to Cys Li-Fraumeni syndrome | ATTTGCGTGTGGAGTATTTGGATGACAGAAACACTTTTCGACA TAGTGTGGTGGTGCCCTATGAGCCGCCTGAGGTCTGGTTTGC AACTGGGGTCTCTGGGAGGAGGGTTAAGGGTGGTT | 285 |
| | AACCACCCTTAACCCCTCCTCCCAGAGACCCCAGTTGCAAAC CAGACCTCAGGCGGCTCATAGGGCACCACCACACTATGTGCGA AAAGTGTCTGTGCATCCAAATACTCCACACGCAAAT | 286 |
| | GGTGCCCTATGAGCCGC | 287 |
| | GCGGCTCATAGGGCACC | 288 |
| cTCT-ACT Ser-227 to Thr Rhabdomyosarcoma | CACAGGTCTCCCCAAGGCGCACTGGCCTCATCTTGGGCCTGT GTTATCTCCTAGGTTGGCTCTGACTGTACCACCATCCACTACA ACTACATGTGTAACAGTTCCTGCATGGGCGGCATGA | 289 |
| | TCATGCCGCCCATGCAGGAAGTGTACACATGTAGTTGTAGT GGATGGTGGTACAGTCAGAGCCAACCTAGGAGATAACACAG GCCCAAGATGAGGCCAGTGCGCCTTGGGGAGACCTGTG | 290 |
| | AGGTTGGCTCTGACTGT | 291 |
| | ACAGTCAGAGCCAACCT | 292 |
| cCAC-AAC His-233 to Asn Glioma | GCACTGGCCTCATCTTGGGCCTGTGTTATCTCCTAGGTTGGC TCTGACTGTACCACCATCCACTACAACCTACATGTGTAACAGTT CCTGCATGGGCGGCATGAACCGGAGGCCCATCCTCA | 293 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | TGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAGGAACTG TTACACATGTAGTTGTAGTGGATGGTGGTACAGTCAGAGCCA ACCTAGGAGATAACACAGGCCCAAGATGAGGCCAGTGC | 294 |
| | CCACCATCCACTACAAC | 295 |
| | GTTGTAGTGGATGGTGG | 296 |
| cAAC-GAC Asn-235 to Asp Adrenocortical carcinoma | GCCTCATCTTGGGCCTGTGTTATCTCCTAGGTTGGCTCTGAC TGTACCACCATCCACTACA A ACTACATGTGTAACAGTTCCTGCA TGGGCGGCATGAACCGGAGGCCCATCCTCACCATCA | 297 |
| | TGATGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCAG GAACTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGTCA GAGCCAACCTAGGAGATAACACAGGCCCAAGATGAGGC | 298 |
| | TCCACTACA A ACTACATG | 299 |
| | CATGTAGTTGTAGTGGA | 300 |
| AAC-AGC Asn-235 to Ser Rhabdomyosarcoma | CCTCATCTTGGGCCTGTGTTATCTCCTAGGTTGGCTCTGACT GTACCACCATCCACTACA A CTACATGTGTAACAGTTCCTGCAT GGGCGGCATGAACCGGAGGCCCATCCTCACCATCAT | 301 |
| | ATGATGGTGAGGATGGGCCTCCGGTTCATGCCGCCCATGCA GAACTGTTACACATGTAGTTGTAGTGGATGGTGGTACAGTC AGAGCCAACCTAGGAGATAACACAGGCCCAAGATGAGG | 302 |
| | CCACTACA A CTACATGT | 303 |
| | ACATGTAGTTGTAGTGGA | 304 |
| ATCc-ATG Ile-251 to Met Glioma | CATCCACTACA A CTACATGTGTAACAGTTCCTGCATGGGCGG CATGAACCGGAGGCCCAT C CTCACCATCATCACACTGGAAGA CTCCAGGTCAGGAGCCACTTGCCACCCTGCACACTGG | 305 |
| | CCAGTGTGCAGGGTGGCAAGTGGCTCCTGACCTGGAGTCTT CCAGTGTGATGATGGTGA G ATGGGCCTCCGGTTCATGCCG CCCATGCAGGAAGTGTACACATGTAGTTGTAGTGGATG | 306 |
| | AGGCCCAT C CTCACCAT | 307 |
| | ATGGTGAG G ATGGGCCT | 308 |
| ACA-ATA Thr-256 to Ile Glioblastoma | ACATGTGTAACAGTTCCTGCATGGGCGGCATGAACCGGAGG CCCATCCTCACCATCATCA C ACTGGAAGACTCCAGGTCAGGA GCCACTTGCCACCCTGCACACTGGCCTGCTGTGCCCA | 309 |
| | TGGGGCACAGCAGGCCAGTGTGCAGGGTGGCAAGTGGCTCC TGACCTGGAGTCTTCCAGT G TGATGATGGTGAGGATGGGCCT CCGGTTCATGCCGCCCATGCAGGAAGTGTACACATGT | 310 |
| | CATCATCA C ACTGGAAG | 311 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | CTTCCAGT <u>G</u> TGATGATG | 312 |
| CTG-CAG Leu-257 to Gln Li-Fraumeni syndrome | TGTGTAACAGTTCCTGCATGGGCGGCATGAACCGGAGGCCC ATCCTCACCATCATCACACT <u>G</u> GGAAGACTCCAGGTCAGGAGCC ACTTGCCACCCTGCACACTGGCCTGCTGTGCCCCAGCC | 313 |
| | GGCTGGGGCACAGCAGGCCAGTGTGCAGGGTGGCAAGTGG CTCCTGACCTGGAGTCTTCC <u>A</u> GTGTGATGATGGTGAGGATGG GCCTCCGGTTCATGCCGCCCATGCAGGAAGTGTACACA | 314 |
| | CATCACACT <u>G</u> GGAAGACT | 315 |
| | AGTCTTCC <u>A</u> GTGTGATG | 316 |
| CTG-CCG Leu-265 to Pro Li-Fraumeni syndrome | GACCTGATTTCTTACTGCCTCTTGCTTCTTTTTCTATCCTG AGTAGTGGTAATCTACT <u>T</u> GGGACGGAACAGCTTTGAGGTGCGT GTTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGA | 317 |
| | TCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCAC CTCAAAGCTGTTCCGTCCC <u>A</u> GTAGATTACCACTACTCAGGATA GGAAAAGAGAAGCAAGAGGCAGTAAGGAAATCAGGTC | 318 |
| | TAATCTACT <u>G</u> GGACGGA | 319 |
| | TCCGTCCC <u>A</u> GTAGATTA | 320 |
| gCGT-TGT Arg-273 to Cys Li-Fraumeni syndrome | TGCTTCTCTTTTCCTATCCTGAGTAGTGGTAATCTACTGGGAC GGAACAGCTTTGAGGTG <u>C</u> GTGTTTGTGCCTGTCCTGGGAGAG ACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAG | 321 |
| | CTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGGTCTCTCC CAGGACAGGCACAAACAC <u>G</u> CACCTCAAAGCTGTTCCGTCCCA GTAGATTACCACTACTCAGGATAGGAAAAGAGAAGCA | 322 |
| | TTGAGGTG <u>C</u> GTGTTTGT | 323 |
| | ACAAACAC <u>G</u> CACCTCAA | 324 |
| TGT-TAT Cys-275 to Tyr Li-Fraumeni syndrome | CTTTTCCTATCCTGAGTAGTGGTAATCTACTGGGACGGAACA GCTTTGAGGTGCGTGTTT <u>G</u> TGCCTGTCCTGGGAGAGACCGG CGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCC | 325 |
| | GGCTCCCCTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGG TCTCTCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTC CGTCCCAGTAGATTACCACTACTCAGGATAGGAAAAG | 326 |
| | GCGTGTTT <u>G</u> TGCCTGTC | 327 |
| | GACAGGCACAAACACGC | 328 |
| CCT-CTT Pro-278 to Leu Breast cancer | TCCTGAGTAGTGGTAATCTACTGGGACGGAACAGCTTTGAGG TGCGTGTTTGTGCCTGT <u>C</u> TGGGAGAGACCGGCGCACAGAG GAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGA | 329 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | TCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATTACCACTACTCAGGA | 330 |
| | TGCCTGTCC <u>T</u> GGGAGAG | 331 |
| | CTCTCCCAGGACAGGCA | 332 |
| AGA-AAA Arg-280 to Lys Glioma | GTAGTGGTAATCTACTGGGACGGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGAGGAAGAG AATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCC | 333 |
| | GGCAGCTCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGGTCTCTCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCCGTCCCAGTAGATTACCACTAC | 334 |
| | TCCTGGGAGAGACCGGC | 335 |
| | GCCGGTCTCTCCAGGA | 336 |
| GAA-GCA Glu-286 to Ala Adrenocortical carcinoma | GGAACAGCTTTGAGGTGCGTGTTTGTGCCTGTCCTGGGAGAGACCGGCGCACAGAGGAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCCGGAGAGG | 337 |
| | CCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGCTCCCTTTCTTGCGGAGATTCTCTTCCTCTGTGCGCCGGTCTCTCCCAGGACAGGCACAAACACGCACCTCAAAGCTGTTCC | 338 |
| | AGAGGAAGAGAATCTCC | 339 |
| | GGAGATTCTCTTCCTCT | 340 |
| CGA-CCA Arg-306 to Pro Rhabdomyosarcoma | AAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCCCAGGGAGCACTAAGCGAGGTAAGCAAGCAGGACAAGAAGCGGTGGAGGAGACCAAGGGTGCA GTTATGCCTCAGAT | 341 |
| | ATCTGAGGCATAACTGCACCCTTGGTCTCCTCCACCGCTTCTTGTCCTGCTTGCTTACCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTT | 342 |
| | CACTAAGCGAGGTAAGC | 343 |
| | GCTTACCTCGCTTAGTG | 344 |
| gCGA-TGA Arg-306 to Term Li-Fraumeni syndrome | GAAGAGAATCTCCGCAAGAAAGGGGAGCCTCACCACGAGCTGCCCCAGGGAGCACTAAGCGAGGTAAGCAAGCAGGACAAGAAGCGGTGGAGGAGACCAAGGGTGCA GTTATGCCTCAGA | 345 |
| | TCTGAGGCATAACTGCACCCTTGGTCTCCTCCACCGCTTCTTGTCCTGCTTGCTTACCTCGCTTAGTGCTCCCTGGGGGCAGCTCGTGGTGAGGCTCCCCTTTCTTGCGGAGATTCTCTT | 346 |
| | GCACTAAGCGAGGTAAG | 347 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | CTTACCTC <u>G</u> CTTAGTGC | 348 |
| gCGC-TGC Arg-337 to Cys Osteosarcoma | GGTACTGTGAATATACTTACTTCTCCCCCTCCTCTGTTGCTGC AGATCCGTGGGCGTGAGC <u>G</u> CTTCGAGATGTTCCGAGAGCTG AATGAGGCCTTGGA <u>A</u> CTCAAGGATGCCCAGGCTGGGA | 349 |
| | TCCCAGCCTGGGCATCCTTGAGTTCCAAGGCCTCATTGAGCT CTCGGAACATCTCGAAGC <u>G</u> CTCACGCCACGGATCTGCAGC AACAGAGGAGGGGGAGAAGTAAGTATATTACAGTACC | 350 |
| | GGCGTGAGC <u>G</u> CTTCGAG | 351 |
| | CTCGAAGC <u>G</u> CTCACGCC | 352 |
| CTG-CCG Leu-344 to Pro Li-Fraumeni syndrome | CTCCCCCTCCTCTGTTGCTGCAGATCCGTGGGCGTGAGCGCT TCGAGATGTTCCGAGAGCT <u>G</u> AATGAGGCCTTGGA <u>A</u> CTCAAGG ATGCCCAGGCTGGGAAGGAGCCAGGGGGGAGCAGGGC | 353 |
| | GCCCTGCTCCCCCCTGGCTCCTTCCCAGCCTGGGCATCCTTG AGTTCCAAGGCCTCATT <u>C</u> AGCTCTCGGAACATCTCGAAGCGC TCACGCCACGGATCTGCAGCAACAGAGGAGGGGGAG | 354 |
| | CCGAGAGCTGAATGAGG | 355 |
| | CCTCATT <u>C</u> AGCTCTCGG | 356 |

EXAMPLE 7

beta globin

[0207] Hemoglobin, the major protein in the red blood cell, binds oxygen reversibly and is responsible for the cells' capacity to transport oxygen to the tissues. In adults, the major hemoglobin is hemoglobin A, a tetrameric protein consisting of two identical alpha globin chains and two beta globin chains. Disorders involving hemoglobin are among the most common genetic disorders worldwide, with approximately 5% of the world's population being carriers for clinically important hemoglobin mutations. Approximately 300,000 severely affected homozygotes or compound heterozygotes are born each year.

[0208] Mutation of the glutamic acid at position 7 in beta globin to valine causes sickle cell anemia, the clinical manifestations of which are well known. Mutations that cause absence of beta chain cause beta-zero-thalassemia. Reduced amounts of detectable beta globin causes beta-plus-thalassemia. For clinical purposes, beta-thalassemia is divided into thalassemia major (transfusion dependent), thalassemia intermedia (of intermediate severity), and thalassemia minor (asymptomatic). Patients with thalassemia major present in the first year of life with severe anemia; they are unable to maintain a hemoglobin level about 5 gm/dl.

[0209] The beta-thalassemias were among the first human genetic diseases to be examined by means of recombinant DNA analysis. Baysal et al., *Hemoglobin* 19(3-4):213-36 (1995) and others provide a compendium of mutations that result in beta-thalassemia.

[0210] Hemoglobin disorders were among the first to be considered for gene therapy.

- 5 Transcriptional silencing of genes transferred into hematopoietic stem cells, however, poses one of the most significant challenges to its success. If the transferred gene is not completely silenced, a progressive decline in gene expression is often observed. Position effect variegation (PEV) and silencing mechanisms may act on a transferred globin gene residing in chromatin outside of the normal globin locus during the important terminal phases of erythroblast development when globin transcripts normally
- 10 accumulate rapidly despite heterochromatinization and shutdown of the rest of the genome. The attached table discloses the correcting oligonucleotide base sequences for the beta globin oligonucleotides of the invention.

Table 8

Beta Globin Mutations and Genome-Correcting Oligos

15

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Sickle Cell Anemia GLU-7-VAL GAG to GTG | TCTGACACAACCTGTGTTCACTAGCAACCTCAAACAGACACCA TGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCC CTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGA | 357 |
| | TCACCACCAACTTCATCCACGTTACCTTGCCCCACAGGGCA GTAACGGCAGACTTCTCCTCAGGAGTCAGGTGCACCATGGT GTCTGTTTGAGGTTGCTAGTGAACACAGTTGTGTGTCAGA | 358 |
| | GACTCCTGAGGAGAAGT | 359 |
| | ACTTCTCCTCAGGAGTC | 360 |
| Thalassaemia Beta MET-0-ARG ATG to AGG | CTATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCA ACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGA AGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGT | 361 |
| | ACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTC CTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCTA GTGAACACAGTTGTGTGTCAGAAGCAAATGTAAGCAATAG | 362 |
| | AGACACCATGGTGCACC | 363 |
| | GGTGCACCATGGTGTCT | 364 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Thalassaemia Beta MET-0-ILE ATG to ATA | TATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCAA CCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAA GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTG | 365 |
| | CACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCT CCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCT AGTGAACACAGTTGTGTGAGAAGCAAATGTAAGCAATA | 366 |
| | GACACCATGGTGCACCT | 367 |
| | AGGTGCACCATGGTGTGTC | 368 |
| Thalassaemia Beta MET-0-ILE ATG to ATT | TATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCAA CCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAA GTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTG | 369 |
| | CACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCT CCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCT AGTGAACACAGTTGTGTGAGAAGCAAATGTAAGCAATA | 370 |
| | GACACCATGGTGCACCT | 371 |
| | AGGTGCACCATGGTGTGTC | 372 |
| Thalassaemia Beta MET-0-LYS ATG to AAG | CTATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCA ACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGA AGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGT | 373 |
| | ACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTC CTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCTA GTGAACACAGTTGTGTGAGAAGCAAATGTAAGCAATAG | 374 |
| | AGACACCATGGTGCACCT | 375 |
| | GGTGCACCATGGTGTCT | 376 |
| Thalassaemia Beta MET-0-THR ATG to ACG | CTATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGCA ACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGA AGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGT | 377 |
| | ACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTC CTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCTA GTGAACACAGTTGTGTGAGAAGCAAATGTAAGCAATAG | 378 |
| | AGACACCATGGTGCACCT | 379 |
| | GGTGCACCATGGTGTCT | 380 |
| Thalassaemia Beta MET-0-VAL ATG to GTG | TCTATTGCTTACATTTGCTTCTGACACAACCTGTGTTCACTAGC AACCTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAG AAGTCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACG | 381 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | CGTTCACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTCC TCAGGAGTCAGGTGCACCATGGTGTCTGTTTGAGGTTGCTAG TGAACACAGTTGTGTCAGAAGCAAATGTAAGCAATAGA | 382 |
| | CAGACACCATGGTGCAC | 383 |
| | GTGCACCATGGTGTCTG | 384 |
| Thalassaemia Beta TRP-16-Term TGG to TGA | TCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAAGT CTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAA GTTGGTGGTGAAGGCCCTGGGCAGGTTGGTATCAAGGTTA | 385 |
| | TAACCTTGATACCAACCTGCCCAGGGCCTCACCACCAACTTC ATCCACGTTACCTTGCCCACAGGGCAGTAACGGCAGACT TCTCCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGA | 386 |
| | GCCCTGTGGGGCAAGGT | 387 |
| | ACCTTGCCCCACAGGGC | 388 |
| Thalassaemia Beta TRP-16-Term TGG to TAG | CTCAAACAGACACCATGGTGCACCTGACTCCTGAGGAGAAG TCTGCCGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGA AGTTGGTGGTGAAGGCCCTGGGCAGGTTGGTATCAAGGTT | 389 |
| | AACCTTGATACCAACCTGCCCAGGGCCTCACCACCAACTTCA TCCACGTTACCTTGCCCCACAGGGCAGTAACGGCAGACTT CTCCTCAGGAGTCAGGTGCACCATGGTGTCTGTTTGA | 390 |
| | TGCCCTGTGGGGCAAGG | 391 |
| | CCTTGCCCCACAGGGCA | 392 |
| Thalassaemia Beta LYS-18-Term AAG to TAG | ACAGACACCATGGTGCACCTGACTCCTGAGGAGAAGTCTGC CGTTACTGCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTG GTGGTGAAGGCCCTGGGCAGGTTGGTATCAAGGTTACAAG | 393 |
| | CTTGTAACCTTGATACCAACCTGCCCAGGGCCTCACCACCAA CTTCATCCACGTTACCTTGCCCCACAGGGCAGTAACGGCA GACTTCTCCTCAGGAGTCAGGTGCACCATGGTGTCTGT | 394 |
| | TGTGGGGCAAGGTGAAC | 395 |
| | GTTACCTTGCCCCACA | 396 |
| Thalassaemia Beta ASN-20-SER AAC to AGC | CCATGGTGCACCTGACTCCTGAGGAGAAGTCTGCCGTTACT GCCCTGTGGGGCAAGGTGAACGTGGATGAAGTTGGTGGTGA GGCCCTGGGCAGGTTGGTATCAAGGTTACAAGACAGGTT | 397 |
| | AACCTGTCTTGTAACCTTGATACCAACCTGCCCAGGGCCTCA CCACCAACTTCATCCACGTTACCTTGCCCCACAGGGCAGTA ACGGCAGACTTCTCCTCAGGAGTCAGGTGCACCATGG | 398 |
| | CAAGGTGAACGTGGATG | 399 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | | |
| | CATCCACGTTACCTTG | 400 |
| Thalassaemia Beta GLU-23-ALA GAA to GCA | ACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTGG GGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGCCCTGG GCAGGTTGGTATCAAGGTTACAAGACAGGTTTAAGGAGAC | 401 |
| | GTCTCCTTAAACCTGTCTTGTAACCTTGATACCAACCTGCCCA GGGCCTCACCACCAACTTCATCCACGTTACCTTGCCCCACA GGGCAGTAACGGCAGACTTCTCCTCAGGAGTCAGGT | 402 |
| | CGTGGATGAAGTTGGTG | 403 |
| | CACCAACTTCATCCACG | 404 |
| Thalassaemia Beta GLU-23-term GAA to TAA | CACCTGACTCCTGAGGAGAAGTCTGCCGTTACTGCCCTGTG GGGCAAGGTGAACGTGGATGAAGTTGGTGGTGAGGCCCTG GGCAGGTTGGTATCAAGGTTACAAGACAGGTTTAAGGAGA | 405 |
| | TCTCCTTAAACCTGTCTTGTAACCTTGATACCAACCTGCCCAG GGCCTCACCACCAACTTCATCCACGTTACCTTGCCCCACAG GGCAGTAACGGCAGACTTCTCCTCAGGAGTCAGGTG | 406 |
| | ACGTGGATGAAGTTGGT | 407 |
| | ACCAACTTCATCCACGT | 408 |
| Thalassaemia Beta GLU-27-LYS GAG to AAG | GAGGAGAAGACTGCTGTCAATGCCCTGTGGGGCAAAGTGAA CGTGGATGCAGTTGGTGGTGAGGCCCTGGGCAGGTTGGTAT CAAGGTTATAAGAGAGGCTCAAGGAGGCAAATGGAACT | 409 |
| | AGTTTCCATTTGCCTCCTTGAGCCTCTCTTATAACCTTGATAC CAACCTGCCCAGGGCCTCACCACCAACTGCATCCACGTTCA CTTGCCCCACAGGGCATTGACAGCAGTCTTCTCCTC | 410 |
| | TTGGTGGTGAGGCCCTG | 411 |
| | CAGGGCCTCACCACCAA | 412 |
| Thalassaemia Beta GLU-27-Term GAG to TAG | GAGGAGAAGACTGCTGTCAATGCCCTGTGGGGCAAAGTGAA CGTGGATGCAGTTGGTGGTGAGGCCCTGGGCAGGTTGGTAT CAAGGTTATAAGAGAGGCTCAAGGAGGCAAATGGAACT | 413 |
| | AGTTTCCATTTGCCTCCTTGAGCCTCTCTTATAACCTTGATAC CAACCTGCCCAGGGCCTCACCACCAACTGCATCCACGTTCA CTTGCCCCACAGGGCATTGACAGCAGTCTTCTCCTC | 414 |
| | TTGGTGGTGAGGCCCTG | 415 |
| | CAGGGCCTCACCACCAA | 416 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Thalassaemia Beta ALA-28-SER GCC to TCC | GAGAAGACTGCTGTCAATGCCCTGTGGGGCAAAGTGAACGT GGATGCAGTTGGTGGTGAAGGCCCTGGGCAGGTTGGTATCAA GGTTATAAGAGAGGCTCAAGGAGGCAAATGGAAACTGGG | 417 |
| | CCCAGTTTCCATTTGCCTCCTTGAGCCTCTCTTATAACCTTGA TACCAACCTGCCCAGGGCCTCACCACCAACTGCATCCACGTT CACTTTGCCCCACAGGGCATTGACAGCAGTCTTCTC | 418 |
| | GTGGTGAGGCCCTGGGC | 419 |
| | GCCCAGGGCCTCACCAC | 420 |
| Thalassaemia Beta ARG-31-THR AGG to ACG | CTGTCAATGCCCTGTGGGGCAAAGTGAACGTGGATGCAGTT GGTGGTGAGGCCCTGGGCAAGTTGGTATCAAGGTTATAAGA GAGGCTCAAGGAGGCAAATGGAACTGGGCATGTGTAGA | 421 |
| | TCTACACATGCCAGTTTCCATTTGCCTCCTTGAGCCTCTCTT ATAACCTTGATACCAACCTGCCAGGGCCTCACCACCAACTG CATCCACGTTCACTTTGCCCCACAGGGCATTGACAG | 422 |
| | CCTGGGCAGGTTGGTAT | 423 |
| | ATACCAACCTGCCAGG | 424 |
| Thalassaemia Beta Leu-33-GLN CTG to CAG | TGGGTTTCTGATAGGCACTGACTCTCTGTCCCTTGGGCTGTT TTCCTACCCTCAGATTACTGGTGGTCTACCCTTGGACCCAGA GGTTCTTTGAGTCCTTTGGGGATCTGTCCTCTCCTGA | 425 |
| | TCAGGAGAGGACAGATCCCCAAAGGACTCAAAGAACCTCTG GGTCCAAGGGTAGACCACCAAGTAATCTGAGGGTAGGAAAAC AGCCCAAGGGACAGAGAGTCAGTGCCTATCAGAAACCCA | 426 |
| | CAGATTACTGGTGGTCT | 427 |
| | AGACCACCAAGTAATCTG | 428 |
| Thalassaemia Beta TYR-36-Term TAC to TAA | ATAGGCACTGACTCTCTGTCCCTTGGGCTGTTTTCTACCCT CAGATTACTGGTGGTCTACCTTGGACCCAGAGGTTCTTTGA GTCCTTTGGGGATCTGTCCTCTCCTGATGCTGTTATG | 429 |
| | CATAACAGCATCAGGAGAGGACAGATCCCCAAAGGACTCAA AGAACCTCTGGGTCCAAGGGTAGACCACCAAGTAATCTGAGG GTAGGAAAACAGCCCAAGGGACAGAGAGTCAGTGCCTAT | 430 |
| | GTGGTCTACCTTGGAC | 431 |
| | GTCCAAGGGTAGACCAC | 432 |
| Thalassaemia Beta TRP-38-Term TGG to TGA | ACTGACTCTCTGTCCCTTGGGCTGTTTTCTACCCTCAGATTA CTGGTGGTCTACCCTTGGACCCAGAGGTTCTTTGAGTCCTTT GGGGATCTGTCCTCTCCTGATGCTGTTATGGGCAAC | 433 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | GTTGCCCAT AACAGCATCAGGAGAGGACAGATCCCCAAAGG ACTCAAAGAACCTCTGGGTCCAAGGGTAGACCACCAGTAATC TGAGGGTAGGAAAACAGCCCAAGGGACAGAGAGTCAGT | 434 |
| | TACCCTTG <u>G</u> ACCCAGAG | 435 |
| | CTCTGGGTCCAAGGGTA | 436 |
| Thalassaemia Beta TRP-38-Term TGG to TAG | CACTGACTCTCTGTCCCTTGGGCTGTTTTCTACCCTCAGAT TACTGGTGGTCTACCCTTGACCCAGAGGTTCTTTGAGTCCT TTGGGGATCTGTCCTCTCCTGATGCTGTTATGGGCAA | 437 |
| | TTGCCCAT AACAGCATCAGGAGAGGACAGATCCCCAAAGGA CTCAAAGAACCTCTGGGTCCAAGGGTAGACCACCAGTAATCT GAGGGTAGGAAAACAGCCCAAGGGACAGAGAGTCAGTG | 438 |
| | CTACCCTTGACCCAGA | 439 |
| | TCTGGGTCCAAGGGTAG | 440 |
| Thalassaemia Beta GLN-40-Term CAG-TAG | ACTCTCTGTCCCTTGGGCTGTTTTCTACCCTCAGATTACTG GTGGTCTACCCTTGACCCAGAGGTTCTTTGAGTCCTTTGGG GATCTGTCCTCTCCTGATGCTGTTATGGGCAACCCTA | 441 |
| | TAGGGTTGCCCAT AACAGCATCAGGAGAGGACAGATCCCCA AAGGACTCAAAGAACCTCTGGGTCCAAGGGTAGACCACCAG TAATCTGAGGGTAGGAAAACAGCCCAAGGGACAGAGAGT | 442 |
| | CTTGACCCAGAGGTTCT | 443 |
| | GAACCTCTGGGTCCAAG | 444 |
| Thalassaemia Beta GLU-44-Term GAG to TAG | TTGGGCTGTTTTCTACCCTCAGATTACTGGTGGTCTACCCT TGGACCCAGAGGTTCTTTGAGTCCTTTGGGGATCTGTCCTCT CCTGATGCTGTTATGGGCAACCCTAAGGTGAAGGCTC | 445 |
| | GAGCCTTCACCTTAGGGTTGCCCAT AACAGCATCAGGAGAG GACAGATCCCCAAAGGACTCAAAGAACCTCTGGGTCCAAGG GTAGACCACCAGTAATCTGAGGGTAGGAAAACAGCCCAA | 446 |
| | GGTTCTTTGAGTCCTTT | 447 |
| | AAAGGACTCAAAGAACC | 448 |
| Thalassaemia Beta LYS-62-Term AAG to TAG | TTCTTTGAGTCCTTTGGGGATCTGTCCTCTCCTGATGCTGTTA TGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAGGTGCTA GGTGCCCTTAGTGATGGCCTGGCTCACCTGGACAACC | 449 |
| | GGTTGTCCAGGTGAGCCAGGCCATCACTAAAGGCACCTAGC ACCTTCTTGCCATGAGCCTTACCTTAGGGTTGCCCATACA GCATCAGGAGAGGACAGATCCCCAAAGGACTCAAAGAA | 450 |
| | CTAAGGTGAAGGCTCAT | 451 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | | |
| | ATGAGCCTTCACCTTAG | 452 |
| Thalassaemia Beta SER-73-ARG AGT to AGA | TGCTGTTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGA AGGTGCTAGGTGCCTTTAGTGATGGCCTGGCTCACCTGGAC AACCTCAAGGGCACTTTTTCTCAGCTGAGTGAGCTGCAC | 453 |
| | GTGCAGCTCACTCAGCTGAGAAAAAGTGCCCTTGAGGTTGTC CAGGTGAGCCAGGCCATCACTAAAGGCACCTAGCACCTTCT TGCCATGAGCCTTCACCTTAGGGTTGCCATAACAGCA | 454 |
| | GCCTTTAGTGATGGCCT | 455 |
| | AGGCCATCACTAAAGGC | 456 |
| Haemolytic Anaemia GLY-75-VAL GGC to GTC | TTATGGGCAACCCTAAGGTGAAGGCTCATGGCAAGAAGGTG CTAGGTGCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTC AAGGGCACTTTTTCTCAGCTGAGTGAGCTGCACTGTGA | 457 |
| | TCACAGTGCAGCTCACTCAGCTGAGAAAAAGTGCCCTTGAG GTTGTCCAGGTGAGCCAGGCCATCACTAAAGGCACCTAGCA CCTTCTTGCCATGAGCCTTCACCTTAGGGTTGCCATAA | 458 |
| | TAGTGATGGCCTGGCTC | 459 |
| | GAGCCAGGCCATCACTA | 460 |
| Thalassaemia Beta GLU-91-Term GAG to TAG | GCCTTTAGTGATGGCCTGGCTCACCTGGACAACCTCAAGGG CACCTTTGCCACACTGAGTGAGCTGCACTGTGACAAGCTGCA CGTGGATCCTGAGAACTTCAGGGTGAGTCTATGGGACC | 461 |
| | GGTCCCATAGACTCACCCTGAAGTTCTCAGGATCCACGTGCA GCTTGTACAGTGCAGCTCACTCAGTGTGGCAAAGGTGCCC TTGAGGTTGTCCAGGTGAGCCAGGCCATCACTAAAGGC | 462 |
| | CACTGAGTGAGCTGCAC | 463 |
| | GTGCAGCTCACTCAGTG | 464 |
| Thalassaemia Beta VAL-99-MET GTG to ATG | CTGGACAACCTCAAGGGCACTTTTTCTCAGCTGAGTGAGCTG CACTGTGACAAGCTGCACGTGGATCCTGAGAACTTCAGGGT GAGTCCAGGAGATGCTTCACTTTTCTCTTTTACTTTT | 465 |
| | GAAAGTAAAAAGAGAAAAGTGAAGCATCTCCTGGACTCACCC TGAAGTTCTCAGGATCCAAGTGCAGCTTGTACAGTGCAGCT CACTCAGCTGAGAAAAAGTGCCCTTGAGGTTGTCCAG | 466 |
| | AGCTGCACGTGGATCCT | 467 |
| | AGGATCCACGTGCAGCT | 468 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Thalassaemia Beta LEU-111-PRO CTG-CCG | CCCTTTTGCTAATCATGTTTCATACCTCTTATCTTCCTCCCACA GCTCCTGGGCAACGTGCTGGTCTGTGTGCTGGCCCATCACT TTGGCAAAGAATTCACCCCACCAGTGCAGGCTGCCTA | 469 |
| | TAGGCAGCCTGCACTGGTGGGGTGAATTCTTTGCCAAAGTG ATGGGCCAGCACACAGACCAGCACGTTGCCCAGGAGCTGTG GGAGGAAGATAAGAGGTATGAACATGATTAGCAAAGGG | 470 |
| | CAACGTGCTGGTCTGTG | 471 |
| | CACAGACCAGCACGTTG | 472 |
| Thalassaemia Beta CYS-113-Term TGT to TGA | GCTAATCATGTTTCATACCTCTTATCTTCCTCCCACAGCTCCTG GGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAA AGAATTCACCCCACCAGTGCAGGCTGCCTATCAGAAA | 473 |
| | TTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCTTTGCC AAAGTGATGGGCCAGCACACAGACCAGCACGTTGCCCAGGA GCTGTGGGAGGAAGATAAGAGGTATGAACATGATTAGC | 474 |
| | CTGGTCTGTGTGCTGGC | 475 |
| | GCCAGCACACAGACCAG | 476 |
| Thalassaemia Beta LEU-115-PRO CTG to CCG | TCATGTTTCATACCTCTTATCTTCCTCCCACAGCTCCTGGGCAA CGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATT CACCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGT | 477 |
| | ACCACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCT TTGCCAAAGTGATGGGCCAGCACACAGACCAGCACGTTGCC CAGGAGCTGTGGGAGGAAGATAAGAGGTATGAACATGA | 478 |
| | CTGTGTGCTGGCCCATC | 479 |
| | GATGGGCCAGCACACAG | 480 |
| Thalassaemia Beta ALA-116-ASP GCC to GAC | TGTTTCATACCTCTTATCTTCCTCCCACAGCTCCTGGGCAACG TGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCA CCCCACCAGTGCAGGCTGCCTATCAGAAAGTGGTGGC | 481 |
| | GCCACCACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAA TTCTTTGCCAAAGTGATGGGCCAGCACACAGACCAGCACGTT GCCCAGGAGCTGTGGGAGGAAGATAAGAGGTATGAACA | 482 |
| | TGTGCTGGCCCATCACT | 483 |
| | AGTGATGGGCCAGCAC | 484 |
| Thalassaemia Beta GLU-122-Term GAA to TAA | TTCCTCCCACAGCTCCTGGGCAACGTGCTGGTCTGTGTGCT GGCCCATCACTTTGGCAAAGAATTCACCCCACCAGTGCAGG CTGCCTATCAGAAAGTGGTGGCTGGTGTGGCTAATGCCC | 485 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | GGGCATTAGCCACACCAGCCACCACTTTCTGATAGGCAGCC TGCACTGGTGGGGTGAATTCTTTGCCAAAGTGATGGGCCAG CACACAGACCAGCACGTTGCCAGGAGCTGTGGGAGGAA | 486 |
| | TTGGCAAAGAATTCACC | 487 |
| | GGTGAATTCTTTGCCAA | 488 |
| Thalassaemia Beta GLN-128-PRO CAG to CCG | GCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAA GAATTCACCCACCAAGTGCAGGCTGCCTATCAGAAAGTGGT GGCTGGTGTGGCTAATGCCCTGGCCACAAGTATCACTA | 489 |
| | TAGTGATACTTGTGGGCCAGGGCATTAGCCACACCAGCCAC CACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCTTT GCCAAAGTGATGGGCCAGCACACAGACCAGCACGTTGC | 490 |
| | ACCAGTGCAGGCTGCCT | 491 |
| | AGGCAGCCTGCACTGGT | 492 |
| Thalassaemia Beta GLN-128-Term CAG to TAG | GGCAACGTGCTGGTCTGTGTGCTGGCCCATCACTTTGGCAA AGAATTCACCCACCAAGTGCAGGCTGCCTATCAGAAAGTGGT GGCTGGTGTGGCTAATGCCCTGGCCACAAGTATCACT | 493 |
| | AGTGATACTTGTGGGCCAGGGCATTAGCCACACCAGCCACC ACTTTCTGATAGGCAGCCTGCACTGGTGGGGTGAATTCTTTG CCAAAGTGATGGGCCAGCACACAGACCAGCACGTTGCC | 494 |
| | CACCAGTGCAGGCTGCC | 495 |
| | GGCAGCCTGCACTGGTG | 496 |
| Thalassaemia Beta GLN-132-LYS CAG to AAG | GTCTGTGTGCTGGCCCATCACTTTGGCAAAGAATTCACCCCA CCAGTGCAGGCTGCCTATCAGAAAGTGGTGGCTGGTGTGGC TAATGCCCTGGCCACAAGTATCACTAAGCTCGCTTTC | 497 |
| | GAAAGCGAGCTTAGTGATACTTGTGGGCCAGGGCATTAGCC ACACCAGCCACCACTTTCTGATAGGCAGCCTGCACTGGTGG GGTGAATTCTTTGCCAAAGTGATGGGCCAGCACACAGAC | 498 |
| | CTGCCTATCAGAAAGTG | 499 |
| | CACTTTCTGATAGGCAG | 500 |

EXAMPLE 8

Retinoblastoma

- [0211] Retinoblastoma (RB) is an embryonic neoplasm of retinal origin. It almost
5 always presents in early childhood and is often bilateral. The risk of osteogenic sarcoma is increased

500-fold in bilateral retinoblastoma patients, the bone malignancy being at sites removed from those exposed to radiation treatment of the eye tumor.

[0212] The retinoblastoma susceptibility gene (pRB; pRb) plays a pivotal role in the regulation of the cell cycle. pRB restrains cell cycle progression by maintaining a checkpoint in late G₁ that controls commitment of cells to enter S phase. The critical role that pRB plays in cell cycle regulation explains its status as archetypal tumor suppressor: loss of pRB function results in an inability to maintain control of the G₁ checkpoint; unchecked progression through the cell cycle is, in turn, a hallmark of neoplasia.

[0213] Blanquet *et al.*, *Hum. Molec. Genet.* 4: 383-388 (1995) performed a mutation survey of the RB1 gene in 232 patients with hereditary or nonhereditary retinoblastoma. They systematically explored all 27 exons and flanking sequences, as well as the promoter. All types of point mutations were represented and found to be unequally distributed along the RB1 gene sequence. In the population studied, exons 3, 8, 18, and 19 were preferentially altered. The attached table discloses the correcting oligonucleotide base sequences for the retinoblastoma oligonucleotides of the invention.

Table 9

pRB Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Retinoblastoma Trp99Term TGG-TAG | AATATTTGATCTTTATTTTTGTTCCAGGGAGGTTATATTCAA AAGAAAAGGAACTGTGGGGAATCTGTATCTTTATTGCAGCA GTTGACCTAGATGAGATGTCGTTCACTTTTACTGA | 501 |
| | TCAGTAAAAGTGAACGACATCTCATCTAGGTCAACTGCTGCA ATAAAGATACAGATTCCCACAGTTCCTTTTCTTTTGAATATA ACCTCCCTGGGAACAAAAATAAAGATCAAATATT | 502 |
| | GGAAGTGTGGGGAATCT | 503 |
| | AGATTCCTCCACAGTTCC | 504 |
| Retinoblastoma Glu137Asp GAA-GAT | ATTTACTTTTTCTATTCTTTCCTTTGTAGTGTCCATAAATTCTT TAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGATAAT GCTATGTCAAGACTGTTGAAGAAGTATGATGTA | 505 |
| | TACATCATACTTCTTCAACAGTCTTGACATAGCATTATCAACT TTGGTACTGGTATCAATTCTTTTAGTAAGTTAAAGAATTTATG GACACTACAAAGGAAAGAATAGAAAAAGTAAAT | 506 |
| | CTAAAAGAAATTGATAC | 507 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | GTATCAAT <u>T</u> TCTTTTAG | 508 |
| Retinoblastoma Glu137Term GAA-TAA | TGATTTACTTTTTTCTATTCTTTCTTTGTAGTGTCCATAAATT CTTTAACTTACTAAAAGAAATTGATACCAGTACCAAAGTTGAT AATGCTATGTCAAGACTGTTGAAGAAGTATGATG | 509 |
| | CATCATACTTCTTCAACAGTCTTGACATAGCATTATCAACTTT GGTACTGGTATCAATTTCTTTTAGTAAGTTAAAGAATTTATGG ACACTACAAAGGAAAGAATAGAAAAAAGTAAATCA | 510 |
| | TACTAAAAGAAATTGAT | 511 |
| | ATCAATTTCTTTTAGTA | 512 |
| Retinoblastoma Gln176Term C | AAAATGTTAAAAAGTCATAATGTTTTCTTTTCAGGACATGTG AACTTATATATTTGACACAACCCAGCAGTTCGTAAGTAGTTCA CAGAATGTTATTTTCACTTAAAAAAAAGATTTT | 513 |
| | AAAATCTTTTTTTTTAAGTGAAAAATAACATTCTGTGAACTACT TACGAACTGCTGGGTTGTGTCAAATATATAAGTTCACATGTCC TGAAAAGAAAAACATTATGACTTTTAAACATTTT | 514 |
| | ATTTGACACAACCCAGC | 515 |
| | GCTGGGTTGTGTCAAAT | 516 |
| Retinoblastoma Ile185Thr ATA-ACA | TGATACATTTTCTGTTTTTTTTCTGCTTTCTATTTGTTTAATA GGATATCTACTGAAAATAATTCTGCATTGGTGCTAAAAGTTTC TTGGATCACATTTTATTAGCTAAAGGTAAGTT | 517 |
| | AACTTACCTTTAGCTAATAAAAATGTGATCCAAGAACTTTTA GCACCAATGCAGAATTTATTTTCAGTAGATATCCTATTAAACAA ATAGAAAGCAGAAAAAAACAGGAAAAATGTATCA | 518 |
| | TACTGAAATAAATTCTG | 519 |
| | CAGAATTTATTTTCAGTA | 520 |
| Retinoblastoma Gln207Term CAA-TAA | AAAGATCTGAATCTCTAACTTTCTTTAAAAATGTACATTTTTTT TTCAGGGGAAGTATTCAAATGGAAGATGATCTGGTGATTTTC ATTTTCAGTTAATGCTATGTGTCCTTGACTATTTTA | 521 |
| | TAAAATAGTCAAGGACACATAGCATTAACTGAAATGAAATCAC CAGATCATCTTCCATTTGTAATACTTCCCCTGAAAAAAAATG TACATTTTTAAAGAAAGTTAGAGATTCAGATCTTT | 522 |
| | AAGTATTACAATGGAA | 523 |
| | TTCCATTTGTAATACTT | 524 |
| Retinoblastoma Arg251Term CGA to TGA | GTTCTTATCTAATTTACCACTTTTACAGAAACAGCTGTTATAC CCATTAATGGTTCACCTCGAACACCCAGGCGAGGTCAGAACAA GGAGTGCACGGATAGCAAAACAAGTAGAAAATGATA | 525 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | TATCATTCTTAGTTGTTTTGCTATCCGTGCACTCCTGTTCTG ACCTCGCCTGGGTGTTCCAGGTGAACCATTAAATGGGTATAAC AGCTGTTTCTGTAAAAGTGGTAAATTAGATAAGAAC | 526 |
| | GTTACCTCGAACACCC | 527 |
| | GGGTGTTCCAGGTGAAC | 528 |
| Retinoblastoma Arg255Term CGA to TGA | TTTACCACTTTTACAGAAACAGCTGTTATACCCATTAAATGGTT CACCTCGAACACCCAGGCGAGGTGAGAACAGGAGTGACCGG ATAGCAAAACAACCTAGAAAATGATACAAGAATTATTG | 529 |
| | CAATAATTCTTGTATCATTTTTCTAGTTGTTTTGCTATCCGTGCA CTCCTGTTCTGACCTCGCCTGGGTGTTGAGGTGAACCATTAA ATGGGTATAACAGCTGTTTCTGTAAAAGTGGTAAA | 530 |
| | CACCCAGGCGAGGTCAG | 531 |
| | CTGACCTCGCCTGGGTG | 532 |
| Retinoblastoma Gln266Te | ATTAATGGTTCACCTCGAACACCCAGGCGAGGTGAGAACAG GAGTGCACGGATAGCAAAACAACCTAGAAAATGATACAAGAAT TATTGAAGTTCTCTGTAAAGAACATGAATGTAATATAG | 533 |
| | CTATATTACATTCATGTTCTTTACAGAGAACTTCAATAATTCTT GTATCATTTTTCTAGTTGTTTTGCTATCCGTGCACTCCTGTTCT GACCTCGCCTGGGTGTTGAGGTGAACCATTAAAT | 534 |
| | TAGCAAAACAACCTAGAA | 535 |
| | TTCTAGTTGTTTTGCTA | 536 |
| Retinoblastoma Arg320Term CGA to TGA | TGACATGTAAAGGATAATTGTCAGTGACTTTTTCTTTCAAGG TTGAAAATCTTTCTAAACGATACGAAGAAATTTATCTTAAAAAT AAAGATCTAGATGCAAGATTATTTTTGGATCATG | 537 |
| | CATGATCCAAAAATAATCTTGCATCTAGATCTTTATTTTAAAGA TAAATTTCTTCGTATCGTTTAGAAAGATTTTCAACCTTGAAAG AAAAAAGTCACTGACAATTATCCTTTACATGTCA | 538 |
| | TTTCTAAACGATACGAA | 539 |
| | TTCGTATCGTTTAGAAA | 540 |
| Retinoblastoma Gln354Term CAG to TAG | ACAAATTGTAAATTTTCAGTATGTGAATGACTTCACTTATTGTT ATTTAGTTTTGAAACAAGAGAACACCACGAAAAAGTAACCTT GATGAAGAGGTGAATGTAATTCCTCCACACACTC | 541 |
| | GAGTGTGTGGAGGAATTACATTACCTCTTCATCAAGGTTAC TTTTTCGTGGTGTTCTCTGTGTTTCAAACTAAATAACAATAA GTGAAGTCATTCACATACTGAAAATTTACAATTTGT | 542 |
| | TTGAAACAAGAGAACAA | 543 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | TGTTCTCT <u>G</u> TGTTTCAA | 544 |
| Retinoblastoma Arg358Gly CGA to GGA | TTTTCAGTATGTGAATGACTTCACTTATTGTTATTTAGTTTTGA AACACAGAGAACACCAC <u>G</u> AAAAAGTAACCTTGATGAAGAGGT GAATGTAATTCCTCCACACACTCCAGTTAGGTATG | 545 |
| | CATACCTAACTGGAGTGTGTGGAGGAATTACATTCACCTCTT CATCAAGGTTACTTTTT <u>C</u> GTGGTGTTCTCTGTGTTTCAAACT AAATAACAATAAGTGAAGTCATTCACATACTGAAAA | 546 |
| | GAACACCAC <u>G</u> AAAAAGT | 547 |
| | ACTTTTT <u>C</u> GTGGTGTTT | 548 |
| Retinoblastoma Ar | TTTTCAGTATGTGAATGACTTCACTTATTGTTATTTAGTTTTGA AACACAGAGAACACCAC <u>G</u> AAAAAGTAACCTTGATGAAGAGGT GAATGTAATTCCTCCACACACTCCAGTTAGGTATG | 549 |
| | CATACCTAACTGGAGTGTGTGGAGGAATTACATTCACCTCTT CATCAAGGTTACTTTTT <u>C</u> GTGGTGTTCTCTGTGTTTCAAACT AAATAACAATAAGTGAAGTCATTCACATACTGAAAA | 550 |
| | GAACACCAC <u>G</u> AAAAAGT | 551 |
| | ACTTTTT <u>C</u> GTGGTGTTT | 552 |
| Retinoblastoma Ser397Term TCA to TAA | CTGTTATGAACACTATCCAACAATTAATGATGATTTTAAATTCA GCAAGTGATCAACCTT <u>C</u> AGAAAATCTGATTTTCTATTTTAACTG TAAGCCATATATGAAACATTATTTATTGTAATAT | 553 |
| | ATATTACAATAAATAATGTTTCATATATGGCTTACGTTAAAATA GGAAATCAGATTTTCT <u>G</u> AAGGTTGATCACTTGCTGAATTTAAA ATCATCATTAAATTGTTGGATAGTGTTCATAACAG | 554 |
| | TCAACCTT <u>C</u> AGAAAATC | 555 |
| | GATTTTCT <u>G</u> AAGGTTGA | 556 |
| Retinoblastoma Arg445Term CGA to TGA | TTTCATAATTGTGATTTTCTAAAATAGCAGGCTCTTATTTTTCT TTTTGTTTGTGTTAG <u>C</u> GATACAACTTGGAGTTGCTTGTAT TACCGAGTAATGGAATCCATGCTTAAATCAGTAA | 557 |
| | TTACTGATTTAAGCATGGATTCCATTACTCGGTAATACAAGCG AACTCCAAGTTTGTATC <u>G</u> CTACAAACAAACAAAAAGAAAAATA AGAGCCTGCTATTTTAGAAAATCACAATTATGAAA | 558 |
| | GTTTGTAG <u>C</u> GATACAAA | 559 |
| | TTTGTATC <u>G</u> CTACAAAC | 560 |
| Retinoblastoma Arg455Term CGA to TGA | GCTCTTATTTTTCTTTTTGTTTGTGTTGTAGCGATACAACTTGG AGTTGCTTGTATTAC <u>G</u> GAGTAATGGAATCCATGCTTAAATCA GTAAGTTAAAAACAATATAAAAAAATTTAGCCG | 561 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | CGGCTGAAATTTTTTATATTGTTTTAACTTACTGATTTAAGC ATGGATTCCATTACTC <u>G</u> GTAATACAAGCGAACTCCAAGTTTGT ATCGCTACAAACAAACAAAAAGAAAAATAAGAGC | 562 |
| | TGTATTAC <u>C</u> GAGTAATG | 563 |
| | CATTACTC <u>G</u> GTAATACA | 564 |
| Retinoblastoma Arg552Term CGA to TGA | ATCGAAAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAA ATGATAAAACATTTAGA <u>C</u> GATGTGAACATCGAATCATGGAAT CCCTTGCATGGCTCTCAGTAAGTAGCTAAATAATTG | 565 |
| | CAATTATTTAGCTACTTACTGAGAGCCATGCAAGGGATTCCAT GATTGATGTTACATC <u>G</u> TTCTAAATGTTTTATCATTTCTCTTG TCAAGTTGCCTTCTGCTTTGATAAACTTTTCGAT | 566 |
| | ATTTAGA <u>A</u> C <u>G</u> ATGTGAA | 567 |
| | TTCACATC <u>G</u> TTCTAAAT | 568 |
| Retinoblastoma Cys553Term TGT to TGA | AAGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGAT AAAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT GCATGGCTCTCAGTAAGTAGCTAAATAATTGAAGAA | 569 |
| | TTCTTCAATTATTTAGCTACTTACTGAGAGCCATGCAAGGGAT TCCATGATTGATGTT <u>C</u> ACATCGTTCTAAATGTTTTATCATTTT TCTTGTCAGTTGCCTTCTGCTTTGATAAACTT | 570 |
| | GAACGATGTGAACATCG | 571 |
| | CGATGTT <u>C</u> ACATCGTTC | 572 |
| Retinoblastoma Glu554Term GAA to TAA | AGTTTTATCAAAGCAGAAGGCAACTTGACAAGAGAAATGATA AAACATTTAGAACGATGTGAACATCGAATCATGGAATCCCTT GCATGGCTCTCAGTAAGTAGCTAAATAATTGAAGAAA | 573 |
| | TTTCTTCAATTATTTAGCTACTTACTGAGAGCCATGCAAGGGA TTCCATGATTGATGTT <u>C</u> ACATCGTTCTAAATGTTTTATCATTT CTTTGTCAAGTTGCCTTCTGCTTTGATAAACT | 574 |
| | AACGATGTGAACATCGA | 575 |
| | TCGATGTT <u>C</u> ACATCGTT | 576 |
| Retinoblastoma Ser567Leu TCA to TTA | TACCTGGGAAAATTATGCTTACTAATGTGGTTTTAATTTATC ATGTTTCATATAGGATT <u>C</u> ACCTTTATTTGATCTTATTAACAAT CAAAGGACCGAGAAGGACCAACTGATCACCTTGA | 577 |
| | TCAAGGTGATCAGTTGGTCCTTCTCGGTCCTTTGATTGTTTAA TAAGATCAAATAAAGGTGAATCCTATATGAAACATGATGAAAT TAAACCACATTAGTAAGCATAATTTCCAGGTA | 578 |
| | ATAGGATT <u>C</u> ACCTTTAT | 579 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | ATAAAGGTGAATCCTAT | 580 |
| Retinoblastoma Gln575Term CAA to TAA | AATGTGGTTTTAATTTTCATCATGTTTCATATAGGATTCACCTTT ATTTGATCTTATTAACAATCAAAGGACCGAGAAGGACCAACT GATCACCTTGAATCTGCTTGTCTCTTAATCTTC | 581 |
| | GAAGATTAAGAGGACAAGCAGATTCAAGGTGATCAGTTGGTC CTTCTCGGTCCTTTGATTGTTTAATAAGATCAAATAAAGGTGA ATCCTATATGAAACATGATGAAATTAACCACATT | 582 |
| | TTATTAAACAATCAAAG | 583 |
| | CTTTGATTGTTTAATAA | 584 |
| Retinoblastoma Arg579Term CGA to TGA | ATTTTCATCATGTTTCATATAGGATTCACCTTTATTTGATCTTAT TAAACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGA ATCTGCTTGTCTCTTAATCTTCTCTCCAGAATA | 585 |
| | TATTCTGGAGAGGAAGATTAAGAGGACAAGCAGATTCAAGGT GATCAGTTGGTCCTTCTCGGTCCTTTGATTGTTTAATAAGATC AAATAAAGGTGAATCCTATATGAAACATGATGAAAT | 586 |
| | CAAAGGACCGAGAAGGA | 587 |
| | TCCTTCTCGGTCCTTTG | 588 |
| Retinoblastoma Glu580Term GAA to TAA | TCATCATGTTTCATATAGGATTCACCTTTATTTGATCTTATTA ACAATCAAAGGACCGAGAAGGACCAACTGATCACCTTGAATC TGCTTGTCTCTTAATCTTCTCTCCAGAATAATC | 589 |
| | GATTATTCTGGAGAGGAAGATTAAGAGGACAAGCAGATTCAA GGTGATCAGTTGGTCCTTCTCGGTCCTTTGATTGTTTAATAAG ATCAAATAAAGGTGAATCCTATATGAAACATGATGA | 590 |
| | AGGACCGAGAAGGACCA | 591 |
| | TGGTCCTTCTCGGTCCT | 592 |
| Retinoblastoma Ser634Term TCA to TGA | AGAAAAAGGTTCAACTACGCGTGTAATTCTACTGCAAATG CAGAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCA TTGAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGG | 593 |
| | CCTTTTTTATAAAACAGTGAAAGAGAGGTAGATTTCATGGCT TCTGGGTCTGGAAGGCTGAGGTTGCTTGTGTCTCTGCATTG CAGTAGAATTTACACGCGTAGTTGAACCTTTTTTCT | 594 |
| | AGCAACCTCAGCCTTCC | 595 |
| | GGAAGGCTGAGGTTGCT | 596 |
| Retinoblastoma Ala635P | AAAAAAGGTTCAACTACGCGTGTAATTCTACTGCAAATGCA GAGACACAAGCAACCTCAGCCTTCCAGACCCAGAAGCCATT GAAATCTACCTCTCTTTCACTGTTTTATAAAAAAGGTT | 597 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | AACCTTTTTTATAAAACAGTGAAAGAGAGGTAGATTTCAATGG CTTCTGGGTCTGGAAGGCTGAGGTTGCTTGTGTCTCTGCATT TGCAGTAGAATTTACACGCGTAGTTGAACCTTTTTT | 598 |
| | CAACCTCAGCCTTCCAG | 599 |
| | CTGGAAGGCTGAGGTTG | 600 |
| Retinoblastoma Gln639Term CAG to TAG | ACTACGCGTGTAATTCTACTGCAAATGCAGAGACACAAGCA ACCTCAGCCTTCCAGACCCAGAAGCCATTGAAATCTACCTCT CTTCACTGTTTTATAAAAAAGGTTAGTAGATGATTA | 601 |
| | TAATCATCTACTAACCTTTTTTATAAAACAGTGAAAGAGAGGT AGATTTCAATGGCTTCTGGGTCTGGAAGGCTGAGGTTGCTTG TGTCTCTGCATTTGCAGTAGAATTTACACGCGTAGT | 602 |
| | TCCAGACCCAGAAGCCA | 603 |
| | TGGCTTCTGGGTCTGGA | 604 |
| Retinoblastoma L | TTGTAATTCAAAATGAACAGTAAAAATGACTAATTTTTCTTATT CCCACAGTGTATCGGCTAGCCTATCTCCGGCTAAATACACTT TGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGA | 605 |
| | TCTAATTCTGGGTGCTCAGACAGAAGGCGTTCACAAAGTGTA TTTAGCCGGAGATAGGCTAGCCGATACACTGTGGGAATAAG AAAAATTAGTCATTTTTACTGTTTCAATTTGAATTACAA | 606 |
| | GTATCGGCTAGCCTATC | 607 |
| | GATAGGCTAGCCGATAC | 608 |
| Retinoblastoma Arg661Trp CGG to TGG | AATGAACAGTAAAAATGACTAATTTTTCTTATTCCCACAGTGT ATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCC TTCTGTCTGAGCACCCAGAATTAGAACATATCATCT | 609 |
| | AGATGATATGTTCTAATTCTGGGTGCTCAGACAGAAGGCGTT CACAAAGTGATTTAGCCGGAGATAGGCTAGCCGATACACTG TGGGAATAAGAAAAATTAGTCATTTTTACTGTTTCAAT | 610 |
| | CCTATCTCCGGCTAAAT | 611 |
| | ATTTAGCCGGAGATAGG | 612 |
| Retinoblastoma Leu662Pro CTA to CCA | AACAGTAAAAATGACTAATTTTTCTTATTCCCACAGTGTATCG GCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGCCTTCT GTCTGAGCACCCAGAATTAGAACATATCATCTGGAC | 613 |
| | GTCCAGATGATATGTTCTAATTCTGGGTGCTCAGACAGAAGG CGTTCACAAAGTGATTTAGCCGGAGATAGGCTAGCCGATAC ACTGTGGGAATAAGAAAAATTAGTCATTTTTACTGTT | 614 |
| | TCTCCGGCTAAATACAC | 615 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | GTGTATTTAGCCGGAGA | 616 |
| Retinoblastoma Glu675Term GAA to TAA | TATCGGCTAGCCTATCTCCGGCTAAATACACTTTGTGAACGC CTTCTGTCTGAGCACCCAGAAATTAGAACATATCATCTGGACC CTTTCCAGCACACCCTGCAGAATGAGTATGAACTCA | 617 |
| | TGAGTTCATACTCATTCTGCAGGGTGTGCTGGAAAAGGGTCC AGATGATATGTTCTAATTCTGGGTGCTCAGACAGAAGGCGTT CACAAAGTGATTTAGCCGGAGATAGGCTAGCCGATA | 618 |
| | AGCACCCAGAAATTAGAA | 619 |
| | TTCTAATTCTGGGTGCT | 620 |
| Retinoblastoma Gln685Pro CAG to CCG | TTTGTGAACGCCTTCTGTCTGAGCACCCAGAATTAGAACATA TCATCTGGACCCTTTTCCAGCACACCCTGCAGAATGAGTATG AACTCATGAGAGACAGGCATTTGGACCAAGTAAGAAA | 621 |
| | TTTCTTACTTGGTCCAAATGCCTGTCTCTCATGAGTTCATACT CATTCTGCAGGGTGTGCTGGAAAAGGGTCCAGATGATATGTT CTAATTCTGGGTGCTCAGACAGAAGGCGTTCACAAA | 622 |
| | CCTTTTCCAGCACACCC | 623 |
| | GGGTGTGCTGGAAAAGG | 624 |
| Retinoblastoma Cys706Tyr TGT to TAT | AAAACCATGTAATAAAATTCTGACTACTTTTACATCAATTTATT TACTAGATTATGATGTGTTCCATGTATGGCATATGCAAAGTGA AGAATATAGACCTTAAATTCAAATCATTGTAAC | 625 |
| | GTTACAATGATTTTGAATTTAAGGTCTATATTCTTCACTTTGCA TATGCCATACATGGAACACATCATAATCTAGTAAATAAATTGA TGTAAGTAGTCAGAATTTTATTACATGGTTTT | 626 |
| | TATGATGTGTTCCATGT | 627 |
| | ACATGGAACACATCATA | 628 |
| Retinoblastoma Cys712Arg TGC to CGC | TTCTGACTACTTTTACATCAATTTATTTACTAGATTATGATGTG TTCCATGTATGGCATATGCAAAGTGAAGAATATAGACCTTAAA TTCAAATCATTGTAACAGCATACAAGGATCTTC | 629 |
| | GAAGATCCTTGTATGCTGTTACAATGATTTTGAATTTAAGGTC TATATTCTTCACTTTGCATATGCCATACATGGAACACATCATA ATCTAGTAAATAAATTGATGTAAAAGTAGTCAGAA | 630 |
| | ATGGCATATGCAAAGTG | 631 |
| | CACTTTGCATATGCCAT | 632 |
| Retinoblastom TAC to TAA | GTATGGCATATGCAAAGTGAAGAATATAGACCTTAAATTCAAA ATCATTGTAACAGCATACAAGGATCTTCCTCATGCTGTTTTCAG GAGGTAGGTAATTTCCATAGTAAGTTTTTTTGATA | 633 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | TATCAAAAAA <u>A</u> CTTACTATGGAAAATTACCTACCTCCTGAACA GCATGAGGAAGATCCTT <u>G</u> TATGCTGTTACAATGATTTTGAATT TAAGGTCTATATTCTTCACTTTGCATATGCCATAC | 634 |
| | ACAGCATAC <u>A</u> AGGATCT | 635 |
| | AGATCCTT <u>G</u> TATGCTGT | 636 |
| Retinoblastoma Glu748Term GAG to TAG | TTTTTTTTTTTTTTTACTGTTCTTCCTCAGACATTCAAACGTGT TTTGATCAAAGAAGAG <u>G</u> AGTATGATTCTATTATAGTATTCTAT AACTCGGTCTTCATGCAGAGACTGAAAACAAATA | 637 |
| | TATTTGTTTTTCACTCTCTGCATGAAGACCGAGTTATAGAATAC TATAATAGAATCATACT <u>C</u> CTCTTCTTTGATCAAAACACGTTTG AATGTCTGAGGAAGAACAGTAAAAAAAAAAAAAAAAA | 638 |
| | AAGAAGAG <u>G</u> AGTATGAT | 639 |
| | ATCATACT <u>C</u> CTCTTCTT | 640 |
| Retinoblastoma Gln762Term CAG to TAG | GTTTTGATCAAAGAAGAGGAGTATGATTCTATTATAGTATTCT ATAACTCGGTCTTCATG <u>C</u> AGAGACTGAAAACAAATATTTTGCA GTATGCTTCCACCAGGGTAGGTCAAAGTATCCTT | 641 |
| | AAGGATACTTTTGACCTACCCTGGTGAAGCATACTGCAAAA TATTTGTTTTTCACTCTCT <u>G</u> CATGAAGACCGAGTTATAGAATAC TATAATAGAATCATACTCCTCTTCTTTGATCAAAAC | 642 |
| | TCTTCATG <u>C</u> AGAGACTG | 643 |
| | CAGTCTCT <u>G</u> CATGAAGA | 644 |
| Retinoblastoma Arg787Term CGA-TGA | TAATCTACTTTTTTGTTTTGCTCTAGCCCCCTACCTTGTCAC CAATACCTCACATTCTC <u>G</u> AAGCCCTTACAAGTTTCCTAGTTC ACCCTTACGGATTCTTGAGGGAACATCTATATT | 645 |
| | AAATATAGATGTTCCCTCCAGGAATCCGTAAGGGTGAAGTAG GAACTTGTAAGGGCTTC <u>G</u> AGGAATGTGAGGTATTGGTGACA AGGTAGGGGGCTAGAGCAAAAACAAAAAAGTAGATTA | 646 |
| | ACATTCCT <u>C</u> GAAGCCCT | 647 |
| | AGGGCTTC <u>G</u> AGGAATGT | 648 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Retinoblastoma Ser816Term TCA to TGA | CCTTACGGATTCCTGGAGGGAACATCTATATTTACCCCTGA AGAGTCCATATAAAATTT <u>C</u> AGAAGGTCTGCCAACACCAACAA AAATGACTCCAAGATCAAGGTGTGTGTTTTCTCTTA | 649 |
| | TAAAGAGAAAACACACACCTTGATCTTGGAGTCATTTTTGTTG GTGTTGGCAGACCTTCT <u>G</u> AAATTTTATATGGACTCTTCAGGG GTGAAATATAGATGTTCCCTCCAGGAATCCGTAAGG | 650 |
| | TAAAATTT <u>C</u> AGAAGGTC | 651 |
| | GACCTTCT <u>G</u> AAATTTTA | 652 |

EXAMPLE 9

BRCA1 and BRCA2

[0214] Breast cancer is the second major cause of cancer death in American women, with an estimated 44,190 lives lost (290 men and 43,900 women) in the US in 1997. While ovarian cancer accounts for fewer deaths than breast cancer, it still represents 4% of all female cancers. In 1994, two breast cancer susceptibility genes were identified: BRCA1 on chromosome 17 and BRCA2 on chromosome 13. When a woman carries a mutation in either BRCA1 or BRCA2, she is at increased risk of being diagnosed with breast or ovarian cancer at some point in her life.

[0215] Ford *et al.*, *Am. J. Hum. Genet.* 62: 676-689 (1998) assessed the contribution of BRCA1 and BRCA2 to inherited breast cancer by linkage and mutation analysis in 237 families, each with at least 4 cases of breast cancer. Families were included without regard to the occurrence of ovarian or other cancers. Overall, disease was linked to BRCA1 in an estimated 52% of families, to BRCA2 in 32% of families, and to neither gene in 16%, suggesting other predisposition genes. The majority (81%) of the breast-ovarian cancer families were due to BRCA1, with most others (14%) due to BRCA2. Conversely, the majority (76%) of families with both male and female breast cancer were due to BRCA2. The largest proportion (67%) of families due to other genes were families with 4 or 5 cases of female breast cancer only.

[0216] More than 75% of the reported mutations in the BRCA1 gene result in truncated proteins. Couch *et al.*, *Hum. Mutat.* 8: 8-18, 1996. (1996) reported a total of 254 BRCA1 mutations, 132 (52%) of which were unique. A total of 221 (87%) of all mutations or 107 (81%) of the unique mutations are small deletions, insertions, nonsense point mutations, splice variants, and regulatory mutations that result in truncation or absence of the BRCA1 protein. A total of 11 disease-associated missense

mutations (5 unique) and 21 variants (19 unique) as yet unclassified as missense mutations or polymorphisms had been detected. Thirty-five independent benign polymorphisms had been described. The most common mutations were 185delAG and 5382insC, which accounted for 30 (11.7%) and 26 (10.1%), respectively, of all the mutations.

5 **[0217]** Most BRCA2 mutations are predicted to result in a truncated protein product. The smallest known cancer-associated deletion removes from the C terminus only 224 of the 3,418 residues constituting BRCA2, suggesting that these terminal amino acids are critical for BRCA2 function. Studies (Spain *et al.*, Proc. Natl. Acad. Sci. 96:13920-13925 (1999)) suggest that such truncations eliminate or interfere with 2 nuclear localization signals that reside within the final 156 residues of BRCA2, suggesting that the vast majority of BRCA2 mutants are nonfunctional because they are not translocated into the nucleus.

10 **[0218]** The attached table discloses the correcting oligonucleotide base sequences for the BRCA1 and BRCA2 oligonucleotides of the invention.

Table 10

BRCA1 Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Breast Cancer Met-1-Ile ATG to ATT | CTGCGCTCAGGAGGCCTTCACCCTCTGCTCTGGGTAAAGTT CATTGGAACAGAAAGAAATGGATTTATCTGCTCTTCGCGTTG AAGAAGTACAAAATGTCATTAATGCTATGCAGAAAATC | 653 |
| | GATTTTCTGCATAGCATTAAATGACATTTTGTACTTCTTCAACG CGAAGAGCAGATAAATCCATTTCTTTCTGTTCCAATGAACTTT ACCCAGAGCAGAGGGTGAAGGCCTCCTGAGCGCAG | 654 |
| | AAAGAAATGGATTTATC | 655 |
| | GATAAATCCATTTCTTT | 656 |
| Breast Cancer Val-11-Ala GTA to GCA | CTGGGTAAAGTTCATTGGAACAGAAAGAAATGGATTTATCTG CTCTTCGCGTTGAAGAAGTACAAAATGTCATTAATGCTATGCA GAAAATCTTAGAGTGTCCCATCTGTCTGGAGTTGAT | 657 |
| | ATCAACTCCAGACAGATGGGACACTCTAAGATTTTCTGCATA GCATTAATGACATTTTGTACTTCTTCAACGCGAAGAGCAGATA AATCCATTTCTTTCTGTTCCAATGAACTTTACCCAG | 658 |
| | TGAAGAAGTACAAAATG | 659 |
| | CATTTTGTACTTCTTCA | 660 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Breast Cancer Ile-21-Val ATC to GTC | ATGGATTTATCTGCTCTTCGCGTTGAAGAAGTACAAAATGTCA TTAATGCTATGCAGAAAATCTTAGAGTGTCCCATCTGTCTGG AGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC | 661 |
| | GGTCACACTTTTGTGGAGACAGGTTCCCTTGATCAACTCCAGAC AGATGGGACACTCTAAGATTTTCTGCATAGCATTAAATGACATT TTGTACTTCTTCAACGCGAAGAGCAGATAAATCCAT | 662 |
| | TGCAGAAAATCTTAGAG | 663 |
| | CTCTAAGATTTTCTGCA | 664 |
| Breast Cancer Leu-22-Ser TTA to TCA | ATTTATCTGCTCTTCGCGTTGAAGAAGTACAAAATGTCATTAA TGCTATGCAGAAAATCTTAGAGTGTCCCATCTGTCTGGAGTT GATCAAGGAACCTGTCTCCACAAAGTGTGACCACAT | 665 |
| | ATGTGGTCACACTTTTGTGGAGACAGGTTCCCTTGATCAACTCC AGACAGATGGGACACTCTAAGATTTTCTGCATAGCATTAAATG ACATTTTGTACTTCTTCAACGCGAAGAGCAGATAAAT | 666 |
| | GAAAATCTTAGAGTGTC | 667 |
| | GACACTCTAAGATTTTC | 668 |
| Breast Cancer Cys-39-Tyr TGT to TAT | AGAAAATCTTAGAGTGTCCCATCTGTCTGGAGTTGATCAAGG AACCTGTCTCCACAAAGTGTGACCACATATTTTGCAAATTTTG CATGCTGAAACTTCTCAACCAGAAGAAAGGGCCTTC | 669 |
| | GAAGGCCCTTTCTTCTGGTTGAGAAGTTTCAGCATGCAAAT TTGCAAATATGTGGTCAACTTTGTGGAGACAGGTTCCCTTG ATCAACTCCAGACAGATGGGACACTCTAAGATTTTCT | 670 |
| | CACAAAGTGTGACCACA | 671 |
| | TGTGGTCAACTTTGTG | 672 |
| Breast Cancer Cys-61-Gly TGT to GGT | CACATATTTTGCAAATTTTGCATGCTGAAACTTCTCAACCAGA AGAAAGGGCCTTCACAGTGTCTTTATGTAAGAATGATATAA CCAAAAGGAGCCTACAAGAAAGTACGAGATTTAGTC | 673 |
| | GACTAAATCTCGTACTTTCTTGTAGGCTCCTTTTGGTTATATC ATTCTTACATAAAGGACACTGTGAAGGCCCTTTCTTCTGGTT GAGAAGTTTCAGCATGCAAATTTGCAAATATGTG | 674 |
| | CTTCACAGTGTCTTTA | 675 |
| | TAAAGGACACTGTGAAG | 676 |
| Breast Cancer Leu-63-Stop TTA to TAA | TTTGCAAATTTTGCATGCTGAAACTTCTCAACCAGAAGAAAGG GCCTTCACAGTGTCTTTATGTAAGAATGATATAACCAAAGG AGCCTACAAGAAAGTACGAGATTTAGTCAACTGT | 677 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | ACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTTTTGG TTATATCATTCTTACATAAAGGACACTGTGAAGGCCCTTTCTT CTGGTTGAGAAGTTTCAGCATGCAAAATTTGCAAA | 678 |
| | GTGTCCTTTATGTAAGA | 679 |
| | TCTTACATAAAGGACAC | 680 |
| Breast Cancer Cys-64-Arg TGT to CGT | TGCAAATTTTGCATGCTGAACTTCTCAACCAGAAGAAAGGG CCTTCACAGTGTCTTTATGTAAGAATGATATAACCAAAAGGA GCCTACAAGAAAGTACGAGATTTAGTCAACTTGTTG | 681 |
| Breast Cancer Cys-64-Gly TGT to GGT | CAACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTTTT GGTTATATCATTCTTACATAAAGGACACTGTGAAGGCCCTTTC TTCTGGTTGAGAAGTTTCAGCATGCAAAATTTGCA | 682 |
| | GTCCTTTATGTAAGAAT | 683 |
| | ATTCTTACATAAAGGAC | 684 |
| Breast Cancer Cys-64-Tyr TGT to TAT | GCAAATTTTGCATGCTGAACTTCTCAACCAGAAGAAAGGGC CTTCACAGTGTCTTTATGTAAGAATGATATAACCAAAAGGAG CCTACAAGAAAGTACGAGATTTAGTCAACTTGTTGA | 685 |
| | TCAACAAGTTGACTAAATCTCGTACTTTCTTGTAGGCTCCTTT TGTTATATCATTCTTACATAAAGGACACTGTGAAGGCCCTTT CTTCTGGTTGAGAAGTTTCAGCATGCAAAATTTGC | 686 |
| | TCCTTTATGTAAGAATG | 687 |
| | CATTCTTACATAAAGGA | 688 |
| Breast Cancer Gln-74-Stop CAA to TAA | CAGAAGAAAGGGCCTTCACAGTGTCTTTATGTAAGAATGAT ATAACCAAAAGGAGCCTACAAGAAAGTACGAGATTTAGTCAA CTTGTTGAAGAGCTATTGAAATCATTGTGCTTTTC | 689 |
| | GAAAAGCACAAATGATTTTCAATAGCTCTTCAACAAGTTGACT AAATCTCGTACTTTCTTGTAGGCTCCTTTTGGTTATATCATTCT TACATAAAGGACACTGTGAAGGCCCTTTCTTCTG | 690 |
| | GGAGCCTACAAGAAAGT | 691 |
| | ACTTTCTTGTAGGCTCC | 692 |
| Breast Cancer Tyr-105-Cys TAT to TGT | AGCTATTGAAAATCATTGTGCTTTTCAGCTTGACACAGGTTT GGAGTATGCAAACAGCTATAATTTTGCAAAAAGGAAAATAA CTCTCCTGAACATCTAAAAGATGAAGTTTCTATCAT | 693 |
| | ATGATAGAACTTCATCTTTTAGATGTTTCAAGGAGAGTTATTT CCTTTTTTGCAAATTATAGCTGTTTGCATACTCCAAACCTGT GTCAAGCTGAAAAGCACAAATGATTTTCAATAGCT | 694 |
| | AAACAGCTATAATTTTG | 695 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | CAAAATTATAGCTGTTT | 696 |
| Breast Cancer Asn-158-Tyr AAC to TAC | CTACAGAGTGAACCCGAAAATCCTTCCTTGCAGGAAACCAGT CTCAGTGTCCAACCTCTCTAACCTTGGAAGTGTGAGAACTCTG AGGACAAAGCAGCGGATACAACCTCAAAAGACGTCTG | 697 |
| | CAGACGTCTTTTGAGGTTGTATCCGCTGCTTTGTCCTCAGAG TTCTCACAGTTCCAAGGTAGAGAGTTGGACACTGAGACTGG TTTCCTGCAAGGAAGGATTTTCGGGTTCACTCTGTAG | 698 |
| | AACCTCTCTAACCTTGGA | 699 |
| | TCCAAGGTAGAGAGTT | 700 |
| Breast Cancer Gln-169-Stop CAG to TAG | GAAACCAGTCTCAGTGTCCAACCTCTAACCTTGGAAGTGTG AGAAGTCTGAGGACAAAGCAGCGGATACAACCTCAAAAGAC GTCTGTCTACATTGAATTGGGATCTGATTCTTCTGAAG | 701 |
| | CTTCAGAAGAATCAGATCCCAATTCAATGTAGACAGACGTCT TTTGAGGTTGTATCCGCTGCTTTGTCCTCAGAGTTCTCACAG TTCCAAGGTAGAGAGTTGGACACTGAGACTGGTTTC | 702 |
| | GGACAAAGCAGCGGATA | 703 |
| | TATCCGCTGCTTTGTCC | 704 |
| Breast Cancer Trp-353-Stop TGG to TAG | CTCCCAGCACAGAAAAAAGGTAGATCTGAATGCTGATCCCC TGTGTGAGAGAAAAGAATGGAATAAGCAGAACTGCCATGCT CAGAGAATCCTAGAGATACTGAAGATGTTCTTGGAT | 705 |
| | ATCCAAGGAACATCTTCAGTATCTCTAGGATTCTCTGAGCAT GGCAGTTTCTGCTTATTCCATTCTTTTCTCTCACACAGGGGAT CAGCATTGAGATCTACCTTTTTTCTGTGCTGGGAG | 706 |
| | AAAAGAATGGAATAAGC | 707 |
| | GCTTATTCCATTCTTTT | 708 |
| Breast Cancer Ile-379-Met ATT to ATG | ATGCTCAGAGAATCCTAGAGATACTGAAGATGTTCTTGGAT AACACTAAATAGCAGCATTCAGAAAGTTAATGAGTGGTTTTCC AGAAGTGATGAACTGTTAGGTTCTGATGACTCACAT | 709 |
| | ATGTGAGTCATCAGAACCTAACAGTTCATCACTTCTGGAAAA CCACTCATTAACTTTCTGAATGCTGCTATTTAGTGTATCCAA GGAACATCTTCAGTATCTCTAGGATTCTCTGAGCAT | 710 |
| | AGCAGCATTCAGAAAGT | 711 |
| | ACTTTCTGAATGCTGCT | 712 |
| Breast Cancer Glu-421-Gly GAA to GGA | GGGAGTCTGAATCAAATGCCAAAGTAGCTGATGTATTGGACG TTCTAAATGAGGTAGATGAATATTCTGGTTCTTCAGAGAAAAT AGACTTACTGGCCAGTGATCCTCATGAGGCTTTAAT | 713 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | ATTAAAGCCTCATGAGGATCACTGGCCAGTAAGTCTATTTTCTCTGAAGAACCAGAATATTCATCTACCTCATTTAGAACGTCCAA TACATCAGCTACTTTGGCATTGATTGAGACTCCC | 714 |
| | GGTAGATGAATATTCTG | 715 |
| | CAGAATATTCATCTACC | 716 |
| Breast Cancer Phe-461-Leu TTT to CTT | ATATGTAAAAGTGAAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATAATTGGGAAAACCTATCGGAAGAAG GCAAGCCTCCCCAACTTAAGCCATGTAAGTGAAGATC | 717 |
| | GATTTTCAGTTACATGGCTTAAGTTGGGGAGGCTTGCCTTCTTCCGATAGGTTTTCCCAAATATTTTGTCTTCAATATTACTCTCT ACTGATTTGGAGTGAAGTCTTTCACTTTTACATAT | 718 |
| | ACAAAATATTTGGGAAA | 719 |
| | TTTCCCAAATATTTTGT | 720 |
| Breast Cancer Tyr-465-Leu TAT to GAT | GAAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTGAAGACAAAATATTTGGGAAAACCTATCGGAAGAAGGCAAGCCTCCCC AACTTAAGCCATGTAAGTGAAGTCTAATTATAGGAG | 721 |
| | CTCCTATAATTAGATTTTCAGTTACATGGCTTAAGTTGGGGAGGCTTGCCTTCTTCCGATAGGTTTTCCCAAATATTTTGTCTTCA ATATTACTCTCTACTGATTTGGAGTGAAGTCTTTC | 722 |
| | GGAAAACCTATCGGAAG | 723 |
| | CTTCCGATAGGTTTTCC | 724 |
| Breast Cancer Gly-484-Stop GGA to TGA | ACCTATCGGAAGAAGGCAAGCCTCCCCAACTTAAGCCATGTA ACTGAAAATCTAATTATAGGAGCATTGTTACTGAGCCACAGATAATACAAGAGCGTCCCCTCACAAATAAATTAAAGC | 725 |
| | GCTTTAATTTATTTGTGAGGGGACGCTCTTGATTATCTGTGGCTCAGTAACAAATGCTCCTATAATTAGATTTTCAGTTACATGG CTTAAGTTGGGGAGGCTTGCCTTCTTCCGATAGGT | 726 |
| | TAATTATAGGAGCATT | 727 |
| | AAATGCTCCTATAATTA | 728 |
| Breast Cancer Arg-507-Ile AGA to ATA | TACTGAGCCACAGATAATACAAGAGCGTCCCCTCACAAATA AATTAAAGCGTAAAGGAGACCTACATCAGGCCTTCATCCTG AGGATTTTATCAAGAAAGCAGATTTGGCAGTTCAAAA | 729 |
| | TTTTGAAGTGCCTAATCTGCTTTCTTGATAAAATCCTCAGGAT GAAGGCCTGATGTAGGTCTCCTTTTACGCTTTAATTTATTTGT GAGGGGACGCTCTTGATTATCTGTGGCTCAGTAA | 730 |
| | TAAAAGGAGACCTACAT | 731 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | ATGTAGGT <u>C</u> TCCTTTTA | 732 |
| Breast Cancer Ser-510-Stop TCA to TGA | CACAGATAATACAAGAGCGTCCCCTCACAAATAAATTAAAGC GTAAAAGGAGACCTACAT <u>C</u> AGGCCTTCATCCTGAGGATTTTA TCAAGAAAGCAGATTTGGCAGTTCAAAAGACTCCTGA | 733 |
| | TCAGGAGTCTTTTGAAGTGCCAAATCTGCTTTCTTGATAAAAT CCTCAGGATGAAGGCCT <u>G</u> ATGTAGGTCTCCTTTTACGCTTTA ATTTATTTGTGAGGGGACGCTCTTGATTATCTGTG | 734 |
| | ACCTACAT <u>C</u> AGGCCTTC | 735 |
| | GAAGGCCT <u>G</u> ATGTAGGT | 736 |
| Breast Cancer Gln-526-Stop CAA to TAA | AGGAGACCTACATCAGGCCTTCATCCTGAGGATTTTATCAAG AAAGCAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAAT CAGGGAACCTAACCAACGGAGCAGAATGGTCAAGTGA | 737 |
| | TCACTTGACCATTCTGCTCCGTTTGGTTAGTTCCCTGATTTAT CATTTCAGGAGTCTTTT <u>G</u> AAGTGCCAAATCTGCTTTCTTGATA AAATCCTCAGGATGAAGGCCTGATGTAGGTCTCCT | 738 |
| | TGGCAGTTCAAAAGACT | 739 |
| | AGTCTTTT <u>G</u> AAGTGCCA | 740 |
| Breast Cancer Gln-541-Stop CAG to TAG | AGGAGACCTACATCAGGCCTTCATCCTGAGGATTTTATCAAG AAAGCAGATTTGGCAGTTCAAAAGACTCCTGAAATGATAAAT CAGGGAACCTAACCAACGGAGCAGAATGGTCAAGTGA | 741 |
| | TCACTTGACCATTCTGCTCCGTTTGGTTAGTTCCCTGATTTAT CATTTCAGGAGTCTTTT <u>G</u> AAGTGCCAAATCTGCTTTCTTGATA AAATCCTCAGGATGAAGGCCTGATGTAGGTCTCCT | 742 |
| | AAACGGAG <u>C</u> AGAATGGT | 743 |
| | ACCATTCT <u>G</u> CTCCGTTT | 744 |
| Breast Cancer Gly-552-Val GGT to GTT | TAAATCAGGGAACTAACCAACGGAGCAGAATGGTCAAGTGA TGAATATTACTAATAGT <u>G</u> TCATGAGAATAAAACAAAAGGTGA TTCTATTTCAGAAATGAGAAAAATCCTAACCCAATAGA | 745 |
| | TCTATTGGGTTAGGATTTTCTCATTCTGAATAGAATCACCTT TTGTTTTATTCTCATGAC <u>C</u> CACTATTAGTAATATTCATCACTTGA CCATTCTGCTCCGTTTGGTTAGTTCCCTGATTTA | 746 |
| | TAATAGT <u>G</u> TCATGAGA | 747 |
| | TCTCATGAC <u>C</u> CACTATTA | 748 |
| Breast Cancer Gln-563-Stop CAG to TAG | GGTCAAGTGATGAATATTACTAATAGTGGTCATGAGAATAAAA CAAAAGGTGATTCTATT <u>C</u> AGAATGAGAAAAATCCTAACCCAAT AGAATCACTCGAAAAAGAATCTGCTTTCAAACGA | 749 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | TCGTTTTGAAAGCAGATTCTTTTTCGAGTGATTCTATTGGGTT AGGATTTTTCTCATTCTGAATAGAATCACCTTTTGTATTCT CATGACCACTATTAGTAATATTCATCACTTGACC | 750 |
| | ATTCTATTGAGAATGAG | 751 |
| | CTCATTCTGAATAGAAT | 752 |
| Ovarian Cancer Lys-607-Stop AAA to TAA | ATAAGCAGCAGTATAAGCAATATGGAAGCTCGAATTAAATATCC ACAATTCAAAAGCACCTAAAAAGAATAGGCTGAGGAGGAAGT CTTCTACCAGGCATATTCATGCGCTTGAAGTAGTAG | 753 |
| | CTACTAGTTCAAGCGCATGAATATGCCTGGTAGAAGACTTCC TCCTCAGCCTATTCTTTTAGGTGCTTTTGAATTGTGGATATT TAATTCGAGTTCCATATTGCTTATACTGCTGCTTAT | 754 |
| | AAGCACCTAAAAAGAAT | 755 |
| | ATTCTTTTAGGTGCTT | 756 |
| Breast Cancer Leu-639-Stop TTG to TAG | ATATTCATGCGCTTGAAGTAGTAGTCAGTAGAAATCTAAGCC CACCTAATTGTACTGAATTGCAAATTGATAGTTGTTCTAGCAG TGAAGAGATAAAGAAAAAAGTACAACCAAATGCC | 757 |
| | GGCATTGGTTGTACTTTTTTTCTTTATCTCTTCACTGCTAGA ACAAGTATCAATTTGCAATTTCAGTACAATTAGGTGGGCTTAGA TTTCTACTGACTACTAGTTCAAGCGCATGAATAT | 758 |
| | TACTGAATTGCAAATTG | 759 |
| | CAATTTGCAATTCAGTA | 760 |
| Breast Cancer Asp-693-Asn GAC to AAC | GAACCTGCAACTGGAGCCAAGAAGAGTAACAAGCCAAATGA ACAGACAAGTAAAAGACATGACAGCGATACTTTCCAGAGCT GAAGTTAACAAATGCACCTGGTTCTTTACTAAGTGTT | 761 |
| | AACACTTAGTAAAAGAACCAGGTGCATTTGTAACTTCAGCTC TGGGAAAGTATCGCTGTATGTCTTTTACTTGTCTGTTCAATTT GGCTTGTTACTCTTCTTGGCTCCAGTTGCAGGTTT | 762 |
| | AAAGACATGACAGCGAT | 763 |
| | ATCGCTGTATGTCTTT | 764 |
| Ovarian Cancer Glu-720-Stop GAA to TAA | CTGAAGTTAACAAATGCACCTGGTTCTTTTACTAAGTGTTCAA ATACCACTGAACTTAAAGAAATTTGTCAATCCTAGCCTTCCAAG AGAAGAAAAAGAAGAGAACTAGAAACAGTTAAAG | 765 |
| | CTTTAACTGTTTCTAGTTTCTTCTTTTCTTCTCTTGAAGG CTAGGATTGACAAATCTTTAAGTTCACTGGTATTTGAACACT TAGTAAAAGAACCAGGTGCATTTGTAACTTCAG | 766 |
| | AACTTAAAGAATTTGTC | 767 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | GACAAATTCTTTAAGTT | 768 |
| Breast Cancer Glu-755-Stop GAA to TAA | CTAGAAACAGTTAAAGTGTCTAATAATGCTGAAGACCCCAA GATCTCATGTTAAGTGGAGAAAGGGTTTTGCAAAGTAAAGA TCTGTAGAGAGTAGCAGTATTTTATTGGTACCTGGTA | 769 |
| | TACCAGGTACCAATGAAATACTGCTACTCTCTACAGATCTTTC AGTTTGCAAACCCTTTCTCCACTTAACATGAGATCTTTGGGG TCTTCAGCATTATTAGACACTTTAACTGTTTCTAG | 770 |
| | TAAGTGGAGAAAGGGTT | 771 |
| | AACCCTTTCTCCACTTA | 772 |
| Breast Cancer Ser-770-Stop TCA to TAA | TCATGTTAAGTGGAGAAAGGGTTTTGCAAAGTAAAGATCTG TAGAGAGTAGCAGTATTTTATTGGTACCTGGTACTGATTATG GCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCAC | 773 |
| | GTGCTAACTTCCAGTAACGAGATACTTTCCTGAGTGCCATAA TCAGTACCAGGTACCAATGAAATACTGCTACTCTCTACAGAT CTTTCAGTTTGCAAACCCTTTCTCCACTTAACATGA | 774 |
| | CAGTATTTTATTGGTAC | 775 |
| | GTACCAATGAAATACTG | 776 |
| Breast Cancer Val-772-Ala GTA to GCA | TAAGTGGAGAAAGGGTTTTGCAAAGTAAAGATCTGTAGAGA GTAGCAGTATTTTATTGGTACCTGGTACTGATTATGGCACTC AGGAAAGTATCTCGTTACTGGAAGTTAGCACTCTAGG | 777 |
| | CCTAGAGTGCTAACTTCCAGTAACGAGATACTTTCCTGAGTG CCATAATCAGTACCAGGTACCAATGAAATACTGCTACTCTCTA CAGATCTTTCAGTTTGCAAACCCTTTCTCCACTTA | 778 |
| | TTCATTGGTACCTGGTA | 779 |
| | TACCAGGTACCAATGAA | 780 |
| Breast Cancer Gln-780-Stop CAG to TAG | ACTGAAAGATCTGTAGAGAGTAGCAGTATTTTATTGGTACCT GGTACTGATTATGGCACTCAGGAAAGTATCTCGTTACTGGAA GTTAGCACTCTAGGGAAGGCAAAAACAGAACCAAATA | 781 |
| | TATTTGGTTCTGTTTTTGCCTTCCCTAGAGTGCTAACTTCCAG TAACGAGATACTTTCCTGAGTGCCATAATCAGTACCAGGTAC CAATGAAATACTGCTACTCTCTACAGATCTTTCAGT | 782 |
| | ATGGCACTCAGGAAAGT | 783 |
| | ACTTTCCTGAGTGCCAT | 784 |
| Breast Cancer Glu-797-Stop GAA to TAA | TATGGCACTCAGGAAAGTATCTCGTTACTGGAAGTTAGCACT CTAGGGAAGGCAAAAACAGAACCAATAAATGTGTGAGTCAG TGTGCAGCATTTGAAAACCCCAAGGGACTAATTCATG | 785 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | CATGAATTAGTCCCTTGGGGTTTTCAAATGCTGCACACTGAC TCACACATTTATTTGGTTCTGTTTTTGCCTTCCCTAGAGTGCT AACTTCCAGTAACGAGATACTTTCCTGAGTGCCATA | 786 |
| | CAAAAACAGAACCAAAT | 787 |
| | ATTTGGTTCTGTTTTTG | 788 |
| Breast Cancer Lys-820-Glu AAA to GAA | AAATGTGTGAGTCAGTGTGCAGCATTTGAAAACCCCAAGGGA CTAATTCATGGTTGTTCCAAAGATAATAGAAATGACACAGAAG GCTTTAAGTATCCATTGGGACATGAAGTTAACCACA | 789 |
| | TGTGGTTAACTTCATGTCCCAATGGATACTTAAAGCCTTCTGT GTCATTTCTATTATCTTTGGAACAACCATGAATTAGTCCCTTG GGGTTTTCAAATGCTGCACACTGACTCACACATTT | 790 |
| | GTTGTTCCAAAGATAAT | 791 |
| | ATTATCTTTGGAACAAC | 792 |
| Breast Cancer Thr-826-Lys ACA to AAA | CAGCATTTGAAAACCCCAAGGGACTAATTCATGGTTGTTCCA AAGATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGG GACATGAAGTTAACCACAGTCGGGAAACAAGCATAGA | 793 |
| | TCTATGCTTGTTTCCCGACTGTGGTTAACTTCATGTCCCAATG GATACTTAAAGCCTTCTGTGTCAATTTCTATTATCTTTGGAACA ACCATGAATTAGTCCCTTGGGGTTTTCAAATGCTG | 794 |
| | AAATGACACAGAGGCT | 795 |
| | AGCCTTCTGTGTCAATTT | 796 |
| Breast Cancer Arg-841-Trp CGG to TGG | GATAATAGAAATGACACAGAAGGCTTTAAGTATCCATTGGGA CATGAAGTTAACCACAGTCGGGAAACAAGCATAGAAATGGAA GAAAGTGAAGTTGATGCTCAGTATTTGCAGAATACAT | 797 |
| | ATGTATTCTGCAAATACTGAGCATCAAGTTCACCTTCTTCCAT TTCTATGCTTGTTTCCCAGACTGTGGTTAACTTCATGTCCCAAT GGATACTTAAAGCCTTCTGTGTCAATTTCTATTATC | 798 |
| | ACCACAGTCGGGAAACA | 799 |
| | TGTTTCCCAGACTGTGGT | 800 |
| Breast Cancer Pro-871-Leu CCG to CTG | AACTTGATGCTCAGTATTTGCAGAATACATTCAAGGTTTCAAA GCGCCAGTCATTTGCTCCGTTTTCAAATCCAGGAAATGCAGA AGAGGAATGTGCAACATTCTCTGCCACTCTGGGTC | 801 |
| | GACCCAGAGTGGGCAGAGAATGTTGCACATTCCTCTTCTGCA TTTCCTGGATTTGAAAACGGAGCAAATGACTGGCGCTTTGAA ACCTTGAATGTATTCTGCAAATACTGAGCATCAAGTT | 802 |
| | ATTTGCTCCGTTTTCAA | 803 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | TTGAAAAC <u>G</u> GAGCAAAT | 804 |
| Breast Cancer Leu-892-Ser TTA to TCA | TTTCAAATCCAGGAAATGCAGAAGAGGAATGTGCAACATTCT CTGCCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCA CTTTTGAATGTGAACAAAAGGAAGAAAATCAAGGAAA | 805 |
| | TTTCCTTGATTTTCTTCCTTTTGTTCACATTCAAAAGTGACTTT TGGACTTTGTTTCTTTAAGGACCCAGAGTGGGCAGAGAATGT TGCACATTCTCTTCTGCATTTCCTGGATTGAAA | 806 |
| | TGGGTCCTTAAAGAAAC | 807 |
| | GTTTCTTTAAGGACCCA | 808 |
| Breast Cancer Glu-908-Stop GAA to TAA | CACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCACTTTT GAATGTGAACAAAAGGAAGAAATCAAGGAAAGAATGAGTCT AATATCAAGCCTGTACAGACAGTTAATATCACTGCAG | 809 |
| | CTGCAGTGATATTAAGTGTCTGTACAGGCTTGATATTAGACTC ATTCTTTCCTTGATTTTCTTCCTTTTGTTCACATTCAAAAGTGA CTTTTGGACTTTGTTTCTTTAAGGACCCAGAGTG | 810 |
| | AAAAGGAAGAAATCAA | 811 |
| | TTGATTTTCTTCCTTTT | 812 |
| Breast Cancer Gly-960-Asp GGC to GAC | ATAATGCCAAATGTAGTATCAAAGGAGGCTCTAGGTTTTGTCT ATCATCTCAGTTCAGAGGCAACGAACTGGACTCATTACTCC AAATAAACATGGACTTTTACAAAACCCATATCGTAT | 813 |
| | ATACGATATGGGTTTTGTAAAGTCCATGTTTATTTGGAGTAA TGAGTCCAGTTTCGTTGCCTCTGAACTGAGATGATAGACAAA ACCTAGAGCCTCCTTTGATACTACATTTGGCATTAT | 814 |
| | G TTCAGAGGCAACGAAA | 815 |
| | TTTCGTTGCCTCTGAAC | 816 |
| Breast Cancer Met-1008-Ile ATG to ATA | ATTTGTTAAACTAAATGTAAGAAAAATCTGCTAGAGGAAAAC TTTGAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAAAT GAGAACATTCCAAGTACAGTGAGCACAATTAGCCGT | 817 |
| | ACGGCTAATTGTGCTCACTGTACTTGGAATGTTCTCATTTCCC ATTTCTCTTTCAGGTGACATTGAATGTTCTCAAAGTTTTCT CTAGCAGATTTTCTTACATTAGTTTAAACAAAT | 818 |
| | CATTCAATGTCACCTGA | 819 |
| | TCAGGTGACATTGAATG | 820 |
| Breast Cancer Thr-1025-Ile ACA to ATA | ACTTTGAGGAACATTCAATGTCACCTGAAAGAGAAATGGGAA ATGAGAACATTCCAAGTACAGTGAGCACAATTAGCCGTAATA ACATTAGAGAAAATGTTTTTAAAGAAGCCAGCTCAAG | 821 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | CTTGAGCTGGCTTCTTTAAAAACATTTTCTCTAATGTTATTAC GGCTAATTGTGCTCACTGACTTTGGAATGTTCTCATTTCCCAT TTCTCTTTCAGGTGACATTGAATGTTCTCCTCAAAGT | 822 |
| | TCCAAGTACAGTGAGCA | 823 |
| | TGCTCACTGACTTTGGA | 824 |
| Breast Cancer Glu-1038-Gly GAA to GGA | ACATTCCAAGTACAGTGAGCACAATTAGCCGTAATAACATTA GAGAAAATGTTTTTAAAGAAGCCAGCTCAAGCAATATTAATGA AGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTAT | 825 |
| | ATACTGGAGCCCACTTCATTAGTACTGGAACCTACTTCATTAA TATTGCTTGAGCTGGCTTCTTTAAAAACATTTTCTCTAATGTTA TTACGGCTAATTGTGCTCACTGTACTTGGAAATGT | 826 |
| | TTTTAAAGAAGCCAGCT | 827 |
| | AGCTGGCTTCTTTAAAA | 828 |
| Breast Cancer Ser-1040-Asn AGC to AAC | CAAGTACAGTGAGCACAATTAGCCGTAATAACATTAGAGAAA ATGTTTTTAAAGAAGCCAGCTCAAGCAATATTAATGAAGTAGG TTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGA | 829 |
| | TCATTAATACTGGAGCCCACTTCATTAGTACTGGAACCTACTT CATTAAATATTGCTTGAGCTGGCTTCTTTAAAAACATTTTCTCTA ATGTTATTACGGCTAATTGTGCTCACTGTACTTG | 830 |
| | AGAAGCCAGCTCAAGCA | 831 |
| | TGCTTGAGCTGGCTTCT | 832 |
| Breast Cancer Val-1047-Ala GTA to GCA | GCCGTAATAACATTAGAGAAAATGTTTTTAAAGAAGCCAGCTC AAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGG CTCCAGTATTAATGAAATAGGTTCCAGTGATGAAAA | 833 |
| | TTTTCATCACTGGAACCTATTTTATTAATACTGGAGCCCACTT CATTAGTACTGGAACCTACTTCATTAATATTGCTTGAGCTGGC TTCTTTAAAAACATTTTCTCTAATGTTATTACGGC | 834 |
| | TAATGAAGTAGGTTCCA | 835 |
| | TGGAACCTACTTCATTA | 836 |
| Breast Cancer Leu-1080-Stop TTG to TAG | AAATAGGTTCCAGTGATGAAAACATTCAAGCAGAACTAGGTA GAAACAGAGGGCCAAAATTGAATGCTATGCTTAGATTAGGGG TTTTGCAACCTGAGGTCTATAAACAAAGTCTTCCTGG | 837 |
| | CCAGGAAGACTTTGTTTATAGACCTCAGGTTGCAAAACCCCT AATCTAAGCATAGCATTCAATTTTGGCCCTCTGTTTCTACCTA GTTCTGCTTGAATGTTTTCATCACTGGAACCTATTT | 838 |
| | GCCAAAATTGAATGCTA | 839 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | TAGCATTCAATTTTGGC | 840 |
| Breast Cancer Leu-1086-Stop TTA to TGA | AAAACATTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAAAT TGAATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGTCT ATAAACAAAGTCTTCCTGGAAGTAATTGTAAGCATCC | 841 |
| | GGATGCTTACAATTACTTCCAGGAAGACTTTGTTTATAGACCT CAGGTTGCAAAACCCCTAATCTAAGCATAGCATTCAATTTTG GCCCTCTGTTTCTACCTAGTTCTGCTTGAATGTTTT | 842 |
| | GCTTAGATTAGGGGTTT | 843 |
| | AAACCCCTAATCTAAGC | 844 |
| Breast Cancer Ser-1130-Stop TCA to TGA | AGCAAGAATATGAAGAAGTAGTTCAGACTGTTAATACAGATTT CTCTCCATATCTGATTTAGATAACTTAGAACAGCCTATGGGA AGTAGTCATGCATCTCAGGTTTGTTCTGAGACACC | 845 |
| | GGTGTCTCAGAACAAACCTGAGATGCATGACTACTTCCATA GGCTGTTCTAAGTTATCTGAAATCAGATATGGAGAGAAATCT GTATTAACAGTCTGAACTACTTCTTCATATTCTTGCT | 846 |
| | TCTGATTTAGATAACT | 847 |
| | AGTTATCTGAAATCAGA | 848 |
| Breast Cancer Lys-1183-Arg AAA to AGA | CTAGTTTTGCTGAAAATGACATTAAGGAAAGTTCTGCTGTTTT TAGCAAAAGCGTCCAGAAAGGAGAGCTTAGCAGGAGTCCTA GCCCTTTCACCCATACACATTTGGCTCAGGGTTACCG | 849 |
| | CGGTAACCCTGAGCCAAATGTGTATGGGTGAAAGGGCTAGG ACTCCTGCTAAGCTCTCCTTCTGGACGCTTTTGCTAAAAACA GCAGAACTTTCCTTAATGTCAATTTTCAGCAAACTAG | 850 |
| | CGTCCAGAAAGGAGAGC | 851 |
| | GCTCTCCTTCTGGACG | 852 |
| Breast Cancer Gln-1200-Stop CAG to TAG | AGCGTCCAGAAAGGAGAGCTTAGCAGGAGTCCTAGCCCTTT CACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCA AGAAATTAGAGTCCTCAGAAGAGAACTTATCTAGTGAGG | 853 |
| | CCTCACTAGATAAGTTCTCTTCTGAGGACTCTAATTTCTTGCC CCCTCTTCGGTAACCCTGAGCCAAATGTGTATGGGTGAAAGG GCTAGGACTCCTGCTAAGCTCTCCTTTCTGGACGCT | 854 |
| | ATTTGGCTCAGGGTTAC | 855 |
| | GTAACCCTGAGCCAAAT | 856 |
| Breast Cancer Arg-1203-Stop CGA to TGA | AAAGGAGAGCTTAGCAGGAGTCCTAGCCCTTTCACCCATACA CATTTGGCTCAGGGTTACCGAAGAGGGGCCAAGAAATTAGA GTCCTCAGAAGAGAACTTATCTAGTGAGGATGAAGAGC | 857 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | GCTCTTCATCCTCACTAGATAAGTTCTCTTCTGAGGACTCTAA TTTCTTGCCCCCTCTTCGGTAACCCTGAGCCAAATGTGTATG GGTGAAAGGGCTAGGACTCCTGCTAAGCTCTCCTTT | 858 |
| | AGGGTTACCGAAGAGGG | 859 |
| | CCCTCTTCGGTAACCCT | 860 |
| Breast Cancer Glu-1214-Stop GAG to TAG | ACCCATACACATTTGGCTCAGGGTTACCGAAGAGGGGCCAA GAAATTAGAGTCCTCAGAAGAGAAGCTTATCTAGTGAGGATGA AGAGCTTCCCTGCTTCCAACACTTGTTATTTGGTAAAG | 861 |
| | CTTTACCAAATAACAAGTGTTGGAAGCAGGGAAGCTCTTCAT CCTCACTAGATAAGTTCTCTTCTGAGGACTCTAATTTCTTGGC CCCTCTTCGGTAACCCTGAGCCAAATGTGTATGGGT | 862 |
| | CCTCAGAAAGAGAAGCTTA | 863 |
| | TAAGTTCTCTTCTGAGG | 864 |
| Breast Cancer Glu-1219-Asp GAG to GAC | TCAGGGTTACCGAAGAGGGGCCAAGAAATTAGAGTCCTCAG AAGAGAAGCTTATCTAGTGAGGATGAAGAGCTTCCCTGCTTCC AACACTTGTTATTTGGTAAAGTAAACAATATACCTTCT | 865 |
| | AGAAGGTATATTGTTTACTTTACCAAATAACAAGTGTTGGAAG CAGGGAAGCTCTTCATCCTCACTAGATAAGTTCTCTTCTGAG GACTCTAATTTCTTGGCCCCTCTTCGGTAACCCTGA | 866 |
| | TCTAGTGAGGATGAAGA | 867 |
| | TCTTCATCCTCACTAGA | 868 |
| Breast Cancer Glu-1221-Stop GAA to TAA | GGTTACCGAAGAGGGGCCAAGAAATTAGAGTCCTCAGAAGA GAAGCTTATCTAGTGAGGATGAAGAGCTTCCCTGCTTCCAACA CTTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT | 869 |
| | ACTGAGAAGGTATATTGTTTACTTTACCAAATAACAAGTGTTG GAAGCAGGGAAGCTCTTCATCCTCACTAGATAAGTTCTCTTC TGAGGACTCTAATTTCTTGGCCCCTCTTCGGTAACC | 870 |
| | GTGAGGATGAAGAGCTT | 871 |
| | AAGCTCTTCATCCTCAC | 872 |
| Breast Cancer Glu-1250-Stop GAG to TAG | TTATTTGGTAAAGTAAACAATATACCTTCTCAGTCTACTAGGC ATAGCACC GTTGCTACCGAGTGTCTGTCTAAGAACACAGAGG AGAATTTATTATCATTGAAGAATAGCTTAAATGACT | 873 |
| | AGTCATTTAAGCTATTCTTCAATGATAATAAATTCTCCTCTGTG TTCTTAGACAGACACTCGGTAGCAACGGTGCTATGCCTAGTA GACTGAGAAGGTATATTGTTTACTTTACCAAATAA | 874 |
| | TTGCTACCGAGTGTCTG | 875 |

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|--|---|------------|
| | CAGACACT <u>C</u> GGTAGCAA | 876 |
| Breast Cancer Ser-1262-Stop TCA to TAA | CTAGGCATAGCACCGTTGCTACCGAGTGTCTGTCTAAGAACA CAGAGGAGAATTTATTAT <u>C</u> ATTGAAGAATAGCTTAAATGACTG CAGTAACCAGGTAATATTGGCAAAGGCATCTCAGGA | 877 |
| | TCCTGAGATGCCTTTGCCAATATTACCTGGTTACTGCAGTCAT TTAAGCTATTCTTCAAT <u>G</u> ATAATAAATTCTCCTCTGTGTTCTTA GACAGACACTCGGTAGCAACGGTGCTATGCCTAG | 878 |
| | TTTATTAT <u>C</u> ATTGAAGA | 879 |
| | TCTTCAAT <u>G</u> ATAATAAA | 880 |
| Breast Cancer Gln-1281-Stop CAG to TAG | TTATCATTGAAGAATAGCTTAAATGACTGCAGTAACCAGGTAA TATTGGCAAAGGCATCT <u>C</u> AGGAACATCACCTTAGTGAGGAAA CAAATGTTCTGCTAGCTTGTTTTCTTCACAGTGCA | 881 |
| | TGCACTGTGAAGAAAACAAGCTAGCAGAACATTTTGTTCCT CACTAAGGTGATGTTCTT <u>G</u> AGATGCCTTTGCCAATATTACCT GGTTACTGCAGTCATTTAAGCTATTCTTCAATGATAA | 882 |
| | AGGCATCT <u>C</u> AGGAACAT | 883 |
| | ATGTTCTT <u>G</u> AGATGCCT | 884 |
| Breast Cancer Gln-1313-Stop CAG to TAG | GCTAGCTTGTTTTCTTCACAGTGCAGTGAATTGGAAGACTTG ACTGCAAATACAAACACCCAGGATCCTTTCTTGATTGGTTCTT CCAAACAAATGAGGCATCAGTCTGAAAGCCAGGGAG | 885 |
| | CTCCCTGGCTTTTCAGACTGATGCCTCATTTGTTTGAAGAAC CAATCAAGAAAGGATCCTT <u>G</u> GGTGTTTGTATTTGCAGTCAAGT CTTCCAATTCAGTGCAGTGTGAAGAAAACAAGCTAGC | 886 |
| | CAAACACCCAGGATCCT | 887 |
| | AGGATCCTT <u>G</u> GGTGTTTG | 888 |
| Breast Cancer Ile-1318-Val ATT to GTT | TCACAGTGCAGTGAATTGGAAGACTTGACTGCAAATACAAAC ACCCAGGATCCTTTCTTG <u>A</u> TTGGTTCTTCCAAACAAATGAGG CATCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACA | 889 |
| | TGTCAGTGCAGTGAATTGGAAGACTTGACTGCAAATACAAAC TTTGTGTTGGAAGAACCAATCAAGAAAGGATCCTGGGTGTTTG TATTTGCAGTCAAGTCTTCCAATTCAGTGCAGTGTGA | 890 |
| | CTTTCTTG <u>A</u> TTGGTTCT | 891 |
| | AGAACCAATCAAGAAAG | 892 |
| Breast Cancer Gln-1323-Stop CAA to TAA | TTGGAAGACTTGACTGCAAATACAAACACCCAGGATCCTTTC TTGATTGGTTCTTCCAAACAAATGAGGCATCAGTCTGAAAGC CAGGGAGTTGGTCTGAGTGACAAGGAATTGGTTTCAG | 893 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | CTGAAACCAATTCCTTGTCACTCAGACCAACTCCCTGGCTTT CAGACTGATGCCTCATTTGTTTGAAGAACCAATCAAGAAAG GATCCTGGGTGTTTGTATTTGCAGTCAAGTCTTCCAA | 894 |
| | CTTCCAAACAAATGAGG | 895 |
| | CCTCATTTGTTTGAAG | 896 |
| Breast Cancer Arg-1347-Gly AGA to GGA | CAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACAAGGAATT GGTTTCAGATGATGAAGAAAGAGGAACGGGCTTGAAGAAA ATAATCAAGAAGAGCAAAGCATGGATTCAAACCTTAGGTA | 897 |
| | TACCTAAGTTTGAATCCATGCTTTGCTCTTCTTGATTATTTTCT TCCAAGCCCGTTCCTCTTTCTTCATCATCTGAAACCAATTCCT TGCACTCAGACCAACTCCCTGGCTTTCAGACTG | 898 |
| | ATGAAGAAAGAGGAACG | 899 |
| | CGTTCCTCTTTCTTCAT | 900 |
| Breast Cancer Gln-1395-Stop CAG to TAG | GAAACAAGCGTCTCTGAAGACTGCTCAGGGCTATCCTCTCAG AGTGACATTTTAAACCACTCAGGTAAAAAGCGTGTGTGTGTGT GCACATGCGTGTGTGTGGTGTCTTTGCATTTCAGTAG | 901 |
| | CTACTGAATGCAAAGGACACCACACACACGCATGTGCACACA CACACACGCTTTTTACCTGAGTGGTTAAATGTCACTCTGAG AGGATAGCCCTGAGCAGTCTTCAGAGACGCTTGTTTC | 902 |
| | TAACCACTCAGGTAAAA | 903 |
| | TTTTACCTGAGTGGTTA | 904 |
| Breast Cancer Gln-1408-Stop CAG to TAG | TGGTGCCATTTATCGTTTTTGAAGCAGAGGGATACCATGCAA CATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAA GCTGTGTTAGAACAGCATGGGAGCCAGCCTTCTAACA | 905 |
| | TGTTAGAAGGCTGGCTCCCATGCTGTTCTAACACAGCTTCTA GTTTCAGCCATTTCTGCTGGAGCTTTATCAGGTTATGTTGCAT GGTATCCCTCTGCTTCAAAAACGATAAATGGCACCA | 906 |
| | TAAAGCTCCAGCAGGAA | 907 |
| | TTCCTGCTGGAGCTTTA | 908 |
| Breast Cancer Arg-1443-Gly CGA to GGA Arg-1443-Stop CGA to TGA | AGCCAGCCTTCTAACAGCTACCCTTCCATCATAAGTGACTCT TCTGCCCTTGAGGACCTGCGAAATCCAGAACAAAGCACATCA GAAAAAGGTGTGTATTGTTGGCCAAACACTGATATCT | 909 |
| | AGATATCAGTGTTTGGCCAACAATACACACCTTTTTCTGATGT GCTTTGTTCTGGATTTCGAGGTCTCAAGGGCAGAAGAGTC ACTTATGATGGAAGGGTAGCTGTTAGAAGGCTGGCT | 910 |
| | AGGACCTGCGAAATCCA | 911 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | TGGATTTC <u>G</u> CAGGTCCT | 912 |
| Breast Cancer Ser-1512-Ile AGT to ATT | CAGAATAGAACTACCCATCTCAAGAGGAGCTCATTAAAGGTT GTTGATGTGGAGGAGCAAC <u>A</u> CAGCTGGAAGAGTCTGGGCCACA CGATTTGACGGAAACATCTTACTTGCCAAGGCAAGATC | 913 |
| | GATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAAATCGTGTG GCCCAGACTCTTCCAGCT <u>G</u> TTGCTCCTCCACATCAACAACCT TAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCTG | 914 |
| | AGGAGCAAC <u>A</u> CAGCTGGAA | 915 |
| | TTCCAGCT <u>G</u> TTGCTCCT | 916 |
| Breast Cancer Gln-1538-Stop CAG to TAG | ATCTTTCTAGGTCATCCCCTTCTAAATGCCCATCATTAGATGA TAGGTGGTACATGCACAGTTGCTCTGGGAGTCTTCAGAATAG AAACTACCCATCTCAAGAGGAGCTCATTAAAGGTTGT | 917 |
| | ACAACCTTAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCT GAAGACTCCCAGAGCAAC <u>T</u> GTGCATGTACCACCTATCATCTA ATGATGGGCATTTAGAAGGGGATGACCTAGAAAGAT | 918 |
| | CATGCACAGTTGCTCTG | 919 |
| | CAGAGCAAC <u>T</u> GTGCATG | 920 |
| Breast Cancer Glu-1541-Stop GAG to TAG | CAGAATAGAACTACCCATCTCAAGAGGAGCTCATTAAAGGTT GTTGATGTGGAGGAGCAAC <u>A</u> CAGCTGGAAGAGTCTGGGCCACA CGATTTGACGGAAACATCTTACTTGCCAAGGCAAGATC | 921 |
| | GATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAAATCGTGTG GCCCAGACTCTTCCAGCT <u>G</u> TTGCTCCTCCACATCAACAACCT TAATGAGCTCCTCTTGAGATGGGTAGTTTCTATTCTG | 922 |
| | AGGAGCAAC <u>A</u> CAGCTGGAA | 923 |
| | TTCCAGCT <u>G</u> TTGCTCCT | 924 |
| Breast Cancer Thr-1561-Ile ACC to ATC | AACTACCCATCTCAAGAGGAGCTCATTAAAGGTTGTTGATGTG GAGGAGCAACAGCTGGAAG <u>A</u> GTCTGGGCCACACGATTTGAC GGAAACATCTTACTTGCCAAGGCAAGATCTAGGTAATA | 925 |
| | TATTACCTAGATCTTGCCTTGGCAAGTAAGATGTTTCCGTCAA ATCGTGTGGCCAGACT <u>C</u> TTCCAGCTGTTGCTCCTCCACATC AACAACCTTAATGAGCTCCTCTTGAGATGGGTAGTT | 926 |
| | AGCTGGAAGAGTCTGGG | 927 |
| | CCCAGACT <u>C</u> TTCCAGCT | 928 |
| Breast Cancer Tyr-1563-Stop TAC to TAG | TTTGTAATTCAACATTCATCGTTGTGTAAATTAACTTCTCCCA TTCCTTTCAGAGGGAAC <u>C</u> CCCTTACCTGGAATCTGGAATCAGC CTCTTCTCTGATGACCCTGAATCTGATCCTTCTGA | 929 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | TCAGAAGGATCAGATTCAGGGTCATCAGAGAAGAGGCTGATT CCAGATTCCAGGTAAGGGGTTCCCTCTGAAAGGAATGGGAG AAGTTTAATTTACACAACGATGAATGTTGAATTACAAA | 930 |
| | AGAGGGAACCCCTTACC | 931 |
| | GGTAAGGGGTTCCCTCT | 932 |
| Breast Cancer Leu-1564-Pro CTG to CCG | CAACATTCATCGTTGTGTAAATTAACTTCTCCCATTCTTTTC AGAGGGAACCCCTTACCTGGAATCTGGAATCAGCCTCTTCTC TGATGACCCTGAATCTGATCCTTCTGAAGACAGAGC | 933 |
| | GCTCTGTCTTCAGAAGGATCAGATTCAGGGTCATCAGAGAAG AGGCTGATTCCAGATTCCAGGTAAGGGGTTCCCTCTGAAAG GAATGGGAGAAGTTTAATTTACACAACGATGAATGTTG | 934 |
| | CCCTTACCTGGAATCTG | 935 |
| | CAGATTCCAGGTAAGGG | 936 |
| Breast Cancer Gln-1604-Stop CAA to TAA | GCCCCAGAGTCAGCTCGTGTGGCAACATACCATCTTCAACC TCTGCATTGAAAGTTCCCAATTGAAAGTTGCAGAATCTGCC CAGAGTCCAGCTGCTGCTCATACTACTGATACTGCTG | 937 |
| | CAGCAGTATCAGTAGTATGAGCAGCAGCTGGACTCTGGGCA GATTCTGCAACTTTCAATTGGGGAACCTTCAATGCAGAGGTT GAAGATGGTATGTTGCCAACACGAGCTGACTCTGGGGC | 938 |
| | AAGTTCCCAATTGAAA | 939 |
| | TTTCAATTGGGGAACCT | 940 |
| Breast Cancer Lys-1606-Glu AAA to GAA | GAGTCAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCA TTGAAAGTTCCCAATTGAAAGTTGCAGAATCTGCCAGAGT CCAGCTGCTGCTCATACTACTGATACTGCTGGGTATA | 941 |
| | TATACCCAGCAGTATCAGTAGTATGAGCAGCAGCTGGACTCT GGGCAGATTCTGCAACTTTCAATTGGGGAACCTTCAATGCAG AGGTTGAAGATGGTATGTTGCCAACACGAGCTGACTC | 942 |
| | CCCAATTGAAAGTTGCA | 943 |
| | TGCAACTTTCAATTGGG | 944 |
| Breast Cancer Met-1628-Thr ATG to ACG | CAGAATCTGCCAGAGTCCAGCTGCTGCTCATACTACTGATA CTGCTGGGTATAATGCAATTGGAAGAAAGTGTGAGCAGGGAG AAGCCAGAATTGACAGCTTCAACAGAAAGGGTCAACAA | 945 |
| | TTGTTGACCCTTTCTGTTGAAGCTGTCAATTCTGGCTTCTCCC TGCTCACACTTTCTTCCATTGCATTATACCCAGCAGTATCAGT AGTATGAGCAGCAGCTGGACTCTGGGCAGATTCTG | 946 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | TAATGCAAT <u>T</u> GGAAGAAA | 947 |
| | TTTCTTCC <u>A</u> TTGCATTA | 948 |
| Breast Cancer Met-1628-Val ATG to GTG | GCAGAATCTGCCCAGAGTCCAGCTGCTGCTCATACTACTGAT ACTGCTGGGTATAATGCA <u>A</u> TGGAAGAAAGTGTGAGCAGGGA GAAGCCAGAATTGACAGCTTCAACAGAAAGGGTCAACA | 949 |
| | TGTTGACCCTTTCTGTTGAAGCTGTCAATTCTGGCTTCTCCCT GCTCACACTTTCTTCC <u>A</u> TTGCATTATACCCAGCAGTATCAGTA GTATGAGCAGCAGCTGGACTCTGGGCAGATTCTGC | 950 |
| | ATAATGCA <u>A</u> TGGAAGAA | 951 |
| | TTCTTCC <u>A</u> TTGCATTAT | 952 |
| Breast Cancer Pro-1637-Leu CCA to CTA | CTCATACTACTGATACTGCTGGGTATAATGCAATGGAAGAAA GTGTGAGCAGGGAGAAGCC <u>C</u> AGAATTGACAGCTTCAACAGAA AGGGTCAACAAAAGAATGTCCATGGTGGTGTCTGGCCT | 953 |
| | AGGCCAGACACCACCATGGACATTCTTTTGTGACCCTTTCT GTTGAAGCTGTCAATTCT <u>G</u> GCTTCTCCCTGCTCACACTTTCTT CCATTGCATTATACCCAGCAGTATCAGTAGTATGAG | 954 |
| | GGAGAAGCC <u>C</u> AGAATTGA | 955 |
| | TCAATTCT <u>G</u> GCTTCTCC | 956 |
| Breast Cancer Met-1652-Ile ATG to ATA | GAGCAGGGAGAAGCCAGAATTGACAGCTTCAACAGAAAGGG TCAACAAAAGAATGTCCAT <u>G</u> TGGTGTCTGGCCTGACCCCAG AAGAATTTGTGAGTGTATCCATATGTATCTCCCTAATG | 957 |
| | CATTAGGGAGATACATATGGATACACTCACAAATTCTTCTGG GGTCAGGCCAGACACCAC <u>C</u> ATGGACATTCTTTTGTGACCCT TTCTGTTGAAGCTGTCAATTCTGGCTTCTCCCTGCTC | 958 |
| | ATGTCCAT <u>G</u> GTGGTGTG | 959 |
| | GACACCAC <u>C</u> ATGGACAT | 960 |
| Breast Cancer Glu-1694-Stop GAG to TAG | CACTTCCTGATTTTGTTTTCAACTTCTAATCCTTTGAGTGTTTT TCATTCTGCAGATGCT <u>G</u> AGTTTGTGTGTGAACGGACACTGAA ATATTTTCTAGGAATTGCGGGAGGAAAATGGGTAG | 961 |
| | CTACCCATTTTCTCCCGCAATTCTAGAAAATATTTTCAGTGT CCGTTACACACAAACT <u>C</u> AGCATCTGCAGAATGAAAAACACT CAAAGGATTAGAAGTTGAAAACAAAATCAGGAAGTG | 962 |
| | CAGATGCT <u>G</u> AGTTTGTG | 963 |
| | CACAAACT <u>C</u> AGCATCTG | 964 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Breast Cancer Gly-1706-Glu GGA to GAA | GTGTTTTTCATTCTGCAGATGCTGAGTTTGTGTGTGAACGGA CACTGAAATATTTTCTAGGAATTGCGGGAGGAAAATGGGTAG TTAGCTATTTCTGTAAGTATAATACTATTTCTCCCCT | 965 |
| | AGGGGAGAAATAGTATTATACTTACAGAAATAGCTAACTACC CATTTTCCTCCCGCAATTCTAGAAAATATTTTCAGTGTCCGTT CACACACAAACTCAGCATCTGCAGAATGAAAAACAC | 966 |
| | TTTTCTAGGAATTGCGG | 967 |
| | CCGCAATTCTAGAAAA | 968 |
| Breast Cancer Ala-1708-Glu GCG to GAG | TTCATTCTGCAGATGCTGAGTTTGTGTGTGAACGGACACTGA AATATTTTCTAGGAATTGCGGGAGGAAAATGGGTAGTTAGCT ATTTCTGTAAGTATAATACTATTTCTCCCCTCCTCCC | 969 |
| | GGGAGGAGGGGAGAAATAGTATTATACTTACAGAAATAGCTA ACTACCCATTTTCCTCCC <u>G</u> CAATTCCTAGAAAATATTTTCAGTG TCCGTTACACACAAACTCAGCATCTGCAGAATGAA | 970 |
| | AGGAATTGCGGGAGGAA | 971 |
| | TTCCTCCC <u>G</u> CAATTCCT | 972 |
| Breast Cancer Val-1713-Ala GTA to GCA | CTGAGTTTGTGTGTGAACGGACACTGAAATATTTTCTAGGAAT TGCGGGAGGAAAATGGGTAGTTAGCTATTTCTGTAAGTATAA TACTATTTCTCCCCTCCTCCCTTAACACCTCAGAA | 973 |
| | TTCTGAGGTGTTAAAGGGAGGAGGGGAGAAATAGTATTATAC TTACAGAAATAGCTAACTACCCATTTTCCTCCCGCAATTCCTA GAAAATATTTTCAGTGTCCGTTACACACAAACTCAG | 974 |
| | AAAATGGGTAGTTAGCT | 975 |
| | AGCTAACTACCCATTTT | 976 |
| Breast Cancer Trp-1718-Stop TGG to TAG | AACGGACACTGAAATATTTTCTAGGAATTGCGGGAGGAAAAT GGGTAGTTAGCTATTTCTGTAAGTATAATACTATTTCTCCCCT CCTCCCTTAACACCTCAGAATTGCATTTTACACC | 977 |
| | GGTGTA AAAATGCAATTCTGAGGTGTTAAAGGGAGGAGGGG AGAAATAGTATTATACTTACAGAAATAGCTAACTACCCATTTT CCTCCCGCAATTCCTAGAAAATATTTTCAGTGTCCGTT | 978 |
| | CTATTTCTGTAAGTATA | 979 |
| | TATACTTACAGAAATAG | 980 |
| Breast Cancer Glu-1725-Stop GAA to TAA | TTCTGCTGTATGTAACCTGTCTTTTCTATGATCTCTTTAGGGG TGACCCAGTCTATTAAAGAAAGAAAATGCTGAATGAGGTAA GTACTTGATGTTACAACTAACCAGAGATATTCATT | 981 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | AATGAATATCTCTGGTTAGTTTGTAAACATCAAGTACTTACCTC ATTCAGCATTTTTCTTTCTTTAATAGACTGGGTACCCCTAAA GAGATCATAGAAAAGACAGGTTACATACAGCAGAA | 982 |
| | CTATTAAAGAAAGAAAA | 983 |
| | TTTTCTTTCTTTAATAG | 984 |
| Breast Cancer Lys-1727-Stop AAA to TAA | TGTATGTAACCTGTCTTTTCTATGATCTCTTTAGGGGTGACCC AGTCTATTAAAGAAAGAAATGCTGAATGAGGTAAGTACTT GATGTTACAACTAACCAGAGATATTCATTCAGTCA | 985 |
| | TGACTGAATGAATATCTCTGGTTAGTTTGTAAACATCAAGTACT TACCTCATTGAGCATTTTCTTTCTTTAATAGACTGGGTACCC CCTAAAGAGATCATAGAAAAGACAGGTTACATACA | 986 |
| | AAGAAAGAAATGCTG | 987 |
| | CAGCATTTTCTTTCTT | 988 |
| Breast Cancer Pro-1749-Arg CCA to CGA | TCTTTCAGCATGATTTTGAAGTCAGAGGAGATGTGGTCAATG GAAGAAACCAAGGTCCAAAGCGAGCAAGAGAATCCCAG GACAGAAAGGTAAAGCTCCCTCCCTCAAGTTGACAAAA | 989 |
| | TTTTGTCAACTTGAGGGAGGGAGCTTTACCTTTCTGTCCTGG GATTCTCTTGCTCGCTTTGGACCTTGGTGGTTTCTTCCATTGA CCACATCTCCTCTGACTTCAAATCATGCTGAAAGA | 990 |
| | CCAAGGTCCAAAGCGAG | 991 |
| | CTCGCTTTGGACCTTGG | 992 |
| Breast Cancer Arg-1751-Stop CGA to TGA | CAGCATGATTTTGAAGTCAGAGGAGATGTGGTCAATGGAAGA AACCACCAAGGTCCAAAGCGAGCAAGAGAATCCCAGGACAG AAAGGTAAAGCTCCCTCCCTCAAGTTGACAAAAATCTC | 993 |
| | GAGATTTTGTCAACTTGAGGGAGGGAGCTTTACCTTTCTGT CCTGGGATTCTCTTGCTCGCTTTGGACCTTGGTGGTTTCTTC CATTGACCACATCTCCTCTGACTTCAAATCATGCTG | 994 |
| | GTCCAAAGCGAGCAAGA | 995 |
| | TCTTGCTCGCTTTGGAC | 996 |
| Breast Cancer Gln-1756-Stop CAG to TAG | GTCAGAGGAGATGTGGTCAATGGAAGAAACCACCAAGGTCC AAAGCGAGCAAGAGAATCCAGGACAGAAAGGTAAAGCTCC CTCCCTCAAGTTGACAAAAATCTCACCCACCACTCTGT | 997 |
| | ACAGAGTGGTGGGGTGAGATTTTGTCAACTTGAGGGAGGG AGCTTTACCTTTCTGTCCTGGGATTCTCTTGCTCGCTTTGGAC CTTGGTGGTTTCTTCCATTGACCACATCTCCTCTGAC | 998 |
| | GAGAATCCAGGACAGA | 999 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | TCTGTCCTGGGATTCTC | 1000 |
| Breast Cancer Met-1775-Arg ATG to AGG | CTCTCTTCTTCCAGATCTTCAGGGGGCTAGAAATCTGTTGCT ATGGGCCCTTCACCAACATGCCACAGGTAAGAGCCTGGGA GAACCCCAGAGTTCCAGCACCAGCCTTTGTCTTACATA | 1001 |
| | TATGTAAGACAAAGGCTGGTGCTGGAACCTCTGGGGTTCTCCC AGGCTCTTACCTGTGGGCATGTTGGTGAAGGGCCCATAGCA ACAGATTTCTAGCCCCCTGAAGATCTGGAAGAAGAGAG | 1002 |
| | CACCAACATGCCACAG | 1003 |
| | CTGTGGGCATGTTGGTG | 1004 |
| Breast Cancer Trp-1782-Stop TGG to TGA | AGTATGCAGATTACTGCAGTGATTTTACATCTAAATGTCCATT TTAGATCAACTGGAATGGATGGTACAGCTGTGTGGTGCTTCT GTGGTGAAGGAGCTTTCATCATTACCCTTGGCACA | 1005 |
| | TGTGCCAAGGGTGAATGATGAAAGCTCCTTCACCACAGAAGC ACCACACAGCTGTACCATCCATTCCAGTTGATCTAAAATGGA CATTTAGATGTAAATCACTGCAGTAATCTGCATACT | 1006 |
| | CTGGAATGGATGGTACA | 1007 |
| | TGTACCATCCATTCCAG | 1008 |
| Breast Cancer Gln-1785-His CAG to CAT | ATTACTGCAGTGATTTTACATCTAAATGTCCATTTTAGATCAA CTGGAATGGATGGTACAGCTGTGTGGTGCTTCTGTGGTGAA GGAGCTTTCATCATTACCCTTGGCACAGTAAGTATT | 1009 |
| | AATACTTACTGTGCCAAGGGTGAATGATGAAAGCTCCTTCAC CACAGAAGCACACACAGCTGTACCATCCATTCCAGTTGATC TAAAATGGACATTTAGATGTAAATCACTGCAGTAAT | 1010 |
| | ATGGTACAGCTGTGTGG | 1011 |
| | CCACACAGCTGTACCAT | 1012 |
| Breast Cancer Glu-1794-Asp GAG to GAT | GTCCATTTTAGATCAACTGGAATGGATGGTACAGCTGTGTGG TGCTTCTGTGGTGAAGGAGCTTTCATCATTACCCTTGGCAC AGTAAGTATTGGGTGCCCTGTCAGAGAGGGAGGACAC | 1013 |
| | GTGTCCTCCCTCTCTGACAGGGCACCCAATACTTACTGTGCC AAGGGTGAATGATGAAAGCTCCTTCACCACAGAAGCACCA CAGCTGTACCATCCATTCCAGTTGATCTAAAATGGAC | 1014 |
| | GTGAAGGAGCTTTCATC | 1015 |
| | GATGAAAGCTCCTTCAC | 1016 |
| Breast Cancer Arg-1835-Stop CGA to TGA | CTCTGCTTGTGTTCTCTGTCTCCAGCAATTGGGCAGATGTGT GAGGCACCTGTGGTGACCCGAGAGTGGGTGTTGGACAGTGT AGCACTCTACCAGTGCCAGGAGCTGGACACCTACCTGA | 1017 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | TCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAGTGCTACA CTGTCCAACACCCACTCTC <u>G</u> GGTCACCACAGGTGCCTCACA CATCTGCCCAATTGCTGGAGACAGAGAACAACAAGCAGAG | 1018 |
| | TGGTGACCC <u>G</u> AGAGTGG | 1019 |
| | CCACTCTC <u>G</u> GGTCACCA | 1020 |
| Breast Cancer Trp-1837-Arg TGG to CGG | TTGTGTTCTCTGTCTCCAGCAATTGGGCAGATGTGTGAGGCA CCTGTGGTGACCCGAGAGT <u>G</u> GGTGTTGGACAGTGTAGCACT CTACCAGTGCCAGGAGCTGGACACCTACCTGATACCCC | 1021 |
| | GGGGTATCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAGT GCTACACTGTCCAACACCC <u>A</u> CTCTCGGGTCACCACAGGTGC CTCACACATCTGCCCAATTGCTGGAGACAGAGAACAACA | 1022 |
| | CCCGAGAGT <u>G</u> GGTGTTG | 1023 |
| | CAACACCC <u>A</u> CTCTCGGG | 1024 |
| Breast Cancer Trp-1837-Stop TGG to TAG | TGTGTTCTCTGTCTCCAGCAATTGGGCAGATGTGTGAGGCAC CTGTGGTGACCCGAGAGT <u>G</u> GGTGTTGGACAGTGTAGCACTC TACCAGTGCCAGGAGCTGGACACCTACCTGATACCCCA | 1025 |
| | TGGGGTATCAGGTAGGTGTCCAGCTCCTGGCACTGGTAGAG TGCTACACTGTCCAACACCC <u>A</u> CTCTCGGGTCACCACAGGTG CCTCACACATCTGCCCAATTGCTGGAGACAGAGAACAACA | 1026 |
| | CCGAGAGT <u>G</u> GGTGTTGG | 1027 |
| | CCAACACCC <u>A</u> CTCTCGG | 1028 |

Table 10

BRCA2 Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Breast cancer PHE32LEU TTT to CTT | GTAAACTAAGGTGGGATTTTTTTTTTAAATAGATTTAGGAC CAATAAGTCTTAATTGGT <u>T</u> TGAAGAACTTTCTTCAGAAGCTCC ACCCTATAATTCTGAACCTGCAGAAGAATCTGAAC | 1029 |
| | G TTCAGATTCTTCTGCAGGTT CAGAATTATAGGGTGGAGCTT CTGAAGAAAGTTCTTCAA <u>A</u> CCAATTAAGACTTATTGGTCCTAA ATCTATTTAAAAAAAATCCCACCTTAGTTTTAAC | 1030 |
| | TTAATTGGT <u>T</u> TGAAGAA | 1031 |
| | TTCTTCAA <u>A</u> CCAATTAA | 1032 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Breast cancer TYR42CYS TAT to TGT | TAGATTTAGGACCAATAAGTCTTAATTGGTTTGAAGAACTTTC TTCAGAAGCTCCACCCTATAATTCTGAACCTGCAGAAGAATC TGAACATAAAAACAACAATTACGAACCAAACCTATT | 1033 |
| | AATAGGTTTGGTTCGTAATTGTTGTTTTATGTTTCAGATTCTTC TGCAGGTTTCAAGATTATAGGGTGGAGCTTCTGAAGAAAGTTC TTCAAACCAATTAAGACTTATTGGTCCTAAATCTA | 1034 |
| | TCCACCCTATAATTCTG | 1035 |
| | CAGAATTATAGGGTGGG | 1036 |
| Breast cancer LYS53ARG AAA to AGA | AAGAACTTTCTTCAGAAGCTCCACCCTATAATTCTGAACCTGC AGAAGAATCTGAACATAAAAACAACAATTACGAACCAAACCTA TTTAAACTCCACAAAGGAAACCATCTTATAATCA | 1037 |
| | TGATTATAAGATGGTTTCCTTTGTGGAGTTTTAAATAGGTTTG GTTTCGTAATTGTTGTTTTATGTTTCAGATTCTTCTGCAGGTTT AGAATTATAGGGTGGAGCTTCTGAAGAAAGTTCTT | 1038 |
| | TGAACATAAAAACAACA | 1039 |
| | TGTTGTTTTATGTTCA | 1040 |
| Breast cancer Phe81Leu TTC to CTC | CTATTTAAACTCCACAAAGGAAACCATCTTATAATCAGCTGG CTTCAACTCCAATAATTTCAAAGAGCAAGGGCTGACTCTGC CGCTGTACCAATCTCCTGTAAAAGAATTAGATAAAT | 1041 |
| | ATTTATCTAATTCTTTTACAGGAGATTGGTACAGCGGCAGAGT CAGCCCTTGCTCTTTGAATATTATTGGAGTTGAAGCCAGCTG ATTATAAGATGGTTTCCTTTGTGGAGTTTTAAATAG | 1042 |
| | CAATAATTTCAAAGAG | 1043 |
| | CTCTTTGAATATTATTG | 1044 |
| Breast cancer TRP194TERM TGG to TAG | GTCAGACACCAAAACATATTTCTGAAAGTCTAGGAGCTGAGG TGGATCCTGATATGTCTTGGTCAAGTTCTTTAGCTACACCACC CACCCTTAGTTCTACTGTGCTCATAGGTAATAATAG | 1045 |
| | CTATTATTACCTATGAGCACAGTAGAACTAAGGGTGGGTGGT GTAGCTAAAGAACTTGACCAAGACATATCAGGATCCACCTCA GCTCCTAGACTTTCAGAAATATGTTTTGGTGTCTGAC | 1046 |
| | TATGTCTTGGTCAAGTT | 1047 |
| | AACTTGACCAAGACATA | 1048 |
| Breast cancer PRO201ARG CCA to CGA | CTGAAAGTCTAGGAGCTGAGGTGGATCCTGATATGTCTTGGT CAAGTTCTTTAGCTACACCACCCACCCTTAGTTCTACTGTGCT CATAGGTAATAATAGCAAATGTGTATTTACAAGAAA | 1049 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | TTTCTTGTAATACACATTTGCTATTATTACCTATGAGCACAGT AGAACTAAGGGTGGGTGGTGTAGCTAAAGAACTTGACCAAG ACATATCAGGATCCACCTCAGCTCCTAGACTTTTCAG | 1050 |
| | AGCTACACCACCCACCC | 1051 |
| | GGGTGGGTGGTGTAGCT | 1052 |
| Breast cancer Pro222Ser CCT to TCT | ACAATACACATAAATTTTTATCTTACAGTCAGAAATGAAGAAG CATCTGAACTGTATTTCTCATGATACTACTGCTGTAAGTAA ATATGACATTGATTAGACTGTTGAAATTGCTAACA | 1053 |
| | TGTTAGCAATTTCAACAGTCTAATCAATGTCATATTTACTTACA GCAGTAGTATCATGAGGAAATACAGTTTCAGATGCTTCTTCAT TTCTGACTGTAAGATAAAAATTTATGTGTATTGT | 1054 |
| | CTGTATTTCTCATGAT | 1055 |
| | ATCATGAGGAAATACAG | 1056 |
| Breast cancer Leu-414-Term TTG to TAG | AATGGTCTCAACTAACCCCTTCAGGTCTAAATGGAGCCCAGA TGGAGAAAATACCCCTATTGCATATTTCTTCATGTGACCAAAA TATTCAGAAAAAGACCTATTAGACACAGAGAACAA | 1057 |
| | TTGTTCTCTGTGTCTAATAGGTCTTTTTCTGAAATATTTTGGTC ACATGAAGAAATATGCAATAGGGGTATTTTCTCCATCTGGGC TCCATTTAGACCTGAAAGGGTTAGTTGAGACCATT | 1058 |
| | ACCCCTATTGCATATTT | 1059 |
| | AAATATGCAATAGGGGT | 1060 |
| Breast cancer, male Cys554Trp TGT to TGG | AGCCTCTGAAAGTGGACTGGAAATACATACTGTTTGCTCACA GAAGGAGGACTCCTTATGTCCAAATTTAATTGATAATGGAAG CTGGCCAGCCACCACCACACAGAATTCTGTAGCTTTG | 1061 |
| | CAAAGCTACAGAATTCTGTGTGGTGGTGGCTGGCCAGCTTC CATTATCAATTAATTTGGACATAAGGAGTCCTCCTTCTGTGA GCAAACAGTATGTATTTCCAGTCCACTTTCAGAGGCT | 1062 |
| | TCCTTATGTCCAAATTT | 1063 |
| | AAATTTGGACATAAGGA | 1064 |
| Breast cancer Lys944Term AAA to TAA | AACTCTACCATGGTTTTATATGGAGACACAGGTGATAAACAA GCAACCCAAGTGTCAATTAAAAAGATTTGGTTTATGTTCTTG CAGAGGAGAACAAAAATAGTGTAAGCAGCATATAA | 1065 |
| | TTATATGCTGCTTTACACTATTTTTGTTCTCCTCTGCAAGAAC ATAAACCAAATCTTTTTTAATTGACACTTGGGTGCTTGTAT CACCTGTGTCTCCATATAAAACCATGGTAGAGTT | 1066 |
| | TGTCAATTAAAAAGAT | 1067 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | ATCTTTTTT <u>A</u> AATTGACA | 1068 |
| Breast cancer, male Glu1320Term GAA to TAA | ATGACTACTGGCACTTTTGTGAAGAAATTACTGAAAATTACA AGAGAAATACTGAAAAT <u>G</u> AAGATAACAAATATACTGCTGCCA GTAGAAATTCTCATAACTTAGAATTTGATGGCAGTG | 1069 |
| | CACTGCCATCAAATTCTAAGTTATGAGAATTTCTACTGGCAGC AGTATATTTGTTATCTT <u>C</u> ATTTTCAGTATTTCTCTTGTAAATTTTC AGTAATTTCTTCAACAAAAGTGCCAGTAGTCAT | 1070 |
| | CTGAAAAT <u>G</u> AAGATAAC | 1071 |
| | GTTATCTT <u>C</u> ATTTTCAG | 1072 |
| Breast cancer Glu1876Term GAA to TAA | CATGAAACAATTAaaaaaAGTGAAAGACATATTTACAGACAGTT TCAGTAAAGTAATTAAG <u>G</u> AAAAACAACGAGAATAAATCAAAAAT TTGCCAAACGAAAATTATGGCAGGTTGTTACGAGG | 1073 |
| | CCTCGTAACAACCTGCCATAATTTTCGTTTGGCAAATTTTGA TTTATTCTCGTTGTTTT <u>C</u> CTTAATTACTTTACTGAAACTGTCTG TAAATATGTCTTTCACTTTTTTAATTGTTTCATG | 1074 |
| | TAATTAAG <u>G</u> AAAAACAAC | 1075 |
| | GTTGTTTT <u>C</u> CTTAATTA | 1076 |
| Breast cancer Ser1882Term TCA to TAA | TGAAAGACATATTTACAGACAGTTTCAGTAAAGTAATTAAGGA AAACAACGAGAATAAAT <u>C</u> AAAAATTTGCCAAACGAAAATTATG GCAGGTTGTTACGAGGCATTGGATGATTCAGAGGA | 1077 |
| | TCCTCTGAATCATCCAATGCCTCGTAACAACCTGCCATAATTT TCGTTTGGCAAATTTTT <u>G</u> ATTTATTCTCGTTGTTTTCCCTTAATT ACTTTACTGAAACTGTCTGTAAATATGTCTTTCA | 1078 |
| | GAATAAAT <u>C</u> AAAAATTT | 1079 |
| | AAATTTTT <u>G</u> ATTTATTC | 1080 |
| Breast cancer Glu1953Term GAA to TAA | AACCAAAATATGTCTGGATTGGAGAAAGTTTCTAAATATCAC CTTGATGTTAGTTTG <u>G</u> AAACTTCAGATATATGTAAATGTAG TATAGGGAAGCTTCATAAGTCAGTCTCATCTGCAA | 1081 |
| | TTGCAGATGAGACTGACTTATGAAGCTTCCCTATACTACATTT ACATATATCTGAAGTTT <u>C</u> CAAACCTAACATCACAAGGTGATATT TTAGAACTTTCTCCAATCCAGACATATTTTGTT | 1082 |
| | TTAGTTTG <u>G</u> AAACTTCA | 1083 |
| | TGAAGTTT <u>C</u> CAAACCTAA | 1084 |
| Breast cancer Ser1970Term TCA to TAA | TTAGTTTGAAACTTCAGATATATGTAAATGTAGTATAGGGAA GCTTCATAAGTCAGTCT <u>C</u> ATCTGCAAACTTTGTGGGATTTTT AGCACAGCAAGTGGAAAATCTGTCCAGGTATCAGA | 1085 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | TCTGATACCTGGACAGATTTTCCACTTGCTGTGCTAAAAATCC CACAAGTATTTGCAGATGAGACTGACTTATGAAGCTTCCCTAT ACTACATTTACATATATCTGAAGTTTCCAACTAA | 1086 |
| | GTCAGTCTCATCTGCAA | 1087 |
| | TTGCAGATGAGACTGAC | 1088 |
| Breast cancer Gln1987Term CAG | AAGTCAGTCTCATCTGCAAATACTTGTGGGATTTTTAGCACAG CAAGTGGAAATCTGTCCAGGTATCAGATGCTTCATTACAAA ACGCAAGACAAGTGTTTTCTGAAATAGAAGATAGTA | 1089 |
| | TACTATCTTCTATTTTCAGAAAACACTTGTCTTGCGTTTTGTAA TGAAGCATCTGATACCTGGACAGATTTTCCACTTGCTGTGCTA AAAATCCCACAAGTATTTGCAGATGAGACTGACTT | 1090 |
| | AATCTGTCCAGGTATCA | 1091 |
| | TGATACCTGGACAGATT | 1092 |
| Breast cancer Ala2466Val GCA to GTA | AAAATAAGATTAATGACAATGAGATTCATCAGTTTAACAAAA CAACTCCAATCAAGCAGCAGCTGTAACCTTTCACAAAGTGTGA AGAAGAACCTTTAGGTATTGTATGACAATTTGTGTG | 1093 |
| | CACACAAATTGTCATACAATACCTAAAGGTTCTTCTTCACACT TTGTGAAAGTTACAGCTGCTGCTTGATTGGAGTTGTTTTTGT AAACTGATGAATCTCATTGTCATTAATCTTATTTT | 1094 |
| | TCAAGCAGCAGCTGTAA | 1095 |
| | TTACAGCTGCTGCTTGA | 1096 |
| Breast cancer Arg2 | AGGCAACGCGTCTTTCCACAGCCAGGCAGTCTGTATCTTGCA AAAACATCCACTCTGCCTCGAATCTCTCTGAAAGCAGCAGTA GGAGGCCAAGTCCCCTCTGCGTGTCTCATAAACAGG | 1097 |
| | CCTGTTTATGAGGACACGCAGAGGGGACTTGGCCTCCTACT GCTGCTTTCAGAGAGATTCCAGGCAGAGTGGATGTTTTTGCA AGATACAGACTGCCTGGCTGTGGAAAGACGCGTTGCCT | 1098 |
| | CTCTGCCTCGAATCTCT | 1099 |
| | AGAGATTCCAGGCAGAG | 1100 |
| Breast cancer Gln2714Term CAA to TAA | ATTCATTGAGCGCAAATATATCTGAACTTCTAGCAATAAAA CTAGTAGTGCAGATACCCAAAAAGTGGCCATTATTGAACTTA CAGATGGGTGGTATGCTGTTAAGGCCCAGTTAGATC | 1101 |
| | GATCTAACTGGGCCTTAACAGCATACCAACCATCTGTAAGTT CAATAATGGCCACTTTTTGGGTATCTGCACTACTAGTTTTATT GCTAGAAGTTTCAGATATATTTGCGCTCAATGAAAT | 1102 |
| | CAGATACCCAAAAAGTG | 1103 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | CACTTTTTGGGTATCTG | 1104 |
| Breast cancer Leu2776Term TTA to TGA | CAGAACTGGTGGGCTCTCCTGATGCCTGTACACCTCTTGAAG CCCCAGAATCTCTTATGTTAAAGGTAAATTAATTTGCACTCTT GGTAAAAATCAGTCATTGATTGATTAAATTCTAGA | 1105 |
| | TCTAGAATTTAACTGAATCAATGACTGATTTTTTACCAAGAGTG CAAATTAATTTACCTTTAACATAAGAGATTCTGGGGCTTCAAG AGGTGTACAGGCATCAGGAGAGCCCACCAGTTCTG | 1106 |
| | TCTTATGTTAAAGATTT | 1107 |
| | AAATCTTTAACATAAGA | 1108 |
| Breast cancer Gln2893Term CAG to TAG | CCTTTTGTTTTCTTAGAAAAACACAACAAACCATATTTACCATC ACGTGCACTAACAAGACAGCAAGTTCGTGCTTTGCAAGATGG TGCAGAGCTTTATGAAGCAGTGAAGAATGCAGCAG | 1109 |
| | CTGCTGCATTCTTCACTGCTTCATAAAGCTCTGCACCATCTTG CAAAGCACGAACTTGCTGTCTTGTTAGTGCACGTGATGGTAA ATATGGTTTTGTTGTGTTTTCTAAGAAAACAAAAGG | 1110 |
| | TAACAAGACAGCAAGTT | 1111 |
| | AACTTGCTGTCTTGTTA | 1112 |
| Breast cancer Ala2951Thr GCC to ACC | AATCACAGGCAAATGTTGAATGATAAGAAACAAGCTCAGATC CAGTTGGAAATTAGGAAGGCCATGGAATCTGCTGAACAAAAG GAACAAGGTTTATCAAGGGATGTCACAACCGTGTGGA | 1113 |
| | TCCACACGGTTGTGACATCCCTTGATAAACCTTGTTCTTTTG TTCAGCAGATTCCATGGCCTTCCTAATTTCCAAGTGGATCTGA GCTTGTTTCTTATCATTCAACATTTGCCTGTGATT | 1114 |
| | TTAGGAAGGCCATGGAA | 1115 |
| | TTCCATGGCCTTCCTAA | 1116 |
| Breast cancer Met3118Th | ACAATTTACTGGCAATAAAGTTTTGGATAGACCTTAATGAGGA CATTATTAAGCCTCATATGTTAATTGCTGCAAGCAACCTCCAG TGCGGACCAGAATCCAAATCAGGCCTTCTACTTT | 1117 |
| | AAAGTAAGAAGGCCTGATTTGGATTCTGGTCGCCACTGGAG GTTGCTTGCAGCAATTAACATATGAGGCTTAATAATGTCCTCA TTAAGGTCTATCCAAAACCTTTATTGCCAGTAAATTGT | 1118 |
| | GCCTCATATGTTAATTG | 1119 |
| | CAATTAACATATGAGGC | 1120 |
| Breast cancer Thr3401Met ACG to ATG | GACTGAAACGACGTTGTACTACATCTCTGATCAAAGAACAGG AGAGTTCCCAGGCCAGTACGGAAGAATGTGAGAAAAATAAG CAGGACACAATTACAATAAAAAATATATCTAAGCATT | 1121 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | AATGCTTAGATATATTTTTTAGTTGTAATTGTGTCCTGCTTATT TTTCTCACATTCTTCCGTA CTGGCCTGGGA ACTCTCCTGTTCT TTGATCAGAGATGTAGTACAACGTCGTTTCAGTC | 1122 |
| | GGCCAGTACGGAAGAAT | 1123 |
| | ATTCTTCCGTA CTGGCC | 1124 |
| Breast cancer Ile3412Val ATT to GTT | AAAGAACAGGAGAGTTCCCAGGCCAGTACGGAAGAATGTGA GAAAAATAAGCAGGACACAATTACA ACTAAAAATATATCTAA GCATTTGCAAAGGCGACAATAAATTATTGACGCTTAA | 1125 |
| | TTAAGCGTCAATAATTTATTGTCGCCTTTGCAAATGCTTAGAT ATATTTTTTAGTTGTAATTGTGTCCTGCTTATTTTTCTCACATT CTCCGTA CTGGCCTGGGA ACTCTCCTGTTCTTT | 1126 |
| | AGGACACAATTACA ACT | 1127 |
| | AGTTGTAATTGTGTCCT | 1128 |

EXAMPLE 10

Cystic Fibrosis - CFTR

[0219] Cystic fibrosis is a lethal disease affecting approximately one in 2,500 live Caucasian births and is the most common autosomal recessive disease in Caucasians. Patients with this disease have reduced chloride ion permeability in the secretory and absorptive cells of organs with epithelial cell linings, including the airways, pancreas, intestine, sweat glands and male genital tract. This, in turn, reduces the transport of water across the epithelia. The lungs and the GI tract are the predominant organ systems affected in this disease and the pathology is characterized by blocking of the respiratory and GI tracts with viscous mucus. The chloride impermeability in affected tissues is due to mutations in a specific chloride channel, the cystic fibrosis transmembrane conductance regulator protein (CFTR), which prevents normal passage of chloride ions through the cell membrane (Welsh et al., Neuron, 8:821-829 (1992)). Damage to the lungs due to mucus blockage, frequent bacterial infections and inflammation is the primary cause of morbidity and mortality in CF patients and, although maintenance therapy has improved the quality of patients' lives, the median age at death is still only around 30 years. There is no effective treatment for the disease, and therapeutic research is focused on gene therapy using exogenous transgenes in viral vectors and/or activating the defective or other chloride channels in the cell membrane to normalize chloride permeability (Tizzano et al., J. Pediat., 120:337-349 (1992)). However, the death of a teenage patient treated with an adenovirus vector carrying an exogenous CFTR gene in clinical trials in the late 1990's has impacted this area of research.

[0220] The oligonucleotides of the invention for correction of the CFTR gene are attached as a table.

Table 12

CFTR Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Cystic fibrosis Ala46Asp GCT to GAT | AAGGATACAGACAGCGCCTGGAATTGTCAGACATATACCAA TCCCTTCTGTTGATTCTGCTGACAATCTATCTGAAAAATTGGA AAGGTATGTTTCATGTACATTGTTAGTTGAAGAGAG | 1129 |
| | CTCTCTTCAACTAAACAATGTACATGAACATACCTTTCCAATT TTTCAGATAGATTGTCAAGCAGAATCAACAGAAGGGATTGGT ATATGTCTGACAATTCCAGGCGCTGTCTGTATCCTT | 1130 |
| | TGATTCTGCTGACAATC | 1131 |
| | GATTGTCAGCAGAATCA | 1132 |
| Cystic fibrosis Ser50Tyr TCT to TAT | AGCGCCTGGAATTGTCAGACATATACCAAATCCCTTCTGTTG ATTCTGCTGACAATCTATCTGAAAAATTGGAAAGGTATGTTCA TGTACATTGTTTAGTTGAAGAGAGAAATTCATATTA | 1133 |
| | TAATATGAATTTCTCTCTTCAACTAAACAATGTACATGAACATA CCTTTCCAATTTTTTCAGATAGATTGTGAGCAGAATCAACAGAA GGGATTTGGTATATGTCTGACAATTCCAGGCGCT | 1134 |
| | CAATCTATCTGAAAAAT | 1135 |
| | ATTTTTCAGATAGATTG | 1136 |
| Congenital absence of vas deferens Glu56Lys GAA-AAA | AGGACAACATAAAATATTTGCACATGCAACTTATTGGTCCCACT TTTTATTCTTTTGCAGAGAATGGGATAGAGAGCTGGCTTCAA GAAAAATCCTAACTCATTAAATGCCCTTCGGCGAT | 1137 |
| | ATCGCCGAAGGGCATTAAATGAGTTTAGGATTTTTCTTTGAAG CCAGCTCTCTATCCCATTTCTCTGCAAAAGAATAAAAAGTGGG ACCAATAAGTTGCATGTGCAAATATTTTAGTTGTCCT | 1138 |
| | TTTGCAGAGAATGGGAT | 1139 |
| | ATCCCATTTCTCTGCAAA | 1140 |
| Cystic fibrosis Trp57Gly TGG to GGG | AGGACAACATAAAATATTTGCACATGCAACTTATTGGTCCCACT TTTTATTCTTTTGCAGAGAATGGGATAGAGAGCTGGCTTCAA GAAAAATCCTAACTCATTAAATGCCCTTCGGCGAT | 1141 |
| | ATCGCCGAAGGGCATTAAATGAGTTTAGGATTTTTCTTTGAAG CCAGCTCTCTATCCCATTTCTCTGCAAAAGAATAAAAAGTGGG ACCAATAAGTTGCATGTGCAAATATTTTAGTTGTCCT | 1142 |
| | TTTGCAGAGAATGGGAT | 1143 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | ATCCCATT <u>C</u> TCTGCAAA | 1144 |
| Cystic fibrosis Trp57Term TGG to TGA | AACTAAAATATTTGCACATGCAACTTATTGGTCCCACCTTTTTAT TCTTTTGCAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAA ATCCTAAACTCATTAAATGCCCTTCGGCGATGTTTT | 1145 |
| | AAAACATCGCCGAAGGGCATTAAATGAGTTTAGGATTTTTCTTT GAAGCCAGCTCTCTATCCATTCTCTGCAAAAAGAATAAAAAAG TGGGACCAATAAGTTGCATGTGCAAATATTTTAGTT | 1146 |
| | AGAGAATGGGATAGAGA | 1147 |
| | TCTCTATCCATTCTCT | 1148 |
| Congenital absence of vas deferens Asp58Asn GAT to AAT | ACTAAAATATTTGCACATGCAACTTATTGGTCCCACCTTTTTATT CTTTTGCAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAA TCCTAAACTCATTAAATGCCCTTCGGCGATGTTTT | 1149 |
| | AAAAACATCGCCGAAGGGCATTAAATGAGTTTAGGATTTTTCTT TGAAGCCAGCTCTCTATCCATTCTCTGCAAAAAGAATAAAAA GTGGGACCAATAAGTTGCATGTGCAAATATTTTAGT | 1150 |
| | GAGAATGGGATAGAGAG | 1151 |
| | CTCTCTATCCATTCTC | 1152 |
| Cystic fibrosis Glu60Term GAG to TAG | ATATTTGCACATGCAACTTATTGGTCCCACCTTTTTATTCTTTTG CAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAA ACTCATTAAATGCCCTTCGGCGATGTTTTTTCTGGA | 1153 |
| | TCCAGAAAAAACATCGCCGAAGGGCATTAAATGAGTTTAGGAT TTTTCTTTGAAGCCAGCTCTCTATCCATTCTCTGCAAAAGAA TAAAAGTGGGACCAATAAGTTGCATGTGCAAATAT | 1154 |
| | GGGATAGAGAGCTGGCT | 1155 |
| | AGCCAGCTCTCTATCCC | 1156 |
| Cystic fibrosis | GGTCCCACCTTTTTATTCTTTTGCAGAGAATGGGATAGAGAGC TGGCTTCAAAGAAAAATCCTAAACTCATTAAATGCCCTTCGGC GATGTTTTTTCTGGAGATTTATGTTCTATGGAATCTT | 1157 |
| | AAGATTCCATAGAACATAAATCTCCAGAAAAAACATCGCCGA AGGGCATTAAATGAGTTTAGGATTTTTCTTTGAAGCCAGCTCTC TATCCATTCTCTGCAAAAGAATAAAAAGTGGGACC | 1158 |
| | GAAAAATCCTAAACTCA | 1159 |
| | TGAGTTTAGGATTTTTCT | 1160 |
| Cystic fibrosis Arg74Trp CGG to TGG | TGCAGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCT AAACTCATTAAATGCCCTTCGGCGATGTTTTTTCTGGAGATTTA TGTTCTATGGAATCTTTTTATATTTAGGGGTAAGGA | 1161 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | TCCTTACCCCTAAATATAAAAAAGATTCCATAGAACATAAATCT CCAGAAAAAACATCGCCGAGGGGCATTAATGAGTTTAGGATT TTTCTTTGAAGCCAGCTCTCTATCCCATTCTCTGCA | 1162 |
| | ATGCCCTTCGGCGATGT | 1163 |
| | ACATCGCCGAGGGGCAT | 1164 |
| Congenital absence of vas deferens ARG75GLN CGA | GAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAAC TCATTAATGCCCTTCGGCGATGTTTTTCTGGAGATTTATGTT CTATGGAATCTTTTATATTTAGGGGTAAGGATCTC | 1165 |
| | GAGATCCTTACCCCTAAATATAAAAAAGATTCCATAGAACATAA ATCTCCAGAAAAAACATCGCCGAGGGGCATTAATGAGTTTAG GATTTTTCTTTGAAGCCAGCTCTCTATCCCATTCTC | 1166 |
| | CCTTCGGCGATGTTTT | 1167 |
| | AAAAACATCGCCGAAGG | 1168 |
| Cystic fibrosis Arg75Leu CGA to CTA | GAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAAC TCATTAATGCCCTTCGGCGATGTTTTTCTGGAGATTTATGTT CTATGGAATCTTTTATATTTAGGGGTAAGGATCTC | 1169 |
| | GAGATCCTTACCCCTAAATATAAAAAAGATTCCATAGAACATAA ATCTCCAGAAAAAACATCGCCGAGGGGCATTAATGAGTTTAG GATTTTTCTTTGAAGCCAGCTCTCTATCCCATTCTC | 1170 |
| | CCTTCGGCGATGTTTT | 1171 |
| | AAAAACATCGCCGAAGG | 1172 |
| Cystic fibrosis Arg75Term CGA to TGA | AGAGAATGGGATAGAGAGCTGGCTTCAAAGAAAAATCCTAAA CTCATTAATGCCCTTCGGCGATGTTTTTCTGGAGATTTATGT TCTATGGAATCTTTTATATTTAGGGGTAAGGATCT | 1173 |
| | AGATCCTTACCCCTAAATATAAAAAAGATTCCATAGAACATAAA TCTCCAGAAAAAACATCGCCGAGGGGCATTAATGAGTTTAGG ATTTTTCTTTGAAGCCAGCTCTCTATCCCATTCTCT | 1174 |
| | CCCTTCGGCGATGTTTT | 1175 |
| | AAAACATCGCCGAAGG | 1176 |
| Cystic fibrosis Gly85Glu GGA to GAA | AAAATCCTAAACTCATTAATGCCCTTCGGCGATGTTTTTCTG GAGATTTATGTTCTATGGAATCTTTTATATTTAGGGGTAAGG ATCTCATTTGTACATTCATTATGTATCACATAACT | 1177 |
| | AGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCC CTAAATATAAAAAAGATTCCATAGAACATAAATCTCCAGAAAA ACATCGCCGAGGGGCATTAATGAGTTTAGGATTTT | 1178 |
| | GTTCTATGGAATCTTT | 1179 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--------------------------------------|--|------------|
| | AAAAGATTCCATAGAAC | 1180 |
| Cystic fibrosis G | AAAATCCTAAACTCATTAAATGCCCTTCGGCGATGTTTTTCTG GAGATTTATGTTCTATGGAATCTTTTATATTTAGGGGTAAGG ATCTCATTTGTACATTCATTATGTATCACATAACT | 1181 |
| | AGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCC CTAAATATAAAAAGATTCCATAGAACATAAATCTCCAGAAAAA ACATCGCCGAAGGGCATTAAATGAGTTTAGGATTTT | 1182 |
| | GTTCTATGGAATCTTTT | 1183 |
| | AAAAGATTCCATAGAAC | 1184 |
| Cystic fibrosis Leu88S | AACTCATTAAATGCCCTTCGGCGATGTTTTTCTGGAGATTTAT GTTCTATGGAATCTTTTATATTTAGGGGTAAGGATCTCATTT GTACATTCATTATGTATCACATAACTATATGCATT | 1185 |
| | AATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGA TCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAATCT CCAGAAAAAACATCGCCGAAGGGCATTAAATGAGTT | 1186 |
| | AATCTTTTATATTTAG | 1187 |
| | CTAAATATAAAAAGATT | 1188 |
| Cystic fibrosis Phe87Leu TTT to CTT | CCTAAACTCATTAAATGCCCTTCGGCGATGTTTTTCTGGAGAT TTATGTTCTATGGAATCTTTTATATTTAGGGGTAAGGATCTC ATTTGTACATTCATTATGTATCACATAACTATATG | 1189 |
| | CATATAGTTATGTGATACATAATGAATGTACAAATGAGATCCT TACCCCTAAATATAAAAAGATTCCATAGAACATAAATCTCCAG AAAAACATCGCCGAAGGGCATTAAATGAGTTTAGG | 1190 |
| | ATGGAATCTTTTATAT | 1191 |
| | ATATAAAAAGATTCCAT | 1192 |
| Cystic fibrosis Leu88Term TTA to TGA | AACTCATTAAATGCCCTTCGGCGATGTTTTTCTGGAGATTTAT GTTCTATGGAATCTTTTATATTTAGGGGTAAGGATCTCATTT GTACATTCATTATGTATCACATAACTATATGCATT | 1193 |
| | AATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGA TCCTTACCCCTAAATATAAAAAGATTCCATAGAACATAAATCT CCAGAAAAAACATCGCCGAAGGGCATTAAATGAGTT | 1194 |
| | AATCTTTTATATTTAG | 1195 |
| | CTAAATATAAAAAGATT | 1196 |
| Cystic fibrosis Leu88Term TTA to TAA | AACTCATTAAATGCCCTTCGGCGATGTTTTTCTGGAGATTTAT GTTCTATGGAATCTTTTATATTTAGGGGTAAGGATCTCATTT GTACATTCATTATGTATCACATAACTATATGCATT | 1197 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|-----------------------------------|--|------------|
| | AATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCCCTAAATATAAAAAAGATTCCATAGAACATAAATCTCCAGAAAAACATCGCCGAAGGGCATTAAATGAGTT | 1198 |
| | AATCTTTTTATATTTAG | 1199 |
| | CTAAATATAAAAAAGATT | 1200 |
| Cystic fibrosis Gly91Ar | AATGCCCTTCGGCGATGTTTTTCTGGAGATTTATGTTCTATGGAATCTTTTTATATTTAGGGGTAAGGATCTCATTGTACATTCATTATGTATCACATAACTATATGCATTTTTGTGAT | 1201 |
| | ATCACAAAAATGCATATAGTTATGTGATACATAATGAATGTACAAATGAGATCCTTACCCCTAAATATAAAAAAGATTCCATAGAACATAAATCTCCAGAAAAACATCGCCGAAGGGCATT | 1202 |
| | TATATTTAGGGGTAAGG | 1203 |
| | CCTTACCCCTAAATATA | 1204 |
| Cystic fibrosis Gln98A | AATAAATGAAATTTAATTTCTCTGTTTTTCCCCTTTTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCATA GCTTCCTATGACCCGGATAACAAGGAGGAACGCTC | 1205 |
| | GAGCGTTCCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAAAAGGGGAAAAACAGAGAAATTAATTTTCATTTATT | 1206 |
| | AGCAGTACAGCCTCTCT | 1207 |
| | AGAGAGGCTGTACTGCT | 1208 |
| Cystic fibrosis Gln98Term CAG-TAG | AAATAAATGAAATTTAATTTCTCTGTTTTTCCCCTTTTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAACGCT | 1209 |
| | AGCGTTCCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAAAAGGGGAAAAACAGAGAAATTAATTTTCATTTATT | 1210 |
| | AAGCAGTACAGCCTCTC | 1211 |
| | GAGAGGCTGTACTGCT | 1212 |
| Cystic fibrosis Ser108Ph | CCCTTTTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCATAGGCTTATG | 1213 |
| | CATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTTCCTCCTTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTACTGCTTTGGTGACTTCCTACAAAAGGG | 1214 |
| | CATAGCTTCCTATGACC | 1215 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | GGTCATAGGAAGCTATG | 1216 |
| Cystic fibrosis Tyr109Cys TAT to TGT | TTTTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGG GAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAAC GCTCTATCGCGATTTATCTAGGCATAGGCTTATGCCT | 1217 |
| | AGGCATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTTCC TCCTTGTTATCCGGGTCA T AGGAAGCTATGATTCTTCCCAGT AAGAGAGGCTGTA C TGCTTTGGTGACTTCCTACAAA | 1218 |
| | AGCTTCCTATGACCCGG | 1219 |
| | CCGGGTCATAGGAAGCT | 1220 |
| Cystic fibrosis Asp110Hi | TTGTAGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGA AGAATCATAGCTTCCTATGACCCGGATAACAAGGAGGAACGC TCTATCGCGATTTATCTAGGCATAGGCTTATGCCTTC | 1221 |
| | GAAGGCATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTT CCTCCTTGTTATCCGGGTCA T AGGAAGCTATGATTCTTCCCA GTAAGAGAGGCTGTA C TGCTTTGGTGACTTCCTACAA | 1222 |
| | CTTCCTATGACCCGGAT | 1223 |
| | ATCCGGGTCA T AGGAAG | 1224 |
| Congenital absence of vas deferens Pro111Leu CCG to CTG | AGGAAGTCACCAAAGCAGTACAGCCTCTCTTACTGGGAAGAA TCATAGCTTCCTATGACCCGGGATAACAAGGAGGAACGCTCTA TCGCGATTTATCTAGGCATAGGCTTATGCCTTCTCTT | 1225 |
| | AAGAGAAGGCATAAGCCTATGCCTAGATAAATCGCGATAGAG CGTTCCTCCTTGTTATCCGGGTCATAGGAAGCTATGATTCTT CCCAGTAAGAGAGGCTGTA C TGCTTTGGTGACTTCCT | 1226 |
| | CTATGACCCGGGATAACA | 1227 |
| | TGTTATCCGGGTCATAG | 1228 |
| Cystic fibrosis A | GTACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGAC CCGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGC ATAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGC | 1229 |
| | GCAGTGTCTCACATAAAGAGAAGGCATAAGCCTATGCCTA GATAAATCGCGATAGAGCGTTCCTCCTTGTTATCCGGGTCAT AGGAAGCTATGATTCTTCCCAGTAAGAGAGGCTGTAC | 1230 |
| | AGGAGGAACGCTCTATC | 1231 |
| | GATAGAGCGTTCCTCCT | 1232 |
| Cystic fibrosis Arg117H | TACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACC CGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCA TAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCT | 1233 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|-------------------------------|---|------------|
| | AGCAGTGTCTCACAATAAAGAGAAGGCATAAGCCTATGCCT AGATAAATCGCGATAGAGCGTTCCTCCTTGTATCCGGGTCA TAGGAAGCTATGATTCTTCCAGTAAGAGAGGCTGTA | 1234 |
| | GGAGGAACGCTCTATCG | 1235 |
| | CGATAGAGCGTTCCTCC | 1236 |
| Cystic fibrosis Arg117L | TACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACC CGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCA TAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCT | 1237 |
| | AGCAGTGTCTCACAATAAAGAGAAGGCATAAGCCTATGCCT AGATAAATCGCGATAGAGCGTTCCTCCTTGTATCCGGGTCA TAGGAAGCTATGATTCTTCCAGTAAGAGAGGCTGTA | 1238 |
| | GGAGGAACGCTCTATCG | 1239 |
| | CGATAGAGCGTTCCTCC | 1240 |
| Cystic fibrosis Arg117P | TACAGCCTCTCTTACTGGGAAGAATCATAGCTTCCTATGACC CGGATAACAAGGAGGAACGCTCTATCGCGATTTATCTAGGCA TAGGCTTATGCCTTCTCTTTATTGTGAGGACACTGCT | 1241 |
| | AGCAGTGTCTCACAATAAAGAGAAGGCATAAGCCTATGCCT AGATAAATCGCGATAGAGCGTTCCTCCTTGTATCCGGGTCA TAGGAAGCTATGATTCTTCCAGTAAGAGAGGCTGTA | 1242 |
| | GGAGGAACGCTCTATCG | 1243 |
| | CGATAGAGCGTTCCTCC | 1244 |
| Cystic fibrosis | CTCTTACTGGGAAGAATCATAGCTTCCTATGACCCGGATAAC AAGGAGGAACGCTCTATCGCGATTTATCTAGGCATAGGCTTA TGCCTTCTCTTTATTGTGAGGACACTGCTCCTACACC | 1245 |
| | GGTGTAGGAGCAGTGTCTCACAATAAAGAGAAGGCATAAG CCTATGCCTAGATAAATCGCGATAGAGCGTTCCTCCTTGTTA TCCGGGTCATAGGAAGCTATGATTCTTCCAGTAAGAG | 1246 |
| | GCTCTATCGCGATTTAT | 1247 |
| | ATAAATCGCGATAGAGC | 1248 |
| Cystic fibrosis Tyr122Te | GGGAAGAATCATAGCTTCCTATGACCCGGATAACAAGGAGG AACGCTCTATCGCGATTTATCTAGGCATAGGCTTATGCCTTCT CTTTATTGTGAGGACACTGCTCCTACACCCAGCCATT | 1249 |
| | AATGGCTGGGTGTAGGAGCAGTGTCTCACAATAAAGAGAA GGCATAAGCCTATGCCTAGATAAATCGCGATAGAGCGTTCCT CCTTGTTATCCGGGTCATAGGAAGCTATGATTCTTCCC | 1250 |
| | GCGATTTATCTAGGCAT | 1251 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|-------------------------------|---|------------|
| | ATGCCTAGATAAAATCGC | 1252 |
| Cystic fibrosis | TAGCTTCCTATGACCCGGATAACAAGGAGGAACGCTCTATCG CGATTTATCTAGGCATAGGCTTATGCCTTCTCTTTATTGTGAG GACACTGCTCCTACACCCAGCCATTTTTGGCCTTCA | 1253 |
| | TGAAGGCCAAAAATGGCTGGGTGTAGGAGCAGTGTCTCAC AATAAGAGAAGGCATAAGCCTATGCCTAGATAAAATCGCGAT AGAGCGTTCCTCCTTGTATCCGGGTCATAGGAAGCTA | 1254 |
| | AGGCATAGGCTTATGCC | 1255 |
| | GGCATAAGCCTATGCCT | 1256 |
| Cystic fibrosis H | TCGCGATTTATCTAGGCATAGGCTTATGCCTTCTCTTTATTGT GAGGACACTGCTCCTACACCCAGCCATTTTTGGCCTTCATCA CATTGGAATGCAGATGAGAATAGCTATGTTTAGTTT | 1257 |
| | AACTAAACATAGCTATTCTCATCTGCATTCCAATGTGATGAA GGCCAAAAATGGCTGGGTGTAGGAGCAGTGTCTCACAATA AAGAGAAGGCATAAGCCTATGCCTAGATAAAATCGCGA | 1258 |
| | GCTCCTACACCCAGCCA | 1259 |
| | TGGCTGGGTGTAGGAGC | 1260 |
| Cystic fibrosis Ala141A | TTTATCTAGGCATAGGCTTATGCCTTCTCTTTATTGTGAGGAC ACTGCTCCTACACCCAGCCATTTTTGGCCTTCATCACATTGG AATGCAGATGAGAATAGCTATGTTTAGTTTGATTGA | 1261 |
| | TAAATCAAATAAACATAGCTATTCTCATCTGCATTCCAATGT GATGAAGGCCAAAAATGGCTGGGTGTAGGAGCAGTGTCTC ACAATAAGAGAAGGCATAAGCCTATGCCTAGATAAA | 1262 |
| | ACACCCAGCCATTTTTG | 1263 |
| | CAAAAATGGCTGGGTGT | 1264 |
| Cystic fibrosis Ile148T | GCCTTCTCTTTATTGTGAGGACACTGCTCCTACACCCAGCCA TTTTTGGCCTTCATCACATTGGAATGCAGATGAGAATAGCTAT GTTTAGTTTGATTTATAAGAAGGTAATACTTCCTTG | 1265 |
| | CAAGGAAGTATTACCTTCTTATAAATAAACTAAACATAGCTA TTCTCATCTGCATTCCAATGTGATGAAGGCCAAAAATGGCTG GGTGTAGGAGCAGTGTCTCACAATAAAGAGAAGGC | 1266 |
| | TCATCACATTGGAATGC | 1267 |
| | GCATTCCAATGTGATGA | 1268 |
| Cystic fibrosis Gly149Ar | CTTCTCTTTATTGTGAGGACACTGCTCCTACACCCAGCCATTT TTGGCCTTCATCACATTGGAATGCAGATGAGAATAGCTATGT TTAGTTTGATTTATAAGAAGGTAATACTTCCTTGCA | 1269 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | TGCAAGGAAGTATTACCTTCTTATAAATCAAACATAACATAGC TATTCTCATCTGCATTCCAATGTGATGAAGGCCAAAAATGGCT GGGTGTAGGAGCAGTGTCTCACAATAAAGAGAAG | 1270 |
| | ATCACATTGGAATGCAG | 1271 |
| | CTGCATTCCAATGTGAT | 1272 |
| Cystic fibrosis GI | TTTATTGTGAGGACACTGCTCCTACACCCAGCCATTTTTGGC CTTCATCACATTGGAATGCAGATGAGAATAGCTATGTTTAGTT TGATTATAAGAAGGTAATACTTCCTTGACAGGCC | 1273 |
| | GGCCTGTGCAAGGAAGTATTACCTTCTTATAAATCAAACATAA CATAGCTATTCTCATCTGCATTCCAATGTGATGAAGGCCAAAA ATGGCTGGGTGTAGGAGCAGTGTCTCACAATAA | 1274 |
| | TTGGAATGCAGATGAGA | 1275 |
| | TCTCATCTGCATTCCAA | 1276 |
| Cystic fibrosis | AATATATTTGTATTTTGTGTTGAAATTATCTAACTTTCCATTT TTCTTTTAGACTTTAAAGCTGTCAAGCCGTGTTCTAGATAAAA TAAGTATTGGACAACCTGTTAGTCTCCTTTCCA | 1277 |
| | TGGAAAGGAGACTAACAAGTTGTCCAATACTTATTTTATCTAG AACACGGCTTGACAGCTTTAAAGTCTAAAAGAAAAATGGAAA GTTAGATAATTTCAACAAACAAAATACAAATATATT | 1278 |
| | AGACTTTAAAGCTGTCA | 1279 |
| | TGACAGCTTTAAAGTCT | 1280 |
| Cystic fibrosis Ile175Val ATA-GTA | TTATCTAACTTTCCATTTTTCTTTTAGACTTTAAAGCTGTCAAG CCGTGTTCTAGATAAAAATAAGTATTGGACAACCTGTTAGTCTC CTTTCCAACAACCTGAACAAATTTGATGAAGTAT | 1281 |
| | ATACTTCATCAAATTTGTTTCAAGTTGTTGGAAAGGAGACTAAC AAGTTGTCCAATACTTATTTTATCTAGAACACGGCTTGACAGC TTTAAAGTCTAAAAGAAAAATGGAAAGTTAGATAA | 1282 |
| | TAGATAAAAATAAGTATT | 1283 |
| | AATACTTATTTTATCTA | 1284 |
| Cystic fibrosis G | TTTCCATTTTTCTTTTAGACTTTAAAGCTGTCAAGCCGTGTTCT AGATAAAATAAGTATTGGACAACCTGTTAGTCTCCTTTCCAAC AACCTGAACAAATTTGATGAAGTATGTACCTATT | 1285 |
| | AATAGGTACATACTTCATCAAATTTGTTTCAAGTTGTTGGAAAG GAGACTAACAAGTTGTCCAATACTTATTTTATCTAGAACACGG CTTGACAGCTTTAAAGTCTAAAAGAAAAATGGAAA | 1286 |
| | TAAGTATTGGACAACCT | 1287 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|-------------------------------|--|------------|
| | AAGTTGTCCAATACTTA | 1288 |
| Cystic fibrosis His199G | AAGATACAATGACACCTGTTTTGCTGTGCTTTTATTTTCCAG GGACTTGCATTGGCACATTTTCGTGTGGATCGCTCCTTTGCAA GTGGCACTCCTCATGGGGCTAATCTGGGAGTTGTTA | 1289 |
| | TAACAACTCCCAGATTAGCCCCATGAGGAGTGCCACTTGCAA AGGAGCGATCCACACGAAATGTGCCAATGCAAGTCCCTGGA AAATAAAAGCACAGCAAAAACAGGTGTCATTGTATCTT | 1290 |
| | TTGGCACATTTTCGTGTG | 1291 |
| | CACACGAAATGTGCCAA | 1292 |
| Cystic fibrosis His199T | GGAAGATACAATGACACCTGTTTTGCTGTGCTTTTATTTTCC AGGGACTTGCATTGGCACATTTTCGTGTGGATCGCTCCTTTGC AAGTGGCACTCCTCATGGGGCTAATCTGGGAGTTGT | 1293 |
| | ACAACTCCCAGATTAGCCCCATGAGGAGTGCCACTTGCAAAG GAGCGATCCACACGAAATGTGCCAATGCAAGTCCCTGGAAA ATAAAAGCACAGCAAAAACAGGTGTCATTGTATCTTCC | 1294 |
| | CATTGGCACATTTTCGTG | 1295 |
| | CACGAAATGTGCCAATG | 1296 |
| Cystic fibrosis P | TGTTTTGCTGTGCTTTTATTTTCCAGGGACTTGCATTGGCAC ATTTTCGTGTGGATCGCTCCTTTGCAAGTGGCACTCCTCATGG GGCTAATCTGGGAGTTGTTACAGGCGTCTGCCTTCT | 1297 |
| | AGAAGGCAGACGCCTGTAACAACTCCCAGATTAGCCCCATG AGGAGTGCCACTTGCAAAGGAGCGATCCACACGAAATGTGC CAATGCAAGTCCCTGGAAAATAAAAGCACAGCAAAAACA | 1298 |
| | GGATCGCTCCTTTGCAA | 1299 |
| | TTGCAAAGGAGCGATCC | 1300 |
| Cystic fibrosis L | TTTGCTGTGCTTTTATTTTCCAGGGACTTGCATTGGCACATTT CGTGTGGATCGCTCCTTTGCAAGTGGCACTCCTCATGGGGC TAATCTGGGAGTTGTTACAGGCGTCTGCCTTCTGTGG | 1301 |
| | CCACAGAAGGCAGACGCCTGTAACAACTCCCAGATTAGCCC CATGAGGAGTGCCACTTGCAAAAGGAGCGATCCACACGAAAT GTGCCAATGCAAGTCCCTGGAAAATAAAAGCACAGCAAA | 1302 |
| | CGCTCCTTTGCAAGTGG | 1303 |
| | CCACTTGCAAAAGGAGCG | 1304 |
| Cystic fibrosis Gln220Te | TTCGTGTGGATCGCTCCTTTGCAAGTGGCACTCCTCATGGGG CTAATCTGGGAGTTGTTACAGGCGTCTGCCTTCTGTGGACTT GGTTTCCTGATAGTCCTTGCCCTTTTTCAGGCTGGGC | 1305 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|-------------------------------|--|------------|
| | GCCCAGCCTGAAAAAGGGCAAGGACTATCAGGAAACCAAGT CCACAGAAGGCAGACGCCTGTAACAACTCCCAGATTAGCCC CATGAGGAGTGCCACTTGCAAAGGAGCGATCCACACGAA | 1306 |
| | AGTTGTTACAGGCGTCT | 1307 |
| | AGACGCCTGTAACAACT | 1308 |
| Cystic f | CCTTTGCAAGTGGCACTCCTCATGGGGCTAATCTGGGAGTTG TTACAGGCGTCTGCCTTCTGTGGACTTGGTTTCCTGATAGTC CTTGCCCTTTTTTCAGGCTGGGCTAGGGAGAATGATGA | 1309 |
| | TCATCATTCTCCCTAGCCCAGCCTGAAAAAGGGCAAGGACTA TCAGGAAACCAAGTCCACAAGAAGGCAGACGCCTGTAACAAC TCCCAGATTAGCCCCATGAGGAGTGCCACTTGCAAAGG | 1310 |
| | CTGCCTTCTGTGGACTT | 1311 |
| | AAGTCCACAAGAAGGCAG | 1312 |
| Cystic fibrosis V | TGGGGCTAATCTGGGAGTTGTTACAGGCGTCTGCCTTCTGTG GACTTGGTTTCCTGATAGTCCTTGCCCTTTTTTCAGGCTGGGC TAGGGAGAATGATGATGAAGTACAGGTAGCAACCTAT | 1313 |
| | ATAGGTTGCTACCTGTACTTCATCATCATTCTCCCTAGCCCAG CCTGAAAAAGGGCAAGGACTATCAGGAAACCAAGTCCACAG AAGGCAGACGCCTGTAACAACTCCCAGATTAGCCCCA | 1314 |
| | CCTGATAGTCCTTGCCC | 1315 |
| | GGGCAAGGACTATCAGG | 1316 |
| Cystic fibrosis Gly239A | GTTACAGGCGTCTGCCTTCTGTGGACTTGGTTTCCTGATAGT CCTTGCCCTTTTTTCAGGCTGGGCTAGGGAGAATGATGATGAA GTACAGGTAGCAACCTATTTTCATAACTTGAAAGTTT | 1317 |
| | AACTTTCAAGTTATGAAAATAGGTTGCTACCTGTACTTCATC ATCATTCTCCCTAGCCCAGCCTGAAAAAGGGCAAGGACTATC AGGAAACCAAGTCCACAGAAGGCAGACGCCTGTAAC | 1318 |
| | TTTCAGGCTGGGCTAGG | 1319 |
| | CCTAGCCCAGCCTGAAA | 1320 |

EXAMPLE 11

Cyclin-dependent kinase inhibitor 2A - CDKN2A

[0221] The human CDKN2A gene was also designated MTS-1 for multiple tumor suppressor-1 and has been implicated in multiple cancers including, for example, malignant melanoma.

- 5 Malignant melanoma is a cutaneous neoplasm of melanocytes. Melanomas generally have features of asymmetry, irregular border, variegated color, and diameter greater than 6 mm. The precise cause of

melanoma is unknown, but sunlight and heredity are risk factors. Melanoma has been increasing during the past few decades.

[0222] The CDKN2A gene has been found to be homozygously deleted at high frequency in cell lines derived from tumors of lung, breast, brain, bone, skin, bladder, kidney, ovary, and lymphocyte. Melanoma cell lines carried at least one copy of CDKN2A in combination with a deleted allele. Melanoma cell lines that carried at least 1 copy of CDKN2A frequently showed nonsense, missense, or frameshift mutations in the gene. Thus, CDKN2A may rival p53 (see Example 6) in the universality of its involvement in tumorigenesis. The attached table discloses the correcting oligonucleotide base sequences for the CDKN2A oligonucleotides of the invention.

Table 13

CDKN2A Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|----------------------------------|--|------------|
| Melanoma Trp15Term TGG-TAG | GGGCGGCGGGGAGCAGCATGGAGCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGCCGGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGG | 1321 |
| | CCCGCCTCCAGCAGCGCCCGCACCTCCTCTACCCGACCCCGGGCCGCGGCCGTGGCCAGCCAGTCAGCCGAAGGCTCCATGTGCTCCCCGCCGCCGGCTCCATGCTGCTCCCCGCCGCC | 1322 |
| | GGCTGACTGGCTGGCCA | 1323 |
| | TGGCCAGCCAGTCAGCC | 1324 |
| Melanoma Leu16Pro CTG-CCG | CGGCGGGGAGCAGCATGGAGCCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCCACGGCCGCGGCCCGGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGGC | 1325 |
| | GCCCCGCCTCCAGCAGCGCCCGCACCTCCTCTACCCGACC CGGGGCCGCGGCCGTGGCCAGCCAGTCAGCCGAAGGCTCCA TGCTGCTCCCCGCCGCCGGCTCCATGCTGCTCCCCGCCG | 1326 |
| | TGACTGGCTGGCCACGG | 1327 |
| | CCGTGGCCAGCCAGTCA | 1328 |
| Melanoma Gly23Asp GGT-GAT | CGGCGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGCCACGGCCGCGGCCCGGGGTCGGGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGGCGCTGCCCAACGCACCGAATAG | 1329 |
| | CTATTCGGTGCGTTGGGCAGCGCCCCCGCCTCCAGCAGCGCCGCACCTCCTCTACCCGACCCCGGGCCGCGGCCGTGGCCAGCCAGTCAGCCGAAGGCTCCATGCTGCTCCCCGCCGCC | 1330 |
| | GGCCCGGGGTCGGGTAG | 1331 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|-----------------------------------|--|---------------|
| | CTACCCGAC <u>C</u> CCCCGGGCC | 1332 |
| Melanoma Arg24Pro CGG-CCG | CGGCGGGGAGCAGCATGGAGCCTTCGGCTGACTGGCTGGCC ACGGCCGCGGCCCGGGGTC <u>G</u> GGTAGAGGAGGTGCGGGCGC TGCTGGAGGCGGGGGCGCTGCCCAACGCACCGAATAGTTA | 1333 |
| | TAACCTATTCGGTGCGTTGGGACGCGCCCCGCCTCCAGCAGC GCCCCGACCTCCTCTACCC <u>G</u> ACCCCCGGGCCGCGGCCGTGGC CAGCCAGTCAGCCGAAGGCTCCATGCTGCTCCCCGCCG | 1334 |
| | CCGGGGTC <u>G</u> GGTAGAGG | 1335 |
| | CCTCTACCC <u>G</u> ACCCCCG | 1336 |
| Melanoma Leu32Pro CTG-CCG | CGGCTGACTGGCTGGCCACGGCCGCGGCCCGGGGTCTGGGT AGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGGCGCTGCC AACGCACCGAATAGTTACGGTCGGAGGCCGATCCAGGTGGG | 1337 |
| | CCCACCTGGATCGGCCTCCGACCGTAACTATTCGGTGCGTTG GGCAGCGCCCCCGCCTCC <u>A</u> GCAGCGCCCGCACCTCCTCTAC CCGACCCCCGGGCCGCGGCCGTGGCCAGCCAGTCAGCCG | 1338 |
| | GGCGCTGCT <u>I</u> GGAGGCGG | 1339 |
| | CCGCCTCC <u>A</u> GCAGCGCC | 1340 |
| Melanoma Gly35Ala GGG-GCG | GGCTGGCCACGGCCGCGGCCCGGGGTCTGGGTAGAGGAGGT GCGGGCGCTGCTGGAGGCGGG <u>G</u> GGCGCTGCCCAACGCACCG AATAGTTACGGTCGGAGGCCGATCCAGGTGGGTAGAGGGTC | 1341 |
| | GACCTCTACCCACCTGGATCGGCCTCCGACCGTAACTATTC GGTGCGTTGGGACGCGCC <u>C</u> CGCCTCCAGCAGCGCCCGCAC CTCCTCTACCCGACCCCGGGCCGCGGCCGTGGCCAGCC | 1342 |
| | GGAGGCGGG <u>G</u> GGCGCTGC | 1343 |
| | GCAGCGCC <u>C</u> CCGCCTCC | 1344 |
| Melanoma Tyr44Term TACg-TAA | GGTAGAGGAGGTGCGGGCGCTGCTGGAGGCGGGGGCGCTG CCCAACGCACCGAATAGTTA <u>C</u> GGTCGGAGGCCGATCCAGGTG GGTAGAGGGTCTGCAGCGGGAGCAGGGGATGGCGGGCGA | 1345 |
| | TCGCCCCGCCATCCCCTGCTCCCGCTGCAGACCCTCTACCCAC CTGGATCGGCCTCCGACC <u>G</u> TAACTATTCGGTGCGTTGGGCAG CGCCCCCGCCTCCAGCAGCGCCCGCACCTCCTCTACC | 1346 |
| | AATAGTTA <u>C</u> GGTCGGAG | 1347 |
| | CTCCGACC <u>G</u> TAACTATT | 1348 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|----------------------------------|---|---------------|
| Melanoma Met53Ile ATGa-ATC | TCTCCCATACCTGCCCCACCCTGGCTCTGACCACTCTGCTCT CTCTGGCAGGTCATGATGATGGGCAGCGCCCGCGTGGCGGA GCTGCTGCTGCTCCACGGCGCGGAGCCCCAACTGCGCA | 1349 |
| | TGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCTCCG CCACGCGGGCGCTGCCCATCATCATGACCTGCCAGAGAGAG CAGAGTGGTCAGAGCCAGGGTGGGGGCAGGTATGGGAGA | 1350 |
| | GTCATGATGATGGGCAG | 1351 |
| | CTGCCCATCATCATGAC | 1352 |
| Melanoma Met54Ile ATGg-ATT | CCCATACCTGCCCCACCCTGGCTCTGACCACTCTGCTCTCTC TGGCAGGTCATGATGATGGGCAGCGCCCGCGTGGCGGAGCT GCTGCTGCTCCACGGCGCGGAGCCCCAACTGCGCAGAC | 1353 |
| | GTCTGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCT CCGCCACGCGGGCGCTGCCCATCATCATGACCTGCCAGAGA GAGCAGAGTGGTCAGAGCCAGGGTGGGGGCAGGTATGGG | 1354 |
| | ATGATGATGGGCAGCGC | 1355 |
| | GCGCTGCCCATCATCAT | 1356 |
| Melanoma Ser56Ile AGC-ATC | GCCGGCCCCACCCTGGCTCTGACCATTCTGTTCTCTCTGGC AGGTCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTG CTGCTCCACGGCGCGGAGCCCCAACTGCGCCGACCCCGC | 1357 |
| | GCGGGGTGCGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCA GCAGCTCCGCCACTCGGGCGCTGCCCATCATCATGACCTGCC AGAGAGAACAGAATGGTCAGAGCCAGGGTGGGGGCCGGC | 1358 |
| | GATGGGCAGCGCCCGAG | 1359 |
| | CTCGGGCGCTGCCCATC | 1360 |
| Melanoma Ala57Val GCC-GTC | GGCCCCACCCTGGCTCTGACCATTCTGTTCTCTCTGGCAGG TCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTG CTCCACGGCGCGGAGCCCCAACTGCGCCGACCCCGCCAC | 1361 |
| | GTGGCGGGGTGCGCGCAGTTGGGCTCCGCGCCGTGGAGCA GCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATGACCT GCCAGAGAGAACAGAATGGTCAGAGCCAGGGTGGGGGCC | 1362 |
| | GGGCAGCGCCCGAGTGG | 1363 |
| | CCACTCGGCGCTGCCC | 1364 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|-----------------------------------|---|------------|
| Melanoma Arg58Term cCGA-TGA | CCCCACCCTGGCTCTGACCATTCTGTTCTCTCTGGCAGGTCA TGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTC CACGGCGCGGAGCCCAACTGCGCCGACCCCGCCACTC | 1365 |
| | GAGTGGCGGGGTGCGGCGCAGTTGGGCTCCGCGCCGTGGAG CAGCAGCAGCTCCGCCACTCGGGCGCTGCCATCATCATGAC CTGCCAGAGAGAACAGAATGGTCAGAGCCAGGGTGGGGG | 1366 |
| | GCAGCGCCCGAGTGGCG | 1367 |
| | CGCCACTCGGGCGCTGC | 1368 |
| Melanoma Val59Gly GTG-GGG | CACCCTGGCTCTGACCATTCTGTTCTCTCTGGCAGGTCATGAT GATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGCTCCACG GCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCAC | 1369 |
| | GTGAGAGTGGCGGGGTGCGGCGCAGTTGGGCTCCGCGCCGTG GAGCAGCAGCAGCTCCGCCACTCGGGCGCTGCCATCATCAT GACCTGCCAGAGAGAACAGAATGGTCAGAGCCAGGGTG | 1370 |
| | CGCCCGAGTGGCGGAGC | 1371 |
| | GCTCCGCCACTCGGGCG | 1372 |
| Melanoma Leu62Pro CTG-CCG | TCTGACCACTCTGCTCTCTCTGGCAGGTCATGATGATGGGCA GCGCCCGCGTGGCGGAGCTGCTGCTGCTCCACGGCGCGGAG CCCAACTGCGCAGACCCTGCCACTCTACCCGACCGGT | 1373 |
| | ACCGGTCGGGTGAGAGTGGCAGGGTCTGCGCAGTTGGGCTC CGCGCCGTGGAGCAGCAGCAGCTCCGCCACGCGGGCGCTGC CCATCATCATGACCTGCCAGAGAGAGCAGAGTGGTCAGA | 1374 |
| | GGCGGAGCTGCTGCTGC | 1375 |
| | GCAGCAGCAGCTCCGCC | 1376 |
| Melanoma Ala68Val GCG-GTG | TCTGGCAGGTCATGATGATGGGCAGCGCCCGCGTGGCGGAG CTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCAGACCC TGCCACTCTACCCGACCGGTGCATGATGCTGCCCGGGA | 1377 |
| | TCCCGGGCAGCATCATGCACCGGTCGGGTGAGAGTGGCAGG GTCTGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCT CCGCCACGCGGGCGCTGCCATCATCATGACCTGCCAGA | 1378 |
| | CCACGGCGCGGAGCCCA | 1379 |
| | TGGGCTCCGCGCCGTGG | 1380 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|----------------------------------|--|---------------|
| Melanoma Asn71Lys AACT-AAA | CATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTGC TCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTC ACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCCTG | 1381 |
| | CAGGAAGCCCTCCCGGGCAGCGTCGTGCACGGGTCTGGGTGA GAGTGGCGGGGTCTGGCGCAATTGGGCTCCGCGCCGTGGAG CAGCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATG | 1382 |
| | GAGCCCAACTGCGCCGA | 1383 |
| | TCGGCGCAATTGGGCTC | 1384 |
| Melanoma Asn71Ser AAC-AGC | TCATGATGATGGGCAGCGCCCGAGTGGCGGAGCTGCTGCTG CTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCT CACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCCT | 1385 |
| | AGGAAGCCCTCCCGGGCAGCGTCGTGCACGGGTCTGGGTGAG AGTGGCGGGGTCTGGCGCAGTTGGGCTCCGCGCCGTGGAGCA GCAGCAGCTCCGCCACTCGGGCGCTGCCCATCATCATGA | 1386 |
| | GGAGCCCAACTGCGCCG | 1387 |
| | CGGCGCAGTTGGGCTCC | 1388 |
| Melanoma Pro81Leu CCC-CTC | AGCTGCTGCTGCTCCACGGCGCGGAGCCCAACTGCGCCGAC CCCGCCACTCTACCCGACCGGTGCACGACGCTGCCCGGGA GGGCTTCCTGGACACGCTGGTGGTGCTGCACCGGGCCGG | 1389 |
| | CCGGCCCGGTGCAGCACCACCAGCGTGTCCAGGAAGCCCTC CCGGGCAGCGTCGTGCACGGGTCTGGGTGAGAGTGGCGGGG TCGGCGCAGTTGGGCTCCGCGCCGTGGAGCAGCAGCAGCT | 1390 |
| | CACCCGACCGGTGCACG | 1391 |
| | CGTGCACGGGTCTGGGTG | 1392 |
| Melanoma Asp84Tyr cGAC-TAC | CTGCTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCAC TCTACCCGACCCGTGCACGACGCTGCCCGGGAGGGCTTCCT GGACACGCTGGTGGTGCTGCACCGGGCCGGGGCGCGGC | 1393 |
| | GCCGCGCCCCGGCCCGGTGCAGCACCACCAGCGTGTCCAGG AAGCCCTCCCGGGCAGCGTCTGTGCACGGGTCTGGGTGAGAGT GGCGGGGTCTGGCGCAGTTGGGCTCCGCGCCGTGGAGCAG | 1394 |
| | CCGTGCACGACGCTGCC | 1395 |
| | GGCAGCGTCTGTGCACGG | 1396 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|----------------------------------|---|---------------|
| Melanoma Ala85Thr cGCT-ACT | CTCCACGGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCT CACCCGACCCGTGCACGAC <u>G</u> CTGCCCGGGAGGGCTTCCTGG ACACGCTGGTGGTGTCTGCACCGGGCCGGGGCGCGGCTGG | 1397 |
| | CCAGCCGCGCCCCGGCCCGGTGCAGCACCACCAGCGTGTCC AGGAAGCCCTCCCGGGCAG <u>C</u> GTCGTGCACGGGTGCGGTGAG AGTGGCGGGGTGCGCGCAGTTGGGCTCCGCGCCGTGGAG | 1398 |
| | TGCACGAC <u>G</u> CTGCCCGG | 1399 |
| | CCGGGCAG <u>C</u> GTCGTGCA | 1400 |
| Melanoma Arg87Pro CGG-CCG | GCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCGA CCCGTGCACGACGCTGCC <u>C</u> GGGAGGGCTTCCTGGACACGCT GGTGGTGTCTGCACCGGGCCGGGGCGCGGCTGGACGTGCG | 1401 |
| | CGCACGTCCAGCCGCGCCCCGGCCCGGTGCAGCACCACCAG CGTGTCCAGGAAGCCCTCC <u>C</u> GGGCAGCGTCGTGCACGGGTC GGGTGAGAGTGGCGGGGTGCGCGCAGTTGGGCTCCGCGC | 1402 |
| | CGCTGCC <u>C</u> GGGAGGGCT | 1403 |
| | AGCCCTCC <u>C</u> GGGCAGCG | 1404 |
| Melanoma Arg87Trp cCGG-TGG | GGCGCGGAGCCCAACTGCGCCGACCCCGCCACTCTCACCCG ACCCGTGCACGACGCTGCC <u>C</u> GGGAGGGCTTCCTGGACACGC TGGTGGTGTCTGCACCGGGCCGGGGCGCGGCTGGACGTGC | 1405 |
| | GCACGTCCAGCCGCGCCCCGGCCCGGTGCAGCACCACCAGC GTGTCCAGGAAGCCCTCC <u>C</u> GGGCAGCGTCGTGCACGGGTGCG GGTGAGAGTGGCGGGGTGCGCGCAGTTGGGCTCCGCGCC | 1406 |
| | ACGCTGCC <u>C</u> GGGAGGGC | 1407 |
| | GCCCTCC <u>C</u> GGGCAGCGT | 1408 |
| Melanoma Leu97Arg CTG-CGG | CTCTACCCGACCGGTGCATGATGCTGCCCGGGAGGGCTTCC TGGACACGCTGGTGGTGTCTGCACCGGGCCGGGGCGCGGCTG GACGTGCGGATGCCTGGGGTCGTCTGCCCGTGGACTT | 1409 |
| | AAGTCCACGGGCAGACGACCCAGGCATCGCGCACGTCCAG CCGCGCCCCGGCCCGGTGC <u>A</u> GCACCACCAGCGTGTCCAGGA AGCCCTCCCGGGCAGCATCATGCACCGGTCGGGTGAGAG | 1410 |
| | GGTGGTGC <u>T</u> GCACCGGG | 1411 |
| | CCCGGTGC <u>A</u> GCACCACC | 1412 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|-----------------------------------|---|------------|
| Melanoma Arg99Pro CGG-CCG | CCCGACCGGTGCATGATGCTGCCCGGGAGGGCTTCCTGGAC ACGCTGGTGGTGTGCTGCACCGGGCCGGGGCGCGGCTGGACGT GCGCGATGCCTGGGGTCGTCTGCCCGTGGACTTGGCCGA | 1413 |
| | TCGGCCAAGTCCACGGGCAGACGACCCCAGGCATCGCGCAC GTCCAGCCGCGCCCCGGCCGGGTGCAGCACCACCAGCGTGT CCAGGAAGCCCTCCCGGGCAGCATCATGCACCGGTTCGGG | 1414 |
| | GCTGCACCGGGCCGGG | 1415 |
| | CCCCGGCCGGGTGCAGC | 1416 |
| Melanoma Gly101Trp cGGG-TGG | CCGGTGCATGATGCTGCCCGGGAGGGCTTCCTGGACACGCT GGTGGTGTGCTGCACCGGGCCGGGGCGCGGCTGGACGTGCGC GATGCCTGGGGTCGTCTGCCCGTGGACTTGCCCGAGGAGC | 1417 |
| | GCTCCTCGGCCAAGTCCACGGGCAGACGACCCCAGGCATCG CGCACGTCCAGCCGCGCCCCGGGCCGGTGCAGCACCACCAG CGTGTCCAGGAAGCCCTCCCGGGCAGCATCATGCACCGG | 1418 |
| | ACCGGGCCGGGGCGCGG | 1419 |
| | CCGCGCCCCGGGCCGGT | 1420 |
| Melanoma Arg107Cys gCGC-TGC | CGGGAGGGCTTCCTGGACACGCTGGTGGTGTGCTGCACCGGGC CGGGGCGCGGCTGGACGTGCGCGATGCCTGGGGTCGTCTGC CCGTGGACTTGGCCGAGGAGCGGGGCCACCGCGACGTTG | 1421 |
| | CAACGTGCGGGTGGCCCCGCTCCTCGGCCAAGTCCACGGGC AGACGACCCCAGGCATCGCGCACGTCCAGCCGCGCCCCGGC CCGGTGCAGCACCACCAGCGTGTCCAGGAAGCCCTCCCG | 1422 |
| | TGGACGTGCGCGATGCC | 1423 |
| | GGCATCGCGCACGTCCA | 1424 |
| Melanoma Ala118Thr gGCT-ACT | CACCGGGCCGGGGCGCGGCTGGACGTGCGCGATGCCTGGG GCCGTCTGCCCGTGGACCTGGCTGAGGAGCTGGGCCATCGC GATGTGCGACGGTACCTGCGCGCGGCTGCGGGGGGCACCA | 1425 |
| | TGGTGCCCCCGCAGCCGCGCGCAGGTACCGTGCGACATCG CGATGGCCCAGCTCCTCAGCCAGGTCCACGGGCAGACGGCC CCAGGCATCGCGCACGTCCAGCCGCGCCCCGGCCCGGTG | 1426 |
| | TGGACCTGGCTGAGGAG | 1427 |
| | CTCCTCAGCCAGGTCCA | 1428 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|----------------------------------|---|------------|
| Melanoma Val126Asp GTC-GAC | TGCGCGATGCCTGGGGCCGTCTGCCCCTGGACCTGGCTGAG GAGCTGGGCCATCGCGATGTCGCACGGTACCTGCGCGCGGC TGCGGGGGGCACCAGAGGCAGTAACCATGCCCGCATAGA | 1429 |
| | TCTATGCGGGCATGGTTACTGCCTCTGGTGCCCCCGCAGCC GCGCGCAGGTACCGTGCGACATCGCGATGGCCCAGCTCCTC AGCCAGGTCCACGGGCAGACGGCCCCAGGCATCGCGCA | 1430 |
| | TCGCGATGTCGCACGGT | 1431 |
| | ACCGTGCGACATCGCGA | 1432 |

EXAMPLE 12

Adenomatous polyposis of the colon - APC

[0223] Adenomatous polyposis of the colon is characterized by adenomatous polyps of the colon and rectum; in extreme cases the bowel is carpeted with a myriad of polyps. This is a viciously premalignant disease with one or more polyps progressing through dysplasia to malignancy in untreated gene carriers with a median age at diagnosis of 40 years.

[0224] Mutations in the APC gene are an initiating event for both familial and sporadic colorectal tumorigenesis and many alleles of the APC gene have been identified. Carcinoma may arise at any age from late childhood through the seventh decade with presenting features including, for example, weight loss and inanition, bowel obstruction, or bloody diarrhea. Cases of new mutation still present in these ways but in areas with well organized registers most other gene carriers are detected. The attached table discloses the correcting oligonucleotide base sequences for the APC oligonucleotides of the invention.

Table 14

APC Mutations And Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Adenomatous polyposis coli Arg121Term AGA-TGA | GGATCTGTATCAAGCCGTTCTGGAGAGTGCAGTCCTGTTCTT ATGGGTTTCATTTCCAAGAAGAGGGTTTGTAAATGGAAGCAGA GAAAGTACTGGATATTTAGAAGAACTTGAGAAAGAGA | 1433 |
| | TCTCTTTCTCAAGTTCTTCTAAATATCCAGTACTTTCTCTGCTT CCATTTACAAACCCTCTTCTTGGAAATGAACCCATAGGAACAG GACTGCACTCTCCAGAACGGCTTGATACAGATCC | 1434 |
| | TTCCAAGAAGAGGGTTT | 1435 |
| | AAACCCTCTTCTTGAA | 1436 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| Adenomatous polyposis coli Trp157Term TGG-TAG | AAAAAAAAAATAGGTCATTGCTTCTTGCTGATCTTGACAAAGA AGAAAAGGAAAAAGACTG <u>G</u> TATTACGCTCAACTTCAGAATCTC ACTAAAAGAATAGATAGTCTTCCTTTAACTGAAAA | 1437 |
| | TTTTCAGTTAAAGGAAGACTATCTATTCTTTTAGTGAGATTCTG AAGTTGAGCGTAATAC <u>C</u> AGTCTTTTTCCTTTTCTTCTTTGTCAA GATCAGCAAGAAGCAATGACCTATTTTTTTTTT | 1438 |
| | AAAAGACTG <u>G</u> TATTACG | 1439 |
| | CGTAATAC <u>C</u> AGTCTTTT | 1440 |
| Adenomatous polyposis coli Tyr159Term TAC-TAG | AAATAGGTCATTGCTTCTTGCTGATCTTGACAAAGAAGAAAAG GAAAAAGACTGGTATTAC <u>G</u> GCTCAACTTCAGAATCTCACTAAAA GAATAGATAGTCTTCCTTTAACTGAAAATGTAAGT | 1441 |
| | ACTTACATTTTCAGTTAAAGGAAGACTATCTATTCTTTTAGTGA GATTCTGAAGTTGAGC <u>G</u> TAATACCAGTCTTTTTCCTTTTCTTCT TTGTCAAGATCAGCAAGAAGCAATGACCTATTT | 1442 |
| | TGGTATTAC <u>G</u> GCTCAACT | 1443 |
| | AGTTGAGC <u>G</u> TAATACCA | 1444 |
| Adenomatous polyposis coli Gln163Term CAG-TAG | TTGCTTCTTGCTGATCTTGACAAAGAAGAAAAGGAAAAAGACT GGTATTACGCTCAACTT <u>C</u> AGAATCTCACTAAAAGAATAGATAG TCTTCCTTTAACTGAAAATGTAAGTAACTGGCAGT | 1445 |
| | ACTGCCAGTTACTTACATTTTCAGTTAAAGGAAGACTATCTATT CTTTTAGTGAGATTCT <u>G</u> AAGTTGAGCGTAATACCAGTCTTTTT CCTTTTCTTCTTTGTCAAGATCAGCAAGAAGCAA | 1446 |
| | CTCAACTT <u>C</u> AGAATCTC | 1447 |
| | GAGATTCT <u>G</u> AAGTTGAG | 1448 |
| Adenomatous polyposis coli Arg168Term AGA-TGA | CTTGACAAAGAAGAAAAGGAAAAAGACTGGTATTACGCTCAAC TTCAGAATCTCACTAAA <u>A</u> GAATAGATAGTCTTCCTTTAACTGAA AATGTAAGTAACTGGCAGTACAACCTATTTGAAA | 1449 |
| | TTTCAAATAAGTTGTACTGCCAGTTACTTACATTTTCAGTTAAA GGAAGACTATCTATTCTTTTAGTGAGATTCTGAAGTTGAGCGT AATACCAGTCTTTTTCTTTTCTTCTTTGTCAAG | 1450 |
| | TCACTAAA <u>A</u> GAATAGAT | 1451 |
| | ATCTATTCTTTTAGTGA | 1452 |
| Adenomatous polyposis coli Ser171Ile AGT-ATT | AAGAAAAGGAAAAAGACTGGTATTACGCTCAACTTCAGAATCT CACTAAAAGAATAGATAGTCTTCCTTTAACTGAAAATGTAAGTA ACTGGCAGTACAACCTATTTGAACTTTAATAAC | 1453 |
| | GTTATTAAAGTTTCAAATAAGTTGTACTGCCAGTTACTTACATT TTCAGTTAAAGGAAGACTATCTATTCTTTTAGTGAGATTCTGAA GTTGAGCGTAATACCAGTCTTTTTCTTTTCTT | 1454 |
| | AATAGATAGTCTTCCTT | 1455 |
| | AAGGAAGACTATCTATT | 1456 |
| Adenomatous polyposis coli Gln181Term | GATTAACGTAAATACAAGATATTGATACTTTTTTATTATTTGTG GTTTTAGTTTTCTTAC <u>C</u> AAACAGATATGACCAGAAGGCAATTG GAATATGAAGCAAGGCAAATCAGAGTTGCGATGG | 1457 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|--------------|
| CAA-TAA | CCATCGCAACTCTGATTTGCCTTGCTTCATATTCCAATTGCCT TCTGGTCATATCTGTTT <u>G</u> TAAGGAAAACATAAAACCACAAATAAT AAAAAAGTATCAATATCTTGTATTTACGTTAATC | 1458 |
| | TTTCCTTACAAACAGAT ATCTGTTT <u>G</u> TAAGGAAA | 1459 1460 |
| | | |
| Adenomatous polyposis coli Glu190Term GAA-TAA | CTTTTTATTATTTGTGGTTTTAGTTTTCTTACAAACAGATATG ACCAGAAGGCAATTGGAATATGAAGCAAGGCAATCAGAGTT GCGATGGAAGAACAACTAGGTACCTGCCAGGATA | 1461 |
| | TATCCTGGCAGGTACCTAGTTGTTCTTCCATCGCAACTCTGAT TTGCCTTGCTTCATATT <u>C</u> CAATTGCCTTCTGGTCATATCTGTTT GTAAGGAAAACATAAAACCACAAATAATAAAAAAG | 1462 |
| | GGCAATTGGAATATGAA | 1463 |
| | TTCATATTCCAATTGCC | 1464 |
| Adenomatous polyposis coli Gln208Term CAG-TAG | CAATTGGAATATGAAGCAAGGCAAATCAGAGTTGCGATGGAA GAACAACAGGTACCTGCCAGGATATGGAAAAACGAGCACAG GTAAGTTACTTGTCTTAAGTGATAAAACAGCGAAGA | 1465 |
| | TCTTCGCTGTTTTATCACTTAGAAACAAGTAACTTACCTGTGCT CGTTTTTCCATATCCTGCGCAGGTACCTAGTTGTTCTTCCATCG CAACTCTGATTTGCCTTGCTTCATATTCCAATTG | 1466 |
| | GTACCTGCCAGGATATG | 1467 |
| | CATATCCTGGCAGGTAC | 1468 |
| Adenomatous polyposis coli Arg213Term CGA-TGA | GCAAGGCAAATCAGAGTTGCGATGGAAGAACAACAGGTACC TGCCAGGATATGGAAAAACGAGCACAGGTAAGTTACTTGTTTC TAAGTGATAAAACAGCGAAGAGCTATTAGGAATAAA | 1469 |
| | TTTATTCCTAATAGCTCTTCGCTGTTTTATCACTTAGAAACAAG TAACTTACCTGTGCTC <u>G</u> TTTTTCCATATCCTGGCAGGTACCTA GTTGTTCTTCCATCGCAACTCTGATTTGCCTTGC | 1470 |
| | TGGAAAAACGAGCACAG | 1471 |
| | CTGTGCTC <u>G</u> TTTTTCCA | 1472 |
| Adenomatous polyposis coli Arg232Term CGA-TGA | GTTTTATTTTAGCGAAGAATAGCCAGAATTCAGCAAATCGAAA AGGACATACTTCGTATACGACAGCTTTTACAGTCCCAAGCAAC AGAAGCAGAGGTTAGTAAATTGCCTTTCTTGTTTG | 1473 |
| | CAAACAAGAAAGGCAATTTACTAACCTCTGCTTCTGTTGCTTG GGACTGTAAAAGCTGT <u>C</u> TATACGAAGTATGTCCTTTTCGATT TGCTGAATTCTGGCTATTCTTCGCTAAAATAAAAC | 1474 |
| | TTCGTATACGACAGCTT | 1475 |
| | AAGCTGTCGTATACGAA | 1476 |
| Adenomatous polyposis coli Gln233Term CAG-TAG | TTATTTTAGCGAAGAATAGCCAGAATTCAGCAAATCGAAAAGG ACATACTTCGTATACGACAGCTTTTACAGTCCCAAGCAACAGA AGCAGAGGTTAGTAAATTGCCTTTCTTGTTTGTGG | 1477 |
| | CCACAAACAAGAAAGGCAATTTACTAACCTCTGCTTCTGTTGC TTGGGACTGTAAAAGCTGTCGTATACGAAGTATGTCCTTTTCG ATTTGCTGAATTCTGGCTATTCTTCGCTAAAATAA | 1478 |

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| Adenomatous polyposis coli Gln247Term CAG-TAG | GTATACGAC <u>C</u> AGCTTTTA | 1479 |
| | TAAAAGCT <u>G</u> TCGTATAC | 1480 |
| | AGAAAGCCTACACCATTTTTGCATGTACTGATGTAACTCCATCTTAACAGAGGTCATCTCAGAACAAAGCATGAAACCGGCTCACATGATGCTGAGCGGCAGAATGAAGGTCAAGGAGTGG | 1481 |
| | CCACTCCTTGACCTTCATTCTGCCGCTCAGCATCATGTGAGCCGTTTCATGCTTGTCTGAGATGACCTCTGTAAAGATGGAGTTAACATCAGTACATGCAAAAATGGTGTAGGCTTTCT | 1482 |
| | GGTCATCTCAGAACAAAG | 1483 |
| | CTTGTTCTGAGATGACC | 1484 |
| Adenomatous polyposis coli Gly267Term GGA-TGA | CAGAACAAGCATGAAACCGGCTCACATGATGCTGAGCGGCAG AATGAAGGTCAAGGAGTGGGAGAAATCAACATGGCAACTTCTGGTAATGGTCAGGTAAATAAATTATTTTATCATATTT | 1485 |
| | AAATATGATAAAATAATTTATTTACCTGACCATTACCAGAAAGTTGCCATGTTGATTTCTCCCACTCCTTGACCTTCATTCTGCCGCTCAGCATCATGTGAGCCGGTTTCATGCTTGTCTG | 1486 |
| | AAGGAGTGGGAGAAATC | 1487 |
| | GATTTCTCCCACTCCTT | 1488 |
| Adenomatous polyposis coli Glu443Term GAA-TAA | CTTCAAATAACAAAGCATTATGGTTTATGTTGATTTTATTTTCA GTGCCAGCTCCTGTTGAACATCAGATCTGTCCTGCTGTGTGT GTTCTAATGAAACTTTTCATTTGATGAAGAGCATA | 1489 |
| | TATGCTCTTCATCAAATGAAAGTTTCATTAGAACACACACAGCAGGACAGATCTGATGTTCAACAGGAGCTGGCACTGAAAAATAAAATCAACATAAACCATAATGCTTTGTTATTTGAAG | 1490 |
| | CTCCTGTTGAACATCAG | 1491 |
| | CTGATGTTCAACAGGAG | 1492 |
| Adenomatous polyposis coli SER457TER TCA-TAA | CAGTGCCAGCTCCTGTTGAACATCAGATCTGTCCTGCTGTGTGTGTTCTAATGAAACTTTTCATTTGATGAAGAGCATAGACATGC AATGAATGAACTAGGTAAGACAAAAATGTTTTTTAA | 1493 |
| | TAAAAAACATTTTTGTCTTACCTAGTTCATTTCATTGCATGTCTATGCTCTTCATCAAATGAAAGTTTCATTAGAACACACACAGCAGGACAGATCTGATGTTCAACAGGAGCTGGCACTG | 1494 |
| | GAAACTTTTCATTTGATG | 1495 |
| | CATCAAATGAAAGTTTC | 1496 |
| Adenomatous polyposis coli Gln473Term CAG-TAG | AGTTGTTTTATTTTAGATGATTGTCTTTTTCCTCTTGCCCTTTTT AAATTAGGGGGACTACAGGCCATTGCAGAATTATTGCAAGTG GACTGTGAAATGTACGGGCTTACTAATGACCACT | 1497 |
| | AGTGGTCATTAGTAAGCCCGTACATTTTACAGTCCACTTGCAA TAATTCTGCAATGGCCTGTAGTCCCCCTAATTTAAAAGGGCAAGAGGAAAAAGACAATCATCTAAAATAAAACAACCT | 1498 |
| | GGGGACTACAGGCCATT | 1499 |
| | AATGGCCTGTAGTCCCC | 1500 |

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| Adenomatous polyposis coli Tyr486Term TAC-TAG | TTTAAATTAGGGGGACTACAGGCCATTGCAGAATTATTGCAA GTGGACTGTGAAATGTACGGGCTTACTAATGACCACTACAGT ATTACACTAAGACGATATGCTGGAATGGCTTTGACA | 1501 |
| | TGTCAAAGCCATTCCAGCATATCGTCTTAGTGTAATACTGTAG TGGTCATTAGTAAGCCCGTACATTTACAGTCCACTTGCAATA ATTCTGCAATGGCCTGTAGTCCCCCTAATTTAAAA | 1502 |
| | GAAATGTACGGGCTTAC | 1503 |
| | GTAAGCCCCGTACATTTT | 1504 |
| Adenomatous polyposis coli Arg499Term CGA-TGA | TTGCAAGTGGACTGTGAAATGTATGGGCTTACTAATGACCACT ACAGTATTACACTAAGACGATATGCTGGAATGGCTTTGACAAA CTTGACTTTTGGAGATGTAGCCAACAAGGTATGTT | 1505 |
| | AACATACCTTGTGGCTACATCTCCAAAAGTCAAGTTTGTCAA AGCCATTCCAGCATATCGTCTTAGTGTAATACTGTAGTGGTCA TTAGTAAGCCCATACATTTACAGTCCACTTGCAA | 1506 |
| | CACTAAGACGATATGCT | 1507 |
| | AGCATATCGTCTTAGTG | 1508 |
| Adenomatous polyposis coli Tyr500Term TAT-TAG | AGTGGACTGTGAAATGTATGGGCTTACTAATGACCACTACAGT ATTACACTAAGACGATATGCTGGAATGGCTTTGACAACTTGA CTTTTGGAGATGTAGCCAACAAGGTATGTTTTTAT | 1509 |
| | ATAAAACATACCTTGTGGCTACATCTCCAAAAGTCAAGTTT GTCAAAGCCATTCCAGCATATCGTCTTAGTGTAATACTGTAGT GGTCATTAGTAAGCCCATACATTTACAGTCCACT | 1510 |
| | AGACGATATGCTGGAAT | 1511 |
| | ATTCCAGCATATCGTCT | 1512 |
| Adenomatous polyposis coli Lys586Term AAA-TAA | GACAAATCCAACTCTAATTAGATGACCCATATTCTGTTTCTTA CTAGGAATCAACCCTCAAAAGCGTATTGAGTGCCTTATGGAAT TTGTCAGCACATTGCACTGAGAATAAAGCTGATA | 1513 |
| | TATCAGCTTTATTCTCAGTGCAATGTGCTGACAAATTCCATAA GGCACTCAATACGCTTTTGAGGGTTGATTCTAGTAAGAAACA GAATATGGGTCATCTAATTAGAGTTGGAATTTGTC | 1514 |
| | CAACCCTCAAAAGCGTA | 1515 |
| | TACGCTTTTGAGGGTTG | 1516 |
| Adenomatous polyposis coli Leu592Term TTA-TGA | TAGATGACCCATATTCTGTTTCTTACTAGGAATCAACCCTCAA AAGCGTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACT GAGAATAAAGCTGATATATGTGCTGTAGATGGTGC | 1517 |
| | GCACCATCTACAGCACATATATCAGCTTTATTCTCAGTGCAAT GTGCTGACAAATTCCATAAGGCACTCAATACGCTTTTGAGGGT TGATTCTAGTAAGAAACAGAATATGGGTCATCTA | 1518 |
| | GAGTGCCTTATGGAATT | 1519 |
| | AATTCCATAAGGCACTC | 1520 |

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| Adenomatous polyposis coli Trp593Term TGG-TAG | ATGACCCATATTCTGTTTCTTAGGAATCAACCCTCAAAGCGTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACTGAG AATAAAGCTGATATATGTGCTGTAGATGGTGCACT | 1521 |
| | AGTGCAACCATCTACAGCACATATATCAGCTTTATTCTCAGTGC AATGTGCTGACAAATTCATAAGGCACTCAATACGCTTTTGAG GGTTGATTCTAGTAAGAAACAGAATATGGGTCAT | 1522 |
| | TGCCTTATGGAATTTGT | 1523 |
| | ACAAATTCATAAGGCA | 1524 |
| Adenomatous polyposis coli Trp593Term TGG-TGA | TGACCCATATTCTGTTTCTTAGGAATCAACCCTCAAAGCGTATTGAGTGCCTTATGGAATTTGTCAGCACATTGCACTGAGA AATAAAGCTGATATATGTGCTGTAGATGGTGCACTT | 1525 |
| | AAGTGCAACCATCTACAGCACATATATCAGCTTTATTCTCAGTGC AATGTGCTGACAAATTCATAAGGCACTCAATACGCTTTTGAG GGTTGATTCTAGTAAGAAACAGAATATGGGTCA | 1526 |
| | GCCTTATGGAATTTGTC | 1527 |
| | GACAAATTCATAAGGC | 1528 |
| Adenomatous polyposis coli Tyr622Term TAC-TAA | TAAAGCTGATATATGTGCTGTAGATGGTGCACTTGCAATTTTTG GTTGGCACTCTTACTTACCGGAGCCAGACAAACACTTTAGCC ATTATTGAAAGTGGAGGTGGGATATTACGGAATGTG | 1529 |
| | CACATTCCGTAATATCCACCTCCACTTTCAATAATGGCTAAA GTGTTTGTCTGGCTCCGGTAAGTAAGAGTGCCAACCAAAAAT GCAAGTGCAACCATCTACAGCACATATATCAGCTTTA | 1530 |
| | CTTACTTACCGGAGCCA | 1531 |
| | TGGCTCCGGTAAGTAAG | 1532 |

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| Adenomatous polyposis coli Gln625Term CAG-TAG | GATATATGTGCTGTAGATGGTGCACTTGCATTTTTGGTTGGCACTCTTACTTACCGGAGCCAGACAAACACTTTAGCCATTATTGA AAGTGGAGGTGGGATATTACGGAATGTGTCCAGCT | 1533 |
| | AGCTGGACACATTCCGTAATATCCACCTCCACTTTCAATAAT GGCTAAAGTGTCTGTCTGGCTCCGGTAAGTAAGAGTGCCAAC CAAAAATGCAAGTGACCATCTACAGCACATATATC | 1534 |
| | ACCGGAGCCAGACAAAC | 1535 |
| | GTTTGTCTGGCTCCGGT | 1536 |
| Adenomatous polyposis coli Leu629Term TTA-TAA | TAGATGGTGCACTTGCATTTTTGGTTGGCACTCTTACTTACCG GAGCCAGACAAACACTTTAGCCATTATTGAAAGTGGAGGTGG GATATTACGGAATGTGTCCAGCTTGATAGCTACAAA | 1537 |
| | TTTGTAGCTATCAAGCTGGACACATTCCGTAATATCCACCTC CACTTTCAATAATGGCTAAAGTGTCTGGCTCCGGTAAGT AAGAGTGCCAACCAAAAATGCAAGTGACCATCTA | 1538 |
| | AAACACTTTAGCCATTA | 1539 |
| | TAATGGCTAAAGTGTCT | 1540 |
| Adenomatous polyposis coli Glu650Term GAG-TAG | GCCATTATTGAAAGTGGAGGTGGGATATTACGGAATGTGTCC AGCTTGATAGCTACAAATGAGGACCACAGGTATATATAGAGTT TTATATTACTTTTAAAGTACAGAATTCATACTCTCA | 1541 |
| | TGAGAGTATGAATCTGTACTTTAAAAGTAATATAAACTCTAT ATATACCTGTGGTCCTCATTGTAGCTATCAAGCTGGACACAT TCCGTAATATCCACCTCCACTTTCAATAATGGC | 1542 |
| | CTACAAATGAGGACCAC | 1543 |
| | GTGGTCCTCATTGTAG | 1544 |
| Adenomatous polyposis coli Trp699Term TGG-TGA | TGCATGTGGAACTTTGTGGAATCTCTCAGCAAGAAATCCTAAA GACCAGGAAGCATTATGGGACATGGGGGCAGTTAGCATGCTC AAGAACCTCATTCAATCAAGCACAAAATGATTGCT | 1545 |
| | AGCAATCATTTTGTGCTTTGAATGAATGAGGTTCTTGAGCATG CTAACTGCCCCCATGTCCATAATGCTTCCTGGTCTTTAGGAT TTCTTGCTGAGAGATTCCACAAAGTTCCACATGCA | 1546 |
| | GCATTATGGGACATGGG | 1547 |
| | CCCATGTCCATAATGC | 1548 |
| Adenomatous polyposis coli Ser713Term TCA-TGA | AAGACCAGGAAGCATTATGGGACATGGGGGCAGTTAGCATGC TCAAGAACCTCATTCAATCAAAGCACAAAATGATTGCTATGGG AAGTGCTGCAGCTTTAAGGAATCTCATGGCAAATAG | 1549 |
| | CTATTTGCCATGAGATTCCTTAAAGCTGCAGCACTTCCCATAG CAATCATTTTGTGCTTTGAATGAATGAGGTTCTTGAGCATGCT AACTGCCCCCATGTCCATAATGCTTCCTGGTCTT | 1550 |
| | CATTCATTCAAAGCACA | 1551 |
| | TGTGCTTTGAATGAATG | 1552 |

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| Adenomatous polyposis coli Ser722Gly AGT-GGT | GGGGCAGTTAGCATGCTCAAGAACCTCATTCAATCAAAGCAC AAAATGATTGCTATGGGAAGTGCTGCAGCTTTAAGGAATCTCA TGGCAAATAGGCCTGCGAAGTACAAGGATGCCAATA | 1553 |
| | TATTGGCATCCTTGTACTTCGCAGGCCTATTTGCCATGAGATT CCTTAAAGCTGCAGCACTTCCCATAGCAATCATTTTGTGCTTT GAATGAATGAGGTTCTTGAGCATGCTAACTGCCCC | 1554 |
| | CTATGGGAAGTGCTGCA | 1555 |
| | TGCAGCACTTCCCATAG | 1556 |
| Adenomatous polyposis coli Leu764Term TTA-TAA | TCTCCTGGCTCAGCTTGCCATCTCTTCATGTTAGGAAACAAA AGCCCTAGAAGCAGAATTAGATGCTCAGCACTTATCAGAACT TTTGACAATATAGACAATTTAAGTCCCAAGGCATC | 1557 |
| | GATGCCTTGGGACTTAAATTGTCTATATTGTCAAAAGTTTCTG ATAAGTGCTGAGCATCTAATTCTGCTTCTAGGGCTTTTTGTTT CCTAACATGAAGAGATGGCAAGCTGAGCCAGGAGA | 1558 |
| | AGCAGAATTAGATGCTC | 1559 |
| | GAGCATCTAATTCTGCT | 1560 |
| Adenomatous polyposis coli Ser784Thr TCT-ACT | TTAGATGCTCAGCACTTATCAGAACTTTTGACAATATAGACA ATTTAAGTCCCAAGGCATCTCATCGTAGTAAGCAGAGACACA GCAAGTCTCTATGGTGATTATGTTTTTGACACCATC | 1561 |
| | GATGGTGTCAAAAACATAATCACCATAGAGACTTGCTGTGTCT CTGCTTACTACGATGAGATGCCTTGGGACTTAAATTGTCTATA TTGTCAAAAGTTTCTGATAAGTGCTGAGCATCTAA | 1562 |
| | CCAAGGCATCTCATCGT | 1563 |
| | ACGATGAGATGCCTTGG | 1564 |
| Adenomatous polyposis coli Arg805Term CGA-TGA | CTCATCGTAGTAAGCAGAGACACAGCAAGTCTCTATGGTGATT ATGTTTTTGACACCAATCGACATGATGATAATAGGTCAGACAT TTTAATACTGGCACATGACTGTCCTTTCACCATAT | 1565 |
| | ATATGGTGAAAGGACAGTCATGTGCCAGTATTAATGTCTGA CCTATTATCATCATGTCCGATTGGTGTCAAAAACATAATCACCAT AGAGACTTGCTGTGTCTCTGCTTACTACGATGAG | 1566 |
| | ACACCAATCGACATGAT | 1567 |
| | ATCATGTCCGATTGGTGT | 1568 |
| Adenomatous polyposis coli Gln879Term CAG-TAG | GGTCTAGGCAACTACCATCCAGCAACAGAAAATCCAGGAAC TCTTCAAAGCGAGGTTTGAGATCTCCACCACTGCAGCCCAG ATTGCCAAAGTCATGGAAGAAGTGTCAGCCATTTCATA | 1569 |
| | TATGAATGGCTGACACTTCTCCATGACTTTGGCAATCTGGGC TGCAGTGGTGGAGATCTGCAAACCTCGCTTTGAAGAAGTTCC TGGATTTTCTGTTGCTGGATGGTAGTTGCCTAGACC | 1570 |
| | GAGGTTTGAGATCTCC | 1571 |
| | GGAGATCTGCAAACCTC | 1572 |

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| Adenomatous polyposis coli Ser932Term TCA-TAA | TACATTGTGTGACAGATGAGAGAAATGCACTTAGAAGAAGCTC TGCTGCCCATACACATTCAAACACTTACAATTTCACTAAGTCG GAAAATTCAAATAGGACATGTTCTATGCCTTATGC | 1573 |
| | GCATAAGGCATAGAACATGTCCTATTTGAATTTTCCGACTTAG TGAAATTGTAAGTGTGGAATGTGTATGGGCAGCAGAGCTTCT TCTAAGTGCATTTCTCTCATCTGTCACACAATGTA | 1574 |
| | TACACATTCAAACACTT | 1575 |
| | AAGTGTTTGAATGTGTA | 1576 |
| Adenomatous polyposis coli Ser932Term TCA-TGA | TACATTGTGTGACAGATGAGAGAAATGCACTTAGAAGAAGCTC TGCTGCCCATACACATTCAAACACTTACAATTTCACTAAGTCG GAAAATTCAAATAGGACATGTTCTATGCCTTATGC | 1577 |
| | GCATAAGGCATAGAACATGTCCTATTTGAATTTTCCGACTTAG TGAAATTGTAAGTGTGGAATGTGTATGGGCAGCAGAGCTTCT TCTAAGTGCATTTCTCTCATCTGTCACACAATGTA | 1578 |
| | TACACATTCAAACACTT | 1579 |
| | AAGTGTTTGAATGTGTA | 1580 |
| Adenomatous polyposis coli Tyr935Term TAC-TAG | GACAGATGAGAGAAATGCACTTAGAAGAAGCTCTGCTGCCCCA TACACATTCAAACACTTACAATTTCACTAAGTCGGAAAATTCAA ATAGGACATGTTCTATGCCTTATGCCAAATTAGAA | 1581 |
| | TTCTAATTTGGCATAAGGCATAGAACATGTCCTATTTGAATTTT CCGACTTAGTGAAATTGTAAGTGTTTGAATGTGTATGGGCAGC AGAGCTTCTTCTAAGTGCATTTCTCTCATCTGTC | 1582 |
| | AACACTTACAATTTAC | 1583 |
| | GTGAAATTGTAAGTGTT | 1584 |
| Adenomatous polyposis coli Tyr935Term TAC-TAA | GACAGATGAGAGAAATGCACTTAGAAGAAGCTCTGCTGCCCCA TACACATTCAAACACTTACAATTTCACTAAGTCGGAAAATTCAA ATAGGACATGTTCTATGCCTTATGCCAAATTAGAA | 1585 |
| | TTCTAATTTGGCATAAGGCATAGAACATGTCCTATTTGAATTTT CCGACTTAGTGAAATTGTAAGTGTTTGAATGTGTATGGGCAGC AGAGCTTCTTCTAAGTGCATTTCTCTCATCTGTC | 1586 |
| | AACACTTACAATTTAC | 1587 |
| | GTGAAATTGTAAGTGTT | 1588 |
| Adenomatous polyposis coli Tyr1000Term TAC-TAA | ACCCTCGATTGAATCCTATTCTGAAGATGATGAAAGTAAGTTT TGCAGTTATGGTCAATACCCAGCCGACCTAGCCCATAAAATAC ATAGTGCAAATCATATGGATGATAATGATGGAGAA | 1589 |
| | TTCTCCATCATTATCATCCATATGATTTGCACTATGTATTTTAT GGGCTAGGTCGGCTGGGTATTGACCATAACTGCAAACTTAC TTTCATCATCTTCAGAATAGGATTCAATCGAGGGT | 1590 |
| | GGTCAATACCCAGCCGA | 1591 |
| | TCGGCTGGGTATTGACC | 1592 |
| Adenomatous polyposis coli Glu1020Term | TACCCAGCCGACCTAGCCCATAAAATACATAGTGCAAATCATA TGGATGATAATGATGGAGAAGTAGATACACCAATAAATTATAG TCTTAAATATTCAGATGAGCAGTTGAACTCTGGAA | 1593 |

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| GAA-TAA | TTCCAGAGTTCAACTGCTCATCTGAATATTTAAGACTATAATTT ATTGGTGTATCTAGTTCTCCATCATTATCATCCATATGATTTGC ACTATGTATTTTATGGGCTAGGTCTGGCTGGGTA | 1594 |
| | ATGATGGAGAACTAGAT | 1595 |
| | ATCTAGTTCTCCATCAT | 1596 |
| Adenomatous polyposis coli Ser1032Term TCA-TAA | ATGAAACCCTCGATTGAATCCTATTCTGAAGATGATGAAAGTA AGTTTTGCAGTTATGGTCAATACCCAGCCGACCTAGCCCATAA AATACATAGTGCAAATCATATGGATGATAATGATG | 1597 |
| | CATCATTATCATCCATATGATTTGCACTATGTATTTTATGGGCT AGGTCGGCTGGGTATTGACCATAACTGCAAACTTACTTTTCAT CATCTTCAGAATAGGATTCAATCGAGGGTTTCAT | 1598 |
| | GTTATGGTCAATACCCA | 1599 |
| | TGGGTATTGACCATAAC | 1600 |
| Adenomatous polyposis coli Gln1041Term CAA-TAA | TGAAGATGATGAAAGTAAGTTTTGCAGTTATGGTCAATACCCA GCCGACCTAGCCCATAAAATACATAGTGCAAATCATATGGATG ATAATGATGGAGAACTAGATACACCAATAAATTAT | 1601 |
| | ATAATTTATTGGTGTATCTAGTTCTCCATCATTATCATCCATAT GATTTGCACTATGTATTTTATGGGCTAGGTCTGGCTGGGTATTG ACCATAACTGCAAACTTACTTTTCATCATCTTCA | 1602 |
| | GCCCATAAAATACATAG | 1603 |
| | CTATGTATTTTATGGGC | 1604 |
| Adenomatous polyposis coli Gln1045Term CAG-TAG | ATAAATTATAGTCTTAAATATTCAGATGAGCAGTTGAACTCTGG AAGGCAAAGTCCTTCAAGAATGAAAGATGGGCAAGACCCAA ACACATAATAGAAGATGAAATAAAACAAAGTGAGC | 1605 |
| | GCTCACTTTGTTTTATTTTCATCTTCTATTATGTGTTTGGGTCTT GCCCATCTTTCACTTCTGTGAAGGACTTTGCCTTCCAGAGTTCA ACTGCTCATCTGAATATTTAAGACTATAATTTAT | 1606 |
| | GTCTTCAAGAATGAA | 1607 |
| | TTCATTCTGTGAAGGAC | 1608 |
| Adenomatous polyposis coli Gln1067Term CAA-TAA | GAAAGATGGGCAAGACCCAAACACATAATAGAAGATGAAATA AAACAAAGTGAGCAAAGACAATCAAGGAATCAAAGTACAACCTT ATCCTGTTTATACTGAGAGCACTGATGATAAACACC | 1609 |
| | GGTGTATATCATCAGTGCTCTCAGTATAAACAGGATAAGTTGT ACTTTGATTCCTTGATTGTCTTTGCTCACTTTGTTTTATTTTCATC TTCTATTATGTGTTTGGGTCTTGCCCATCTTC | 1610 |
| | AGCAAAGACAATCAAGG | 1611 |
| | CCTTGATTGTCTTTGCT | 1612 |
| Adenomatous polyposis coli Tyr1075Term TAT-TAG | AATAGAAGATGAAATAAAACAAAGTGAGCAAAGACAATCAAGG AATCAAAGTACAACCTTATCCTGTTTATACTGAGAGCACTGATG ATAAACACCTCAAGTTCCAACCATTTTTGGACAG | 1613 |
| | CTGTCCAAATGTGGTTGGAAGTTGAGGTGTTTATCATCAGTG CTCTCAGTATAAACAGGATAAGTTGTACTTTGATTCCTTGATT GTCTTTGCTCACTTTGTTTTATTTTCATCTTCTATT | 1614 |

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| | ACAACTTATCCTGTTTA | 1615 |
| | TAAACAGGATAAGTTGT | 1616 |
| Adenomatous polyposis coli Tyr1102Term TAC-TAG | TGATGATAAACACCTCAAGTTCCAACCACATTTTGGACAGCAG GAATGTGTTTCTCCATACAGGTCACGGGGAGCCAATGGTTCA GAAACAAATCGAGTGGGTTCTAATCATGGAATTAAT | 1617 |
| | ATTAATTCCATGATTAGAACCCACTCGATTTGTTTCTGAACCAT TGGCTCCCCGTGACCTGTATGGAGAAACACATTCCTGCTGTC CAAATGTGGTTGGAACCTGAGGTGTTTATCATCA | 1618 |
| | TCTCCATACAGGTCACG | 1619 |
| | CGTGACCTGTATGGAGA | 1620 |
| Adenomatous polyposis coli Ser1110Term TCA-TGA | AACCACATTTTGGACAGCAGGAATGTGTTTCTCCATACAGGTC ACGGGGAGCCAATGGTTGAGAAACAAATCGAGTGGGTTCTAA TCATGGAATTAATCAAAATGTAAGCCAGTCTTTGTG | 1621 |
| | CACAAAGACTGGCTTACATTTTGATTAATTCCATGATTAGAAC CCACTCGATTTGTTTCTGAACCATTTGGCTCCCCGTGACCTGTA TGGAGAAACACATTCCTGCTGTCCAAAATGTGGTT | 1622 |
| | CAATGGTTGAGAAACAA | 1623 |
| | TTGTTTCTGAACCATTG | 1624 |
| Adenomatous polyposis coli Arg1114Term CGA-TGA | GGACAGCAGGAATGTGTTTCTCCATACAGGTCACGGGGAGCC AATGGTTCAGAAACAAATCGAGTGGGTTCTAATCATGGAATTA ATCAAAATGTAAGCCAGTCTTTGTGTCAAGAAGATG | 1625 |
| | CATCTTCTTGACACAAAGACTGGCTTACATTTTGATTAATTCCA TGATTAGAACCCACTCGATTTGTTTCTGAACCATTTGGCTCCCC GTGACCTGTATGGAGAAACACATTCCTGCTGTCC | 1626 |
| | AAACAAATCGAGTGGGT | 1627 |
| | ACCCACTCGATTTGTTT | 1628 |
| Adenomatous polyposis coli Tyr1135Term TAT-TAG | GGGTTCTAATCATGGAATTAATCAAAATGTAAGCCAGTCTTTG TGCAAGAAGATGACTATGAAGATGATAAGCCTACCAATTATA GTGAACGTTACTCTGAAGAAGAACAGCATGAAGAA | 1629 |
| | TTCTTCATGCTGTTCTTCTCAGAGTAACGTTCACTATAATTGG TAGGCTTATCATCTTCTAGTCATCTTCTTGACACAAAGACTG GCTTACATTTTGATTAATTCCATGATTAGAACCC | 1630 |
| | GATGACTATGAAGATGA | 1631 |
| | TCATCTTCTAGTCATC | 1632 |
| Adenomatous polyposis coli Gln1152Term CAG-TAG | GAAGATGACTATGAAGATGATAAGCCTACCAATTATAGTGAAC GTTACTCTGAAGAAGAACAGCATGAAGAAGAGAGACCAA CAAATTATAGCATAAATATAATGAAGAGAAACGTC | 1633 |
| | GACGTTTCTCTTCATTATATTTTATGCTATAATTTGTTGGTCTC TCTTCTTCTTCATGCTGTTCTTCTCAGAGTAACGTTCACTATA ATTGGTAGGCTTATCATCTTCATAGTCATCTTC | 1634 |
| | AAGAAGAACAGCATGAA | 1635 |
| | TTCATGCTGTTCTTCTT | 1636 |

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| Adenomatous polyposis coli Gln1175Term CAG-TAG | GAAGAAGAGAGACCAACAAATTATAGCATAAAATATAATGAAG AGAAACGTCATGTGGATCAGCCTATTGATTATAGTTTAAAATAT GCCACAGATATTCCTTCATCACAGAAACAGTCAT | 1637 |
| | ATGACTGTTTCTGTGATGAAGGAATATCTGTGGCATATTTTAA ACTATAATCAATAGGCTGATCCACATGACGTTTCTCTTCATTAT ATTTATGCTATAATTTGTTGGTCTCTCTTCTTC | 1638 |
| | ATGTGGATCAGCCTATT | 1639 |
| | AATAGGCTGATCCACAT | 1640 |
| Adenomatous polyposis coli Pro1176Leu CCT-CTT | AAGAGAGACCAACAAATTATAGCATAAAATATAATGAAGAGAA ACGTCATGTGGATCAGCCTATTGATTATAGTTTAAAATATGCC ACAGATATTCCTTCATCACAGAAACAGTCATTTTC | 1641 |
| | GAAAATGACTGTTTCTGTGATGAAGGAATATCTGTGGCATATT TTAAACTATAATCAATAGGCTGATCCACATGACGTTTCTCTTCA TTATATTTTATGCTATAATTTGTTGGTCTCTCTT | 1642 |
| | GGATCAGCCTATTGATT | 1643 |
| | AATCAATAGGCTGATCC | 1644 |
| Adenomatous polyposis coli Ala1184Pro GCC-CCC | ATAAAATATAATGAAGAGAAACGTCATGTGGATCAGCCTATTG ATTATAGTTTAAAATATGCCACAGATATTCCTTCATCACAGAAA CAGTCATTTTCATTCTCAAAGAGTTCATCTGGAC | 1645 |
| | GTCCAGATGAACTCTTTGAGAATGAAAATGACTGTTTCTGTGA TGAAGGAATATCTGTGGCATATTTTAACTATAATCAATAGGCT GATCCACATGACGTTTCTCTTCATTATATTTTAT | 1646 |
| | TAAAATATGCCACAGAT | 1647 |
| | ATCTGTGGCATATTTTA | 1648 |
| Adenomatous polyposis coli Ser1194Term TCA-TGA | ATCAGCCTATTGATTATAGTTTAAAATATGCCACAGATATTCCT TCATCACAGAAACAGTCATTTTCATTCTCAAAGAGTTCATCTG GACAAAGCAGTAAACCGAACATATGTCTTCAAG | 1649 |
| | CTTGAAGACATATGTTTCGTTTTACTGCTTTGTCCAGATGAAC TCTTTGAGAATGAAAATGACTGTTTCTGTGATGAAGGAATATC TGTGGCATATTTTAACTATAATCAATAGGCTGAT | 1650 |
| | GAAACAGTCATTTTCAT | 1651 |
| | ATGAAAATGACTGTTTC | 1652 |
| Adenomatous polyposis coli Ser1198Term TCA-TGA | ATTATAGTTTAAAATATGCCACAGATATTCCTTCATCACAGAAA CAGTCATTTTCATTCTCAAAGAGTTCATCTGGACAAAGCAGTA AAACCGAACATATGTCTTCAAGCAGTGAGAATAC | 1653 |
| | GTATTCTCACTGCTTGAAGACATATGTTTCGTTTTACTGCTTT GTCCAGATGAACTCTTTGAGAATGAAAATGACTGTTTCTGTGA TGAAGGAATATCTGTGGCATATTTTAACTATAAT | 1654 |
| | TTCATTCTCAAAGAGTT | 1655 |
| | AACTCTTTGAGAATGAA | 1656 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Adenomatous polyposis coli Gln1228Term CAG-TAG | ACCGAACATATGTCTTCAAGCAGTGAGAATACGTCCACACCTT CATCTAATGCCAAGAGGCAGAATCAGCTCCATCCAGTTCTGC ACAGAGTAGAAGTGGTCAGCCTCAAAGGCTGCCACT | 1657 |
| | AGTGGCAGCCTTTGAGGCTGACCACTTCTACTCTGTGCAGAA CTGGATGGAGCTGATTCTGCCTCTTGGCATTAGATGAAGGTG TGGACGTATTCTCACTGCTTGAAGACATATGTTCCGT | 1658 |
| | CCAAGAGGCAGAATCAG | 1659 |
| | CTGATTCTGCCTCTTGG | 1660 |
| Adenomatous polyposis coli Gln1230Term CAG-TAG | CATATGTCTTCAAGCAGTGAGAATACGTCCACACCTTCATCTA ATGCCAAGAGGCAGAATCAGCTCCATCCAGTTCTGCACAGAG TAGAAGTGGTCAGCCTCAAAGGCTGCCACTTGCAAG | 1661 |
| | CTTGCAAGTGGCAGCCTTTGAGGCTGACCACTTCTACTCTGT GCAGAACTGGATGGAGCTGATTCTGCCTCTTGGCATTAGATG AAGGTGTGGACGTATTCTCACTGCTTGAAGACATATG | 1662 |
| | GGCAGAATCAGCTCCAT | 1663 |
| | ATGGAGCTGATTCTGCC | 1664 |
| Adenomatous polyposis coli Cys1249Term TGC-TGA | TCAGCTCCATCCAAGTTCTGCACAGAGTAGAAGTGGTCAGCC TCAAAAGGCTGCCACTTGCAAAGTTTCTTCTATTAACCAAGAA ACAATACAGACTTATTGTGTAGAAGATACTCCAATA | 1665 |
| | TATTGGAGTATCTTCTACACAATAAGTCTGTATTGTTCTTGGT TAATAGAAGAACTTTGCAAGTGGCAGCCTTTTGAGGCTGAC CACTTCTACTCTGTGCAGAACTTGGATGGAGCTGA | 1666 |
| | GCCACTTGCAAAGTTTC | 1667 |
| | GAAACTTTGCAAGTGGC | 1668 |
| Adenomatous polyposis coli Cys1270Term TGT-TGA | AGTTTCTTCTATTAACCAAGAAACAATACAGACTTATTGTGTAG AAGATACTCCAATATGTTTTTCAAGATGTAGTTCAATTATCATCT TTGTCATCAGCTGAAGATGAAATAGGATGTAAT | 1669 |
| | ATTACATCCTATTTTCATCTTCAGCTGATGACAAAGATGATAATG AACTACATCTTGAAAAACATATTGGAGTATCTTCTACACAATAA GTCTGTATTGTTCTTGGTTAATAGAAGAACT | 1670 |
| | CCAATATGTTTTTCAAG | 1671 |
| | CTTGAAAAACATATTGG | 1672 |
| Adenomatous polyposis coli Ser1276Term TCA-TGA | AAGAAACAATACAGACTTATTGTGTAGAAGATACTCCAATATG TTTTTCAAGATGTAGTTCAATTATCATCTTTGTCATCAGCTGAAG ATGAAATAGGATGTAATCAGACGACACAGGAAGC | 1673 |
| | GCTTCCTGTGTCGTCTGATTACATCCTATTTTCATCTTCAGCTG ATGACAAAGATGATAATGAACATACATCTTGAAAAACATATTGG AGTATCTTCTACACAATAAGTCTGTATTGTTTCTT | 1674 |
| | ATGTAGTTCAATTATCAT | 1675 |
| | ATGATAATGAACATACAT | 1676 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Adenomatous polyposis coli Glu1286Term GAA-TAA | GATACTCCAATATGTTTTCAAGATGTAGTTCATTATCATCTTT GTCATCAGCTGAAGATGAAATAGGATGTAATCAGACGACACA GGAAGCAGATTCTGCTAATACCCTGCAAATAGCAG | 1677 |
| | CTGCTATTTGCAGGGTATTAGCAGAATCTGCTTCCTGTGTCGT CTGATTACATCCTATTTCTATCTTCAGCTGATGACAAAGATGATA ATGAACTACATCTTGAAAAACATATTGGAGTATC | 1678 |
| | CTGAAGATGAAATAGGA | 1679 |
| | TCCTATTTCTATCTTCAG | 1680 |
| Adenomatous polyposis coli Gln1294Term CAG-TAG | TGTAGTTCATTATCATCTTTGTCATCAGCTGAAGATGAAATAG GATGTAATCAGACGACACAGGAAGCAGATTCTGCTAATACCC TGCAAATAGCAGAAATAAAAGAAAAGATTGGAACTA | 1681 |
| | TAGTTCCAATCTTTTCTTTTATTTCTGCTATTTGCAGGGTATTA GCAGAATCTGCTTCCTGTGTCGTCTGATTACATCCTATTTCTAT CTTCAGCTGATGACAAAGATGATAATGAACTACA | 1682 |
| | AGACGACACAGGAAGCA | 1683 |
| | TGCTTCCTGTGTCGTCT | 1684 |
| Predisposition to, association with, colorectal cancer Ile1307Lys ATA-AAA | TAGGATGTAATCAGACGACACAGGAAGCAGATTCTGCTAATA CCCTGCAAATAGCAGAAATAAAAGAAAAGATTGGAACTAGGTC AGCTGAAGATCCTGTGAGCGAAGTTCCAGCAGTGTC | 1685 |
| | GACACTGCTGGAACCTCGCTCACAGGATCTTCAGCTGACCTA GTTCCAATCTTTTCTTTTATTTCTGCTATTTGCAGGGTATTAGC AGAATCTGCTTCCTGTGTCGTCTGATTACATCCTA | 1686 |
| | AGCAGAAATAAAAGAAA | 1687 |
| | TTTCTTTTATTTCTGCT | 1688 |
| Adenomatous polyposis coli Glu1309Term GAA-TAA | CCAAGAAACAATACAGACTTATTGTGTAGAAGATACTCCAATA TGTTTTTCAAGATGTAGTTCATTATCATCTTTGTCATCAGCTGA AGATGAAATAGGATGTAATCAGACGACACAGGAA | 1689 |
| | TTCCTGTGTCGTCTGATTACATCCTATTTCTATCTTCAGCTGATG ACAAAGATGATAATGAAGTACATCTTGAAAAACATATTGGAGT ATCTTCTACACAATAAGTCTGTATTGTTTCTTGG | 1690 |
| | AGATGTAGTTCATTATC | 1691 |
| | GATAATGAAGTACATCT | 1692 |
| Predisposition to Colorectal Cancer Glu1317Gln GAA-CAA | GATTCTGCTAATACCCTGCAAATAGCAGAAATAAAAGAAAAGA TTGGAAGTAGGTCAGCTGAAGATCCTGTGAGCGAAGTTCCAG CAGTGTCACAGCACCCCTAGAACCAAATCCAGCAGAC | 1693 |
| | GTCTGCTGGATTTGGTTCTAGGGTGCTGTGACACTGCTGGAA CTTCGCTCACAGGATCTTCAGCTGACCTAGTTCCAATCTTTTCT TTTTATTTCTGCTATTTGCAGGGTATTAGCAGAATC | 1694 |
| | GGTCAGCTGAAGATCCT | 1695 |
| | AGGATCTTCAGCTGACC | 1696 |
| Adenomatous polyposis coli Gln1328Term | AAAGAAAAGATTGGAAGTAGGTCAGCTGAAGATCCTGTGAGC GAAGTTCCAGCAGTGTCAGCAGCCCTAGAACCAAATCCAGC AGACTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCA | 1697 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| CAG-TAG | TGGCTGATTCTGAAGATAAACTAGAACCCCTGCAGTCTGCTGG ATTTGGTTCTAGGGTGCTGTGACACTGCTGGAACCTCGCTCA CAGGATCTTCAGCTGACCTAGTTCCAATCTTTCTTT | 1698 |
| | CAGTGTCACAGCACCCCT | 1699 |
| | AGGGTGCTGTGACACTG | 1700 |
| Adenomatous polyposis coli Gln1338Term CAG-TAG | GATCCTGTGAGCGAAGTTCCAGCAGTGTACAGCACCCCTAGA ACCAAATCCAGCAGACTGCAGGGTTCTAGTTTATCTTCAGAAT CAGCCAGGCACAAAGCTGTTGAATTTCTTCAGGAG | 1701 |
| | CTCCTGAAGAAAATTCAACAGCTTTGTGCCTGGCTGATTCTGA AGATAAACTAGAACCCTGCAGTCTGCTGGATTTGGTTCTAGG GTGCTGTGACACTGCTGGAACCTTCGCTCACAGGATC | 1702 |
| | GCAGACTGCAGGGTTCT | 1703 |
| | AGAACCCTGCAGTCTGC | 1704 |
| Adenomatous polyposis coli Leu1342Term TTA-TAA | AAGTTCCAGCAGTGTACAGCACCCCTAGAACCAAATCCAGCA GACTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCAGGCACA AAGCTGTTGAATTTCTTCAGGAGCGAAATCTCCCTC | 1705 |
| | GAGGGAGATTTGCTCCTGAAGAAAATTCAACAGCTTTGTGC CTGGCTGATTCTGAAGATAAACTAGAACCCTGCAGTCTGCTG GATTTGGTTCTAGGGTGCTGTGACACTGCTGGAACCT | 1706 |
| | TTCTAGTTTATCTTCAG | 1707 |
| | CTGAAGATAAACTAGAA | 1708 |
| Adenomatous polyposis coli Arg1348Trp AGG-TGG | CAGCACCCCTAGAACCAAATCCAGCAGACTGCAGGGTTCTAGT TTATCTTCAGAATCAGCCAGGCACAAAGCTGTTGAATTTCTT CAGGAGCGAAATCTCCCTCCCGAAAGTGGTGCTCAG | 1709 |
| | CTGAGCACCACTTTGCGGAGGGAGATTTGCTCCTGAAGAAA ATTCAACAGCTTTGTGCTGGCTGATTCTGAAGATAAACTAGA ACCCTGCAGTCTGCTGGATTTGGTTCTAGGGTGCTG | 1710 |
| | AATCAGCCAGGCACAAA | 1711 |
| | TTTGTGCTGGCTGATT | 1712 |
| Adenomatous polyposis coli Gly1357Term GGA-TGA | CTGCAGGGTTCTAGTTTATCTTCAGAATCAGCCAGGCACAAA GCTGTTGAATTTCTTCAGGAGCGAAATCTCCCTCCCGAAAGT GGTGCTCAGACACCCCAAAGTCCACCTGAACACTAT | 1713 |
| | ATAGTGTTCAAGTGGACTTTGGGGTGTCTGAGCACCACTTTC GGGAGGGAGATTTGCTCCTGAAGAAAATTCAACAGCTTTGT GCCTGGCTGATTCTGAAGATAAACTAGAACCCTGCAG | 1714 |
| | TTTCTTCAGGAGCGAAA | 1715 |
| | TTTCGCTCCTGAAGAAA | 1716 |
| Adenomatous polyposis coli Gln1367Term CAG-TAG | CCAGGCACAAAGCTGTTGAATTTCTTCAGGAGCGAAATCTCC CTCCCGAAAGTGGTGCTCAGACACCCCAAAGTCCACCTGAAC ACTATGTTCAAGAGACCCCACTCATGTTTAGCAGAT | 1717 |
| | ATCTGCTAAACATGAGTGGGGTCTCCTGAACATAGTGTTTCA GTGGACTTTGGGGTGTCTGAGCACCACTTTGGGAGGGAGAT TTCGCTCCTGAAGAAAATTCAACAGCTTTGTGCCTGG | 1718 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | GTGGTGCTCAGACACCC | 1719 |
| | GGGTGTCTGAGCACCAC | 1720 |
| Adenomatous polyposis coli Lys1370Term AAA-TAA | AAAGCTGTTGAATTTTCTTCAGGAGCGAAATCTCCCTCCAAAA GTGGTGCTCAGACACCCAAAAGTCCACCTGAACACTATGTTC AGGAGACCCCACTCATGTTTAGCAGATGTACTTCTG | 1721 |
| | CAGAAGTACATCTGCTAAACATGAGTGGGGTCTCCTGAACAT AGTGTTTCAGGTGGACTTTGGGGTGTCTGAGCACCACCTTTTGG AGGGAGATTTTCGCTCCTGAAGAAAATTCAACAGCTTT | 1722 |
| | AGACACCCBAAAGTCCA | 1723 |
| | TGGACTTTTGGGTGTCT | 1724 |
| Adenomatous polyposis coli Ser1392Term TCA-TAA | CACCTGAACACTATGTTTCAGGAGACCCCACTCATGTTTAGCA GATGTACTTCTGTCTAGTTCACTTGATAGTTTTGAGAGTCGTTT GATTGCCAGCTCCGTTTCAGAGTGAACCATGCAGTGG | 1725 |
| | CCACTGCATGGTTCACTCTGAACGGAGCTGGCAATCGAACGA CTCTCAAACTATCAAGTGAAGTACAGAGTACATCTGCTAA ACATGAGTGGGGTCTCCTGAACATAGTGTTTCAGGTG | 1726 |
| | TGTCAGTTCACTTGATA | 1727 |
| | TATCAAGTGAAGTACAG | 1728 |
| Adenomatous polyposis coli Ser1392Term TCA-TGA | CACCTGAACACTATGTTTCAGGAGACCCCACTCATGTTTAGCA GATGTACTTCTGTCTAGTTCACTTGATAGTTTTGAGAGTCGTTT GATTGCCAGCTCCGTTTCAGAGTGAACCATGCAGTGG | 1729 |
| | CCACTGCATGGTTCACTCTGAACGGAGCTGGCAATCGAACGA CTCTCAAACTATCAAGTGAAGTACAGAGTACATCTGCTAA ACATGAGTGGGGTCTCCTGAACATAGTGTTTCAGGTG | 1730 |
| | TGTCAGTTCACTTGATA | 1731 |
| | TATCAAGTGAAGTACAG | 1732 |
| Adenomatous polyposis coli Glu1397Term GAG-TAG | GTTTCAGGAGACCCCACTCATGTTTAGCAGATGTACTTCTGTCA GTTCACTTGATAGTTTTGAGAGTCGTTTCGATTGCCAGCTCCGT TCAGAGTGAACCATGCAGTGGGAATGGTAGGTGGCA | 1733 |
| | TGCCACCTACCATTCCTGCTGTTCACTCTGAACGGAGC TGGCAATCGAACGACTCTCAAACTATCAAGTGAAGTACAGAG AGTACATCTGCTAAACATGAGTGGGGTCTCCTGAAC | 1734 |
| | ATAGTTTTGAGAGTCGT | 1735 |
| | ACGACTCTCAAACTAT | 1736 |
| Adenomatous polyposis coli Lys1449Term AAG-TAG | CAAACCATGCCACCAAGCAGAAGTAAACACCTCCACCACCT CCTCAAACAGCTCAAACCAAGCGAGAAGTACCTAAAAATAAA GCACCTACTGCTGAAAAGAGAGAGAGTGGACCTAAGC | 1737 |
| | GCTTAGGTCCACTCTCTCTTTTCAGCAGTAGGTGCTTTATT TTTAGGTACTTCTCGCTTGGTTTGAGCTGTTTGAGGAGGTGGT GGAGGTGTTTTACTTCTGCTTGGTGGCATGGTTTG | 1738 |
| | CTCAAACCAAGCGAGAA | 1739 |
| | TTCTCGCTTGGTTTGAG | 1740 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Adenomatous polyposis coli Arg1450Term CGA-TGA | ACCATGCCACCAAGCAGAAGTAAACACCTCCACCACCTCCT CAAACAGCTCAAACCAAGCGAGAAGTACCTAAAAATAAGCA CCTACTGCTGAAAAGAGAGAGAGTGGACCTAAGCAAG | 1741 |
| | CTTGCTTAGGTCCACTCTCTCTTTTCAGCAGTAGGTGCTTT ATTTTTAGGTACTTCTCGCTTGTTTTGAGCTGTTTGAGGAGGT GGTGGAGGTGTTTTACTTCTGCTTGGTGGCATGGT | 1742 |
| | AAACCAAGCGAGAAGTA | 1743 |
| | TACTTCTCGCTTGTTTT | 1744 |
| Adenomatous polyposis coli Ser1503Term TCA-TAA | CAGATGCTGATACTTTATTACATTTTCCACGGAAAGTACTCC AGATGGATTTTCTTGTTCCATCCAGCCTGAGTGCTCTGAGCCTC GATGAGCCATTTATACAGAAAGATGTGGAATTAAG | 1745 |
| | CTTAATTCCACATCTTTCTGTATAAATGGCTCATCGAGGCTCA GAGCACTCAGGCTGGATGAACAAGAAAATCCATCTGGAGTAC TTCCGTGGCAAATGTAATAAAGTATCAGCATCTG | 1746 |
| | TTCTTGTTCCATCCAGCC | 1747 |
| | GGCTGGATGAACAAGAA | 1748 |
| Adenomatous polyposis coli Gln1529Term CAG-TAG | CTGAGCCTCGATGAGCCATTTATACAGAAAGATGTGGAATTAA GAATAATGCCTCCAGTTCAGGAAAATGACAATGGGAATGAAA CAGAATCAGAGCAGCCTAAAGAATCAAATGAAAACC | 1749 |
| | GGTTTTCATTTGATTCTTTAGGCTGCTCTGATTCTGTTTCATTC CCATTGTCATTTTCTGAACTGGAGGCATTATTCTTAATTCCAC ATCTTTCTGTATAAATGGCTCATCGAGGCTCAG | 1750 |
| | CTCCAGTTCAGGAAAAT | 1751 |
| | ATTTTCCTGAACTGGAG | 1752 |
| Adenomatous polyposis coli Ser1539Term TCA-TAA | ATGTGGAATTAAGAATAATGCCTCCAGTTCAGGAAAATGACAA TGGAATGAAACAGAATCAGAGCAGCCTAAAGAATCAAATGA AAACCAAGAGAAAGAGGCAGAAAAAACTATTGATTC | 1753 |
| | GAATCAATAGTTTTTCTGCCTCTTTCTCTTGGTTTTCATTTGA TTCTTTAGGCTGCTCTGATTCTGTTTCATTCCCATTGTCATTTT CCTGAACTGGAGGCATTATTCTTAATTCCACAT | 1754 |
| | AACAGAATCAGAGCAGC | 1755 |
| | GCTGCTCTGATTCTGTT | 1756 |
| Adenomatous polyposis coli Ser1567Term TCA-TGA | AAAACCAAGAGAAAGAGGCAGAAAAAACTATTGATTCTGAAAA GGACCTATTAGATGATTGAGATGATGATATTGAAATACTA GAAGAATGTATTATTTCTGCCATGCCAACAAGTC | 1757 |
| | GACTTTGTTGGCATGGCAGAAATAATACATTCTTCTAGTATTTT AATATCATCATCATCTGAATCATCTAATAGGTCCTTTTCAGAAT CAATAGTTTTTCTGCCTCTTTCTCTTGGTTTT | 1758 |
| | AGATGATTGAGATGATG | 1759 |
| | CATCATCTGAATCATCT | 1760 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| Adenomatous polyposis coli Asp1822Val GAC-GTC | AGAGAGTTTTCTCAGACAACAAAGATTCAAAGAAACAGAATTT GAAAAATAATTCCAAGG <u>A</u> CTTCAATGATAAGCTCCCAAATAAT GAAGATAGAGTCAGAGGAAGTTTTGCTTTTGATTCT | 1761 |
| | GAATCAAAGCAAACTTCCTCTGACTCTATCTTCATTATTTGG GAGCTTATCATTGAAGT <u>C</u> CTTGGGAATTATTTTTCAAATTCTGTT TCTTTGAATCTTTGTTGTCTGAGAAACTCTCT | 1762 |
| | TTCCAAGG <u>A</u> CTTCAATG | 1763 |
| | CATTGAAGT <u>C</u> CTTGGAA | 1764 |
| Adenomatous polyposis coli Leu2839Phe CTT-TTT | AAAACTGACAGCACAGAATCCAGTGGAACCCAAAGTCCTAAG CGCCATTCTGGGTCTTAC <u>C</u> TTGTGACATCTGTTTAAAGAGAG GAAGAATGAACTAAGAAAATTCTATGTTAATTACA | 1765 |
| | TGTAATTAACATAGAATTTTCTTAGTTTCATTCTTCCTCTCTTTT AAACAGATGTCACAAG <u>G</u> TAAGACCCAGAATGGCGCTTAGGAC TTTGGGTTCACCTGGATTCTGTGCTGTCAGTTTT | 1766 |
| | GGTCTTAC <u>C</u> TTGTGACA | 1767 |
| | TGTCACAAG <u>G</u> TAAGACC | 1768 |

EXAMPLE 13

Parahemophilia - Factor V Deficiency

[0225] Deficiency in clotting Factor V is associated with a lifelong predisposition to thrombosis. The disease typically manifests itself with usually mild bleeding, although bleeding times and clotting times are consistently prolonged. Individuals that are heterozygous for a mutation in Factor V have lowered levels of factor V but probably never have abnormal bleeding. A large number of alleles with a range of presenting symptoms have been identified. The attached table discloses the correcting oligonucleotide base sequences for the Factor V oligonucleotides of the invention.

Table 15

Factor V Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Factor V deficiency Ala221Val GCC-GTC | TTGACTGAATGCTTATTTTGGCCTGTGTCTCTCCCTCTTTCTCA GATATAACAGTTTGTG <u>C</u> CCATGACCACATCAGCTGGCATCTGC TGGGAATGAGCTCGGGGCCAGAATTATTCTCCAT | 4340 |
| | ATGGAGAATAATTCTGGCCCCGAGCTCATTCCCAGCAGATGC CAGCTGATGTGGTCATGG <u>G</u> CACAACTGTTATATCTGAGAAA GAGGGAGAGACACAGGCCAAAATAAGCATTCAAGTCAA | 1769 |
| | AGTTTGTG <u>C</u> CCATGACC | 1770 |
| | GGTCATGGG <u>C</u> ACAACT | 1771 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Thrombosis Arg306Gly AGG-GGG | TGTCCTAACTCAGCTGGGATGCAGGCTTACATTGACATTAAAA ACTGCCCAAAGAAAACCAAGGAATCTTAAGAAAATAACTCGTGA GCAGAGGCGGCACATGAAGAGGTGGGAATACTTCA | 1772 |
| | TGAAGTATTCCCACCTCTTCATGTGCCGCCTCTGCTCACGAGT TATTTTCTTAAGATTCC ^T GGTTTTCTTTGGGCAGTTTTTAATGT CAATGTAAGCCTGCATCCAGCTGAGTTAGGACA | 1773 |
| | AGAAAACCAAGGAATCTT | 1774 |
| | AAGATTCCT ^T GGTTTTCT | 1775 |
| Thrombosis Arg306Thr AGG-ACG | GTCCTAACTCAGCTGGGATGCAGGCTTACATTGACATTAAAA CTGCCCAAAGAAAACCAAGGAATCTTAAGAAAATAACTCGTGAG CAGAGGCGGCACATGAAGAGGTGGGAATACTTCAT | 1776 |
| | ATGAAGTATTCCCACCTCTTCATGTGCCGCCTCTGCTCACGAG TTATTTTCTTAAGATTCC ^T GGTTTTCTTTGGGCAGTTTTTAATG TCAATGTAAGCCTGCATCCAGCTGAGTTAGGAC | 1777 |
| | GAAAACCAAGGAATCTTA | 1778 |
| | TAAGATTCCT ^T GGTTTTCT | 1779 |
| Increased Risk Thrombosis Arg485Lys AGA-AAA | CCACAGAAAATGATGCCCAGTGCTTAACAAGACCATACTACAG TGACGTGGACATCATGAGAGACATCGCCTCTGGGCTAATAGG ACTACTTCTAATCTGTAAGAGCAGATCCCTGGACAG | 1780 |
| | CTGTCCAGGGATCTGCTCTTACAGATTAGAAGTAGTCCTATTA GCCCAGAGGCGATGTCT ^T TCATGATGTCCACGTCACTGTAGT ATGGTCTTGTTAAGCACTGGGCATCATTTTCTGTGG | 1781 |
| | CATCATGAGAGACATCG | 1782 |
| | CGATGTCT ^T TCATGATG | 1783 |
| Increased Risk Thrombosis Arg506Gln CGA-CAA | ACATCGCCTCTGGGCTAATAGGACTACTTCTAATCTGTAAGAG CAGATCCCTGGACAGGCGAGGAATACAGGTATTTTGTCTTG AAGTAACCTTTAGAAATTCTGAGAATTTCTTCTGG | 1784 |
| | CCAGAAGAAATTCTCAGAATTTCTGAAAGGTTACTTCAAGGAC AAAATACCTGTATTCCT ^T CGCCTGTCCAGGGATCTGCTCTTACA GATTAGAAGTAGTCCTATTAGCCCAGAGGCGATGT | 1785 |
| | GGACAGGCGAGGAATAC | 1786 |
| | GTATTCCT ^T CGCCTGTCC | 1787 |
| Factor V Deficiency Arg506Term CGA-TGA | GACATCGCCTCTGGGCTAATAGGACTACTTCTAATCTGTAAGA GCAGATCCCTGGACAGGCGAGGAATACAGGTATTTTGTCTT GAAGTAACCTTTAGAAATTCTGAGAATTTCTTCTG | 1788 |
| | CAGAAGAAATTCTCAGAATTTCTGAAAGGTTACTTCAAGGACA AAATACCTGTATTCCT ^T CGCCTGTCCAGGGATCTGCTCTTACAG ATTAGAAGTAGTCCTATTAGCCCAGAGGCGATGTC | 1789 |
| | TGGACAGGCGAGGAATA | 1790 |
| | TATTCCT ^T CGCCTGTCCA | 1791 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|-------------------------------------|---|------------|
| Thrombosis Arg712Term CGA-TGA | AGTGATGCTGACTATGATTACCAGAACAGACTGGCTGCAGCA TTAGGAATCAGGTCATTCCGAAACTCATCATTGAATCAGGAAG AAGAAGAGTTCAATCTTACTGCCCTAGCTCTGGAGA | 1792 |
| | TCTCCAGAGCTAGGGCAGTAAGATTGAACTCTTCTTCTTCCTG ATTCAATGATGAGTTTCGGAATGACCTGATTCCTAATGCTGCA GCCAGTCTGTTCTGGTAATCATAGTCAGCATCACT | 1793 |
| | GGTCATTCCGAAACTCA | 1794 |
| | TGAGTTTCGGAATGACC | 1795 |
| Thrombosis His1299Arg CAT-CGT | TCAGTCAGACAAACCTTTCCCCAGCCCTCGGTCAGATGCCCA TTTCTCCAGACCTCAGCCATACAACCCTTTCTCTAGACTTCAG CCAGACAAACCTCTCTCCAGAACTCAGTCAAACAAA | 1796 |
| | TTTGTGTTGACTGAGTTCTGGAGAGAGGTTTGTCTGGCTGAAGT CTAGAGAAAGGGTTGTATGGCTGAGGTCTGGAGAAATGGGCA TCTGACCGAGGGCTGGGGAAGGTTTGTCTGACTGA | 1797 |
| | CCTCAGCCATACAACCC | 1798 |
| | GGTTGTATGGCTGAGG | 1799 |

EXAMPLE 14

Hemophilia - Factor VIII Deficiency

[0226] The attached table discloses the correcting oligonucleotide base sequences for the Factor VIII oligonucleotides of the invention.

5

Table 16

Factor VIII Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|-------------------------------------|--|------------|
| Haemophilia A TyrSCys TAC-TGC | AGCTCTCCACCTGCTTCTTTCTGTGCCTTTTGCGATTCTGCTT TAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAAGTGC ATGGGACTATATGCAAAGTGATCTCGGTGAGCTGCC | 1800 |
| | GGCAGCTCACCGAGATCACTTTGCATATAGTCCCATGACAGT TCCACTGCACCCAGGTAGTATCTTCTGGTGGCACTAAAGCAG AATCGCAAAGGCACAGAAAGAAGCAGGTGGAGAGCT | 1801 |
| | CAGAAGATACTACCTGG | 1802 |
| | CCAGGTAGTATCTTCTG | 1803 |
| Haemophilia A Leu7Arg CTG-CGG | CCACCTGCTTCTTTCTGTGCCTTTTGCGATTCTGCTTTAGTGC CACCAGAAGATACTACCTGGGTGCAGTGGAAGTGCATGGGA CTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGA | 1804 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | TCCACAGGCAGCTCACCGAGATCACTTTGCATATAGTCCCAT GACAGTTCCACTGCACCC <u>A</u> GGTAGTATCTTCTGGTGGCACTA AAGCAGAATCGCAAAGGCACAGAAAGAAGCAGGTGG | 1805 |
| | ATACTACCTGGGTGCAG | 1806 |
| | CTGCACCC <u>A</u> GGTAGTAT | 1807 |
| Haemophilia A Ser(-1)Arg AGTg-AGG | AGTCATGCAAATAGAGCTCTCCACCTGCTTCTTTCTGTGCCTT TTGCGATTCTGCTTTAGIGCCACCAGAAGATACTACCTGGGT GCAGTGGAAGTGTCTATGGGACTATATGCAAAGTGAT | 1808 |
| | ATCACTTTGCATATAGTCCCATGACAGTTCCACTGCACCCAGG TAGTATCTTCTGGTGGC <u>A</u> CTAAAGCAGAATCGCAAAGGCAC AGAAAGAAGCAGGTGGAGAGCTCTATTTGCATGACT | 1809 |
| | TGCTTTAGTGGCACCAG | 1810 |
| | CTGGTGGC <u>A</u> CTAAAGCA | 1811 |
| Haemophilia A Arg(-5)Term gCGA-TGA | CATTTGTAGCAATAAGTCATGCAAATAGAGCTCTCCACCTGCT TCTTTCTGTGCCTTTTG <u>C</u> GATTCTGCTTTAGTGCCACCAGAAG ATACTACCTGGGTGCAGTGGAAGTGTCTATGGGACT | 1812 |
| | AGTCCCATGACAGTTCCACTGCACCCAGGTAGTATCTTCTGG TGGCACTAAAGCAGAATC <u>G</u> CAAAGGCACAGAAAGAAGCAG GTGGAGAGCTCTATTTGCATGACTTATTGCTACAAATG | 1813 |
| | GCCTTTTG <u>C</u> GATTCTGC | 1814 |
| | GCAGAATC <u>G</u> CAAAGGC | 1815 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Haemophilia A Glu11Val GAA-GTA | TTCTGTGCCTTTTGGCATTCTGCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCATGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAGGTAAAG | 1816 |
| | CTTTACCTTTCGTCCACAGGCAGCTCACCGAGATCACTTTGCATATAGTCCCATGACAGTTCCACTGCACCCAGGTAGTATCTTC TGGTGGCACTAAAGCAGAATCGCAAAAGGCACAGAA | 1817 |
| | TGCAGTGGAACTGTCAT | 1818 |
| | ATGACAGTTCCACTGCA | 1819 |
| Haemophilia A Trp14Gly aTGG-GGG | CTTTTGGCATTCTGCTTTAGTGCCACCAGAAGATACTACCTGGGTGCAGTGGAACTGTCAATGGGACTATATGCAAAGTGATCTCGGTGAGCTGCCTGTGGACGCAAGGTAAAGGCATGTCC | 1820 |
| | GGACATGCCTTTACCTTTCGTCCACAGGCAGCTCACCGAGATCACTTTGCATATAGTCCCATGACAGTTCCACTGCACCCAGGTAGTATCTTCTGGTGGCACTAAAGCAGAATCGCAAAAG | 1821 |
| | AACTGTCAATGGGACTAT | 1822 |
| | ATAGTCCCATGACAGTT | 1823 |
| Haemophilia A Tyr46Term TACa-TAA | TTCACGCAGATTTCTCCTAGAGTGCCAAAATCTTTTCCATTC AACACCTCAGTCGTGTACAATAAAGACTCTGTTTGTAGAATTCA CGGATCACCTTTTCAACATCGCTAAGCCAAGGCCA | 1824 |
| | TGGCCTTGGCTTAGCGATGTTGAAAAGGTGATCCGTGAATTC TACAAACAGAGTCTTTTTGTACACGACTGAGGTGTTGAATGGA AAAGATTTTGGCACTCTAGGAGGAAATCTGCGTGAA | 1825 |
| | GTCGTGTACAAAAGAC | 1826 |
| | GTCTTTTTGTACACGAC | 1827 |
| Haemophilia A Asp56Glu GATc-GAA | ATCTTTTCCATTCAACACCTCAGTCGTGTACAAAAGACTCTG TTTGTAGAATTCACGGATCACCTTTTCAACATCGCTAAGCCAA GGCCACCCTGGATGGGTAATGAAAACAATGTTGAA | 1828 |
| | TTCAACATTGTTTTATTACCCATCCAGGGTGGCCTTGGCTTA GCGATGTTGAAAAGGTGATCCGTGAATTCTACAAACAGAGTC TTTTGTACACGACTGAGGTGTTGAATGGAAAAGAT | 1829 |
| | TTCACGGATCACCTTTT | 1830 |
| | AAAAGGTGATCCGTGAA | 1831 |
| Haemophilia A Gly73Val GGT-GTT | TTCTGGAGTACTATCCCCAAGTAACCTTTGGCGGACATCTCAT TCTTACAGGTCTGCTAGTTCCTACCATCCAGGCTGAGGTTTAT GATACAGTGGTCATTACACTTAAGAACATGGCTTC | 1832 |
| | GAAGCCATGTTCTTAAGTGAATGACCACTGTATCATAAACCT CAGCCTGGATGGTAGGACCTAGCAGACCTGTAAGAATGAGAT GTCCGCCAAAGGTTACTTGGGGATAGTACTCCAGAA | 1833 |
| | TCTGCTAGGTCCTACCA | 1834 |
| | TGGTAGGACCTAGCAGA | 1835 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---------------------------------------|--|------------|
| Haemophilia A Glu79Lys tGAG-AAG | CAAGTAACCTTTGGCGGACATCTCATTCTTACAGGTCTGCTAG GTCCTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTAC ACTTAAGAACATGGCTTCCCATCCTGTCAGTCTTC | 1836 |
| | GAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAAATGA CCACTGTATCATAAACCTCAGCCTGGATGGTAGGACCTAGCA GACCTGTAAGAATGAGATGTCCGCCAAAGGTTACTTG | 1837 |
| | TCCAGGCTGAGGTTTAT | 1838 |
| | ATAAACCTCAGCCTGGA | 1839 |
| Haemophilia A Val50Asp GTT-GAT | TAACCTTTGGCGGACATCTCATTCTTACAGGTCTGCTAGGTCC TACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTACACTT AAGAACATGGCTTCCCATCCTGTCAGTCTTCATGC | 1840 |
| | GCATGAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAA ATGACCACTGTATCATAAACCTCAGCCTGGATGGTAGGACCT AGCAGACCTGTAAGAATGAGATGTCCGCCAAAGGTTA | 1841 |
| | GGCTGAGGTTTATGATA | 1842 |
| | TATCATAAACCTCAGCC | 1843 |
| Haemophilia A Asp82Val GAT-GTT | TTGGCGGACATCTCATTCTTACAGGTCTGCTAGGTCCTACCAT CCAGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAA CATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGG | 1844 |
| | CCAACAGCATGAAGACTGACAGGATGGGAAGCCATGTTCTTA AGTGTAATGACCACTGTATCATAAACCTCAGCCTGGATGGTA GGACCTAGCAGACCTGTAAGAATGAGATGTCCGCCAA | 1845 |
| | GGTTTATGATACAGTGG | 1846 |
| | CCACTGTATCATAAACCC | 1847 |
| Haemophilia A Asp82Gly GAT-GGT | TTGGCGGACATCTCATTCTTACAGGTCTGCTAGGTCCTACCAT CCAGGCTGAGGTTTATGATACAGTGGTCATTACACTTAAGAA CATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGG | 1848 |
| | CCAACAGCATGAAGACTGACAGGATGGGAAGCCATGTTCTTA AGTGTAATGACCACTGTATCATAAACCTCAGCCTGGATGGTA GGACCTAGCAGACCTGTAAGAATGAGATGTCCGCCAA | 1849 |
| | GGTTTATGATACAGTGG | 1850 |
| | CCACTGTATCATAAACCC | 1851 |
| Haemophilia A Val85Asp GTC-GAC | ATCTCATTCTTACAGGTCTGCTAGGTCCTACCATCCAGGCTGA GGTTTATGATACAGTGGTCATTACACTTAAGAACATGGCTTCC CATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTA | 1852 |
| | TAGGATACACCAACAGCATGAAGACTGACAGGATGGGAAGCC ATGTTCTTAAGTGTAAATGACCACTGTATCATAAACCTCAGCCT GGATGGTAGGACCTAGCAGACCTGTAAGAATGAGAT | 1853 |
| | TACAGTGGTCATTACAC | 1854 |
| | GTGTAATGACCACTGTA | 1855 |
| Haemophilia A Lys89Thr AAG-ACG | CAGGTCTGCTAGGTCCTACCATCCAGGCTGAGGTTTATGATA CAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTGTCAG TCTTCATGCTGTTGGTGTATCCTACTGGAAAGCTTC | 1856 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
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| | GAAGCTTTCCAGTAGGATACACCAACAGCATGAAGACTGACA GGATGGGAAGCCATGTTCTTAAGTGTAAATGACCACTGTATCAT AAACCTCAGCCTGGATGGTAGGACCTAGCAGACCTG | 1857 |
| | TACACTTAAGAACATGG | 1858 |
| | CCATGTTCTTAAGTGTAA | 1859 |
| | | |
| Haemophilia A Met91Val cATG-GTG | CTGCTAGGTCCTACCATCCAGGCTGAGGTTTATGATACAGTG GTCATTACACTTAAGAACAATGGCTTCCCATCCTGTCAGTCTTC ATGCTGTTGGTGTATCCTACTGGAAAGCTTCTGAGG | 1860 |
| | CCTCAGAAGCTTTCCAGTAGGATACACCAACAGCATGAAGAC TGACAGGATGGGAAGCCATGTTCTTAAGTGTAAATGACCACTG TATCATAAACCTCAGCCTGGATGGTAGGACCTAGCAG | 1861 |
| | TTAAGAACAATGGCTTCC | 1862 |
| | GGAAGCCATGTTCTTAA | 1863 |
| | | |
| Haemophilia A His94Arg CAT-CGT | CTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTACACT TAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGGT GTATCCTACTGGAAAGCTTCTGAGGGTGAGTAAAA | 1864 |
| | TTTTACTCACCTCAGAAGCTTTCCAGTAGGATACACCAACAG CATGAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAA TGACCACTGTATCATAAACCTCAGCCTGGATGGTAG | 1865 |
| | GGCTTCCCATCCTGTCA | 1866 |
| | TGACAGGATGGGAAGCC | 1867 |
| | | |
| Haemophilia A His94Tyr cCAT-TAT | CCTACCATCCAGGCTGAGGTTTATGATACAGTGGTCATTACAC TTAAGAACATGGCTTCCCATCCTGTCAGTCTTCATGCTGTTGG TGTATCCTACTGGAAAGCTTCTGAGGGTGAGTAAA | 1868 |
| | TTTACTCACCTCAGAAGCTTTCCAGTAGGATACACCAACAGC ATGAAGACTGACAGGATGGGAAGCCATGTTCTTAAGTGTAA GACCACTGTATCATAAACCTCAGCCTGGATGGTAGG | 1869 |
| | TGGCTTCCCATCCTGTC | 1870 |
| | GACAGGATGGGAAGCCA | 1871 |
| | | |
| Haemophilia A Leu98Arg CTT-CGT | CTGAGGTTTATGATACAGTGGTCATTACACTTAAGAACATGGC TTCCCATCCTGTCAGTCTTCATGCTGTTGGTGTATCCTACTGG AAAGCTTCTGAGGGTGAGTAAAATACCCTCCTATT | 1872 |
| | AATAGGAGGGTATTTTACTCACCTCAGAAGCTTTCCAGTAG GATACACCAACAGCATGAAGACTGACAGGATGGGAAGCCAT GTTCTTAAGTGTAAATGACCACTGTATCATAAACCTCAG | 1873 |
| | TGTCAGTCTTCATGCTG | 1874 |
| | CAGCATGAAGACTGACA | 1875 |
| | | |
| Haemophilia A Gly102Ser tGGT-AGT | GATACAGTGGTCATTACACTTAAGAACATGGCTTCCCATCCTG TCAGTCTTCATGCTGTTGGTGTATCCTACTGGAAAGCTTCTGA GGGTGAGTAAAATACCCTCCTATTGTCCTGTCATT | 1876 |
| | AATGACAGGACAATAGGAGGGTATTTTACTCACCTCAGAAG CTTTCCAGTAGGATACACCAACAGCATGAAGACTGACAGGAT GGGAAGCCATGTTCTTAAGTGTAAATGACCACTGTATC | 1877 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | ATGCTGTTGGTGTATCC | 1878 |
| | GGATACACCAACAGCAT | 1879 |
| Haemophilia A Glu113Asp GAA-T-GAC | CTTTGAGTGTACAGTGGATATAGAAAGGACAATTTTATTTCTT CCTGCTATAGGAGCTGAATATGATGATCAGACCAGTCAAAGG GAGAAAGAAGATGATAAAGTCTTCCCTGGTGGAAAGC | 1880 |
| | GCTTCCACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTTGA CTGGTCTGATCATCATATTCAGCTCCTATAGCAGGAAGAAATA AAATTGTCCTTTCTATATCCACTGTACACTCAAAG | 1881 |
| | GGAGCTGAATATGATGA | 1882 |
| | TCATCATATTCAGCTCC | 1883 |
| Haemophilia A Tyr114Cys TAT-TGT | TTGAGTGTACAGTGGATATAGAAAGGACAATTTTATTTCTTCC TGCTATAGGAGCTGAATATGATGATCAGACCAGTCAAAGGGA GAAAGAAGATGATAAAGTCTTCCCTGGTGGAAAGCCA | 1884 |
| | TGGCTTCCACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTT GACTGGTCTGATCATCATATTCAGCTCCTATAGCAGGAAGAAA TAAATTGTCCTTTCTATATCCACTGTACACTCAA | 1885 |
| | AGCTGAATATGATGATC | 1886 |
| | GATCATCATATTCAGCT | 1887 |
| Haemophilia A Asp116Gly GAT-GGT | GTACAGTGGATATAGAAAGGACAATTTTATTTCTTCTGCTAT AGGAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAGA AGATGATAAAGTCTTCCCTGGTGGAAAGCCATACATA | 1888 |
| | TATGTATGGCTTCCACCAGGGAAGACTTTATCATCTTCTTTCT CCCTTTGACTGGTCTGATCATCATATTCAGCTCCTATAGCAGG AAGAAATAAAATTGTCCTTTCTATATCCACTGTAC | 1889 |
| | ATATGATGATCAGACCA | 1890 |
| | TGGTCTGATCATCATAT | 1891 |
| Haemophilia A Gln 117Term tCAG-TAG | ACAGTGGATATAGAAAGGACAATTTTATTTCTTCTGCTATAG GAGCTGAATATGATGATCAGACCAGTCAAAGGGAGAAAGAAG ATGATAAAGTCTTCCCTGGTGGAAAGCCATACATATG | 1892 |
| | CATATGTATGGCTTCCACCAGGGAAGACTTTATCATCTTCTTT CTCCCTTTGACTGGTCTGATCATCATATTCAGCTCCTATAGCA GGAAGAAATAAAATTGTCCTTTCTATATCCACTGT | 1893 |
| | ATGATGATCAGACCAGT | 1894 |
| | ACTGGTCTGATCATCAT | 1895 |
| Haemophilia A Thr118Ile ACC-ATC | TGGATATAGAAAGGACAATTTTATTTCTTCTGCTATAGGAGC TGAATATGATGATCAGACCAGTCAAAGGGAGAAAGAAGATGA TAAAGTCTTCCCTGGTGGAAAGCCATACATATGTCTG | 1896 |
| | CAGACATATGTATGGCTTCCACCAGGGAAGACTTTATCATCTT CTTTCTCCCTTTGACTGGTCTGATCATCATATTCAGCTCCTATA GCAGGAAGAAATAAAATTGTCCTTTCTATATCCA | 1897 |
| | TGATCAGACCAGTCAA | 1898 |
| | TTTGAAGTGGTCTGATCA | 1899 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Haemophilia A Glu122Term gGAG-TAG | AGGACAATTTTATTTCTTCCTGCTATAGGAGCTGAATATGATG ATCAGACCAGTCAAAGG <u>G</u> AGAAAGAAGATGATAAAGTCTTCC CTGGTGGAAGCCATACATATGTCTGGCAGGTCCTGA | 1900 |
| | TCAGGACCTGCCAGACATATGTATGGCTTCCACCAGGGAAGA CTTTATCATCTTCTTTCT <u>C</u> CCTTTGACTGGTCTGATCATCATAT TCAGCTCCTATAGCAGGAAGAAATAAAATTGTCCT | 1901 |
| | GTCAAAGG <u>G</u> AGAAAGAA | 1902 |
| | TTCTTTCT <u>C</u> CCTTTGAC | 1903 |
| Haemophilia A Asp126His tGAT-CAT | TTTCTTCCTGCTATAGGAGCTGAATATGATGATCAGACCAGTC AAAGGGAGAAAGAAGAT <u>G</u> ATAAAGTCTTCCCTGGTGGAAGCC ATACATATGTCTGGCAGGTCCTGMAGAGAATGGTC | 1904 |
| | GACCATTCTCTTTCAGGACCTGCCAGACATATGTATGGCTTCC ACCAGGGAAGACTTTAT <u>C</u> ATCTTCTTTCTCCCTTTGACTGGTC TGATCATCATATTCAGCTCCTATAGCAGGAAGAAA | 1905 |
| | AAGAAGAT <u>G</u> ATAAAGTC | 1906 |
| | GACTTTAT <u>C</u> ATCTTCTT | 1907 |
| Haemophilia A Gln139Term gCAG-TAG | AGTCAAAGGGAGAAAGAAGATGATAAAGTCTTCCCTGGTGGA AGCCATACATATGTCTGG <u>C</u> AGGTCCTGAAAGAGAATGGTCCA ATGGCCTCTGACCCACTGTGCCTTACCTACTCATATC | 1908 |
| | GATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATTGGA CCATTCTCTTTCAGGACCT <u>G</u> CCAGACATATGTATGGCTTCCAC CAGGGAAGACTTTATCATCTTCTTTCTCCCTTTGACT | 1909 |
| | ATGTCTGG <u>C</u> AGGTCCTG | 1910 |
| | CAGGACCT <u>G</u> CCAGACAT | 1911 |
| Haemophilia A Val140Ala GTC-GCC | AAAGGGAGAAAGAAGATGATAAAGTCTTCCCTGGTGGAAGCC ATACATATGTCTGGCAGG <u>T</u> CCTGAAAGAGAATGGTCCAATGG CCTCTGACCCACTGTGCCTTACCTACTCATATCTTTC | 1912 |
| | GAAAGATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATT GGACCATTCTCTTTCAGG <u>A</u> CCTGCCAGACATATGTATGGCTT CCACCAGGGAAGACTTTATCATCTTCTTTCTCCCTTT | 1913 |
| | CTGGCAGG <u>T</u> CCTGAAAG | 1914 |
| | CTTTCAGG <u>A</u> CCTGCCAG | 1915 |
| Haemophilia A Asn144Lys AATg-AAA | AGATGATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTG GCAGGTCTGAAAGAGAAT <u>T</u> GGTCCAATGGCCTCTGACCCACT GTGCCTTACCTACTCATATCTTTCTCATGTGGACCTG | 1916 |
| | CAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGTGG GTCAGAGGCCATTGGACC <u>A</u> TTCTCTTTCAGGACCTGCCAGAC ATATGTATGGCTTCCACCAGGGAAGACTTTATCATCT | 1917 |
| | AAAGAGAAT <u>T</u> GGTCCAAT | 1918 |
| | ATTGGACC <u>A</u> TTCTCTTT | 1919 |
| Haemophilia AG Gly145Asp GGT-GAT | ATGATAAAGTCTTCCCTGGTGGAAGCCATACATATGTCTGGC AGGTCCTGAAAGAGAAT <u>G</u> TCCAATGGCCTCTGACCCACTGT GCCTTACCTACTCATATCTTTCTCATGTGGACCTGGT | 1920 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
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| | ACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGT GGGTCAGAGGCCATTGGAC <u>C</u> ATTCTCTTTTCAGGACCTGCCAG ACATATGTATGGCTTCCACCAGGGAAGACTTTATCAT | 1921 |
| | AGAGAATGGTCCAATGG | 1922 |
| | CCATTGGAC <u>C</u> ATTCTCT | 1923 |
| | | |
| Haemophilia A Gly145Val GGT-GTT | ATGATAAAGTCTTCCCTGGTGGAGCCATACATATGTCTGGC AGGTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGT GCCTTACCTACTCATATCTTTCTCATGTGGACCTGGT | 1924 |
| | ACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAGT GGGTCAGAGGCCATTGGAC <u>C</u> ATTCTCTTTTCAGGACCTGCCAG ACATATGTATGGCTTCCACCAGGGAAGACTTTATCAT | 1925 |
| | AGAGAATGGTCCAATGG | 1926 |
| | CCATTGGAC <u>C</u> ATTCTCT | 1927 |
| | | |
| Haemophilia A Pro146Ser tCCA-TCA | GATAAAGTCTTCCCTGGTGGAGCCATACATATGTCTGGCAG GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGC CTTACCTACTCATATCTTTCTCATGTGGACCTGGTAA | 1928 |
| | TTACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACA GTGGGTCAGAGGCCATTGG <u>G</u> ACCATTCTCTTTTCAGGACCTGCC AGACATATGTATGGCTTCCACCAGGGAAGACTTTATC | 1929 |
| | AGAATGGTCCAATGGCC | 1930 |
| | GGCCATTGG <u>G</u> ACCATTCT | 1931 |
| | | |
| Haemophilia A Cys153Trp TGCc-TGG | CCATACATATGTCTGGCAGGTCCTGAAAGAGAATGGTCCAAT GGCCTCTGACCCACTGTGC <u>C</u> TTACCTACTCATATCTTTCTCAT GTGGACCTGGTAAAGACTTGAATTCAGGCCTCATT | 1932 |
| | AATGAGGCCTGAATTCAGTCTTTTACCAGGTCCACATGAGAA AGATATGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATTGG ACCATTCTCTTTTCAGGACCTGCCAGACATATGTATGG | 1933 |
| | CCACTGTGCCTTACCTA | 1934 |
| | TAGGTAAGGCACAGTGG | 1935 |
| | | |
| Haemophilia A Tyr156Term TACT-TAA | TGTCTGGCAGGTCCTGAAAGAGAATGGTCCAATGGCCTCTGA CCCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCTG GTAAAAGACTTGAATTCAGGCCTCATTGGAGCCCTA | 1936 |
| | TAGGGCTCCAATGAGGCCTGAATTCAGTCTTTTACCAGGTC CACATGAGAAAGATATGAGTAGGTAAGGCACAGTGGGTCAGA GGCCATTGGACCATTCTCTTTTCAGGACCTGCCAGACA | 1937 |
| | CTTACCTACTCATATCT | 1938 |
| | AGATATGAGTAGGTAAG | 1939 |
| | | |
| Haemophilia A Ser157Pro cTCA-CCA | GTCTGGCAGGTCCTGAAAGAGAATGGTCCAATGGCCTCTGAC CCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCTGG TAAAAGACTTGAATTCAGGCCTCATTGGAGCCCTAC | 1940 |
| | GTAGGGCTCCAATGAGGCCTGAATTCAGTCTTTTACCAGGT CCACATGAGAAAGATATGAGTAGGTAAGGCACAGTGGGTCAG AGGCCATTGGACCATTCTCTTTTCAGGACCTGCCAGAC | 1941 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | TTACCTACTCATATCTT | 1942 |
| | AAGATATGAGTAGGTAA | 1943 |
| Haemophilia A Ser160Pro tTCT-CCT | GTCCTGAAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGC CTTACCTACTCATATCTTTCTCATGTGGACCTGGTAAAAGACT TGAATTCAGGCCTCATTGGAGCCCTACTAGTATGTA | 1944 |
| | TACATACTAGTAGGGCTCCAATGAGGCCTGAATTCAGTCTTT TACCAGGTCCACATGAGAAAGATATGAGTAGGTAAGGCACAG TGGGTCAGAGGCCATTGGACCATTCTCTTTCAGGAC | 1945 |
| | CATATCTTTCTCATGTG | 1946 |
| | CACATGAGAAAGATATG | 1947 |
| | | |
| Haemophilia A Val162Met tGTG-ATG | AAAGAGAATGGTCCAATGGCCTCTGACCCACTGTGCCTTACC TACTCATATCTTTCTCATGTGGACCTGGTAAAAGACTTGAATT CAGGCCTCATTGGAGCCCTACTAGTATGTAGAGAAG | 1948 |
| | CTTCTCTACATACTAGTAGGGCTCCAATGAGGCCTGAATTCAA GTCTTTTACCAGGTCCACATGAGAAAAGATATGAGTAGGTAAG GCACAGTGGGTCAGAGGCCATTGGACCATTCTCTTT | 1949 |
| | TTTCTCATGTGGACCTG | 1950 |
| | CAGGTCCACATGAGAAA | 1951 |
| | | |
| Haemophilia A Lys166Thr AAA-ACA | CAATGGCCTCTGACCCACTGTGCCTTACCTACTCATATCTTTC TCATGTGGACCTGGTAAAGACTTGAATTCAGGCCTCATTGG AGCCCTACTAGTATGTAGAGAAGGTAAGTGTATGAA | 1952 |
| | TTCATACACTTACCTTCTCTACATACTAGTAGGGCTCCAATGA GGCCTGAATTCAGTCTTTTACCAGGTCCACATGAGAAAAGATA TGAGTAGGTAAGGCACAGTGGGTCAGAGGCCATTG | 1953 |
| | CCTGGTAAAGACTTGA | 1954 |
| | TCAAGTCTTTTACCAGG | 1955 |
| | | |
| Haemophilia A Ser170Leu TCA-TTA | ACCCACTGTGCCTTACCTACTCATATCTTTCTCATGTGGACCT GGTAAAAGACTTGAATTCAGGCCTCATTGGAGCCCTACTAGT ATGTAGAGAAGGTAAGTGTATGAAAGCGTAGGATTG | 1956 |
| | CAATCCTACGCTTTCATACACTTACCTTCTCTACATACTAGTAG GGCTCCAATGAGGCCTGAATTCAAGTCTTTTACCAGGTCCAC ATGAGAAAAGATATGAGTAGGTAAGGCACAGTGGGT | 1957 |
| | CTTGAATTCAGGCCTCA | 1958 |
| | TGAGGCCTGAATTCAAG | 1959 |
| | | |
| Haemophilia A Phe195Val aTTT-GTT | AATGTTCTCACTTCTTTTTTCAGGGAGTCTGGCCAAGGAAAAGA CACAGACCTTGCACAAATTATACTACTTTTTTGCTGTATTTGAT GAAGGTTAGTGAGTCTTAATCTGAATTTTGGATT | 1960 |
| | AATCCAAAATTGAGTTAAGACTCACTAACCTTCATCAAATACA GCAAAAAGTAGTATAAATTTGTGCAAGGTCTGTGTCTTTTCCT TGGCCAGACTCCCTGAAAAAGAAGTGAGAACATT | 1961 |
| | TGCACAAATTTATACTA | 1962 |
| | TAGTATAAATTTGTGCA | 1963 |
| | | |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Haemophilia A Leu198His CTT-CAT | CTTCTTTTTCAGGGAGTCTGGCCAAGGAAAAGACACAGACCT TGCACAAATTTATACTACTTTTGGCTGTATTTGATGAAGGTTAG TGAGTCTTAATCTGAATTTTGGATTCTGAAAGAA | 1964 |
| | TTCTTTTCAGGAATCCAAAATTCAGATTAAGACTCACTAACCTTC ATCAAATACAGCAAAAAGTAGTATAAATTTGTGCAAGGTCTGT GTCTTTTCCTTGGCCAGACTCCCTGAAAAAGAAG | 1965 |
| | TATACTACTTTTGGCTG | 1966 |
| | CAGCAAAAAGTAGTATA | 1967 |
| Haemophilia A Ala200Asp GCT-GAT | TTTCAGGGAGTCTGGCCAAGGAAAAGACACAGACCTTGCACA AATTTATACTACTTTTTGCTGTATTTGATGAAGGTTAGTGAGTC TTAATCTGAATTTTGGATTCTGAAAGAAATCCTC | 1968 |
| | GAGGATTTCTTTTCAGGAATCCAAAATTCAGATTAAGACTCACT AACCTTCATCAAATACAGCAAAAAGTAGTATAAATTTGTGCAA GGTCTGTGTCTTTTCCTTGGCCAGACTCCCTGAAA | 1969 |
| | ACTTTTTGCTGTATTTG | 1970 |
| | CAAATACAGCAAAAAGT | 1971 |
| Haemophilia A Ala200Thr TGT-ACT | TTTTTCAGGGAGTCTGGCCAAGGAAAAGACACAGACCTTGCAC AAATTTATACTACTTTTTGCTGTATTTGATGAAGGTTAGTGAGT CTTAATCTGAATTTTGGATTCTGAAAGAAATCCT | 1972 |
| | AGGATTTCTTTTCAGGAATCCAAAATTCAGATTAAGACTCACTA ACCTTCATCAAATACAGCAAAAAGTAGTATAAATTTGTGCAAG GTCTGTGTCTTTTCCTTGGCCAGACTCCCTGAAAA | 1973 |
| | TACTTTTTGCTGTATTT | 1974 |
| | AAATACAGCAAAAAGTA | 1975 |
| Haemophilia A Val234Phe aGTC-TTC | AACTCCTTGATGCAGGATAGGGATGCTGCATCTGCTCGGGCC TGGCCTAAAATGCACACAGTCAATGGTTATGTAAACAGGTCTC TGCCAGGTATGTACACACCTGCTCAACAATCCTCAG | 1976 |
| | CTGAGGATTGTTGAGCAGGTGTGTACATACCTGGCAGAGACC TGTTTACATAACCATTGACTGTGTGCATTTTAGGCCAGGCCCG AGCAGATGCAGCATCCCTATCCTGCATCAAGGAGTT | 1977 |
| | TGCACACAGTCAATGGT | 1978 |
| | ACCATTGACTGTGTGCA | 1979 |
| Haemophilia A Gly247Glu GGA-GAA | ATTTTCAGATTCTCTACTTCATAGCCATAGGTGTCTTATTCCTAC TTTACAGGTCTGATTGGATGCCACAGGAAATCAGTCTATTGG CATGTGATTGGAATGGGCACCACTCCTGAAGTGCA | 1980 |
| | TGCACTTCAGGAGTGGTGCCCATTCGAATCACATGCCAATAG ACTGATTTCTGTGGCATCCAATCAGACCTGTAAAGTAGGAAT AAGACACCTATGGCTATGAAGTAGAGAATCTGAAAT | 1981 |
| | TCTGATTGGATGCCACA | 1982 |
| | TGTGGCATCCAATCAGA | 1983 |
| Haemophilia A Trp255Cys TGGc-TGT | ATAGGTGTCTTATTCCTACTTTACAGGTCTGATTGGATGCCAC AGGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACT CCTGAAGTGCACTCAATATTCCTCGAAGGTCACACA | 1984 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
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| | TGTGTGACCTTCGAGGAATATTGAGTGCACCTTCAGGAGTGGT GCCCATTCGAATCACATGCCAATAGACTGATTTCTGTGGCAT CCAATCAGACCTGTAAAGTAGGAATAAGACACCTAT | 1985 |
| | GTCTATTGGCATGTGAT | 1986 |
| | ATCACATGCCAATAGAC | 1987 |
| Haemophilia A Trp255Term TGGc-TGA | ATAGGTGTCTTATTCCTACTTTACAGGTCTGATTGGATGCCAC AGGAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACT CCTGAAGTGCACCTCAATATTCCTCGAAGGTCACACA | 1988 |
| | TGTGTGACCTTCGAGGAATATTGAGTGCACCTTCAGGAGTGGT GCCCATTCGAATCACATGCCAATAGACTGATTTCTGTGGCAT CCAATCAGACCTGTAAAGTAGGAATAAGACACCTAT | 1989 |
| | GTCTATTGGCATGTGAT | 1990 |
| | ATCACATGCCAATAGAC | 1991 |
| Haemophilia A His256Leu CAT-CTT | AGGTGTCTTATTCCTACTTTACAGGTCTGATTGGATGCCACAG GAAATCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCC TGAAGTGCACCTCAATATTCCTCGAAGGTCACACATT | 1992 |
| | AATGTGTGACCTTCGAGGAATATTGAGTGCACCTTCAGGAGTG GTGCCCATTCCAATCACATGCCAATAGACTGATTTCTGTGGC ATCCAATCAGACCTGTAAAGTAGGAATAAGACACCT | 1993 |
| | CTATTGGCATGTGATTG | 1994 |
| | CAATCACATGCCAATAG | 1995 |
| Haemophilia A Gly259Arg tGGA-AGA | TATTCCTACTTTACAGGTCTGATTGGATGCCACAGGAAATCAG TCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAAGTGC ACTCAATATTCCTCGAAGGTCACACATTTCTTGTA | 1996 |
| | TCACAAGAAATGTGTGACCTTCGAGGAATATTGAGTGCACCTC AGGAGTGGTGCCCATTCGAATCACATGCCAATAGACTGATT CCTGTGGCATCCAATCAGACCTGTAAAGTAGGAATA | 1997 |
| | ATGTGATTGGAATGGGC | 1998 |
| | GCCCATTCGAATCACAT | 1999 |
| Haemophilia A Val266Gly GTG-GGG | TTGGATGCCACAGGAAATCAGTCTATTGGCATGTGATTGGAA TGGGCACCACTCCTGAAGTGCACCTCAATATTCCTCGAAGGTC ACACATTTCTTGAGGAACCATCGCCAGGCGTCCTT | 2000 |
| | AAGGACGCCTGGCGATGGTTCCTCACAAGAAATGTGTGACCT TCGAGGAATATTGAGTGCACTTCAGGAGTGGTGCCCATTCGA ATCACATGCCAATAGACTGATTTCTGTGGCATCCAA | 2001 |
| | TCCTGAAGTGCACCTCA | 2002 |
| | TTGAGTGCACTTCAGGA | 2003 |
| Haemophilia A Glu272Gly GAA-GGA | CAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAAG TGCACTCAATATTCCTCGAAGGTCACACATTTCTTGAGGAA CCATCGCCAGGCGTCCTTGGAATCTCGCCAATAAC | 2004 |
| | GTTATTGGCGAGATTTCCAAGGACGCCTGGCGATGGTTCCTC ACAAGAAATGTGTGACCTTCGAGGAATATTGAGTGCACCTCA GGAGTGGTGCCCATTCGAATCACATGCCAATAGACTG | 2005 |
| | ATTCCTCGAAGGTCACA | 2006 |

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| | TGTGACCTTCGAGGAAT | 2007 |
| Haemophilia A Glu272Lys cGAA-AAA | TCAGTCTATTGGCATGTGATTGGAATGGGCACCACTCCTGAA GTGCACTCAATATTCCTC <u>G</u> AAGGTCACACATTTCTTGTGAGGA ACCATCGCCAGGCGTCCTTGGAATCTCGCCAATAA | 2008 |
| | TTATTGGCGAGATTTCCAAGGACGCCTGGCGATGGTTCCTCA CAAGAAATGTGTGACCTTC <u>G</u> GAGGAATATTGAGTGCACCTTCAG GAGTGGTGCCCATTCGAATCACATGCCAATAGACTGA | 2009 |
| | TATTCCTC <u>G</u> AAGGTCAC | 2010 |
| | GTGACCTTC <u>G</u> GAGGAATA | 2011 |
| | | |
| Haemophilia A Thr275Ile ACA-ATA | GGCATGTGATTGGAATGGGCACCACTCCTGAAGTGCACCTCAA TATTCCTCGAAGGTCACA <u>C</u> ATTTCTTGTGAGGAACCATCGCCA GGCGTCCTTGGAATCTCGCCAATAACTTTCTTAC | 2012 |
| | GTAAGGAAAGTTATTGGCGAGATTTCCAAGGACGCCTGGCGA TGGTTCCTCACAAGAAAT <u>G</u> TGTGACCTTCGAGGAATATTGAGT GCACTTCAGGAGTGGTGCCCATTCGAATCACATGCC | 2013 |
| | AGGTCACAC <u>A</u> TTTCTTG | 2014 |
| | CAAGAAAT <u>G</u> TGTGACCT | 2015 |
| | | |
| Haemophilia A Val278Ala GTG-GCG | TTGGAATGGGCACCACTCCTGAAGTGCACCTCAATATTCCTCG AAGGTCACACATTTCTT <u>G</u> TGAGGAACCATCGCCAGGCGTCCT TGGAATCTCGCCAATAACTTTCTTACTGCTCAAAC | 2016 |
| | GTTTGAGCAGTAAGGAAAGTTATTGGCGAGATTTCCAAGGAC GCCTGGCGATGGTTCCTC <u>A</u> CAAGAAATGTGTGACCTTCGAGG AATATTGAGTGCACCTCAGGAGTGGTGCCCATTCGAA | 2017 |
| | ATTTCTTG <u>T</u> GAGGAACC | 2018 |
| | GGTTCCTC <u>A</u> CAAGAAAT | 2019 |
| | | |
| Haemophilia A Asn280Ile AAC-ATC | TGGGCACCACTCCTGAAGTGCACCTCAATATTCCTCGAAGGTC ACACATTTCTTGTGAGGA <u>A</u> CCATCGCCAGGCGTCCTTGGA TCTCGCCAATAACTTTCTTACTGCTCAAACACTCTT | 2020 |
| | AAGAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAGATTTCC AAGGACGCCTGGCGATGG <u>I</u> TCCTCACAAGAAATGTGTGACCT TCGAGGAATATTGAGTGCACCTCAGGAGTGGTGCCCA | 2021 |
| | TGTGAGGA <u>A</u> CCATCGCC | 2022 |
| | GGCGATGG <u>I</u> TCCTCACA | 2023 |
| | | |
| Haemophilia A Arg282Cys tCGC-TGC | ACCACTCCTGAAGTGCACCTCAATATTCCTCGAAGGTCACACAT TTCTTGTGAGGAACCAT <u>C</u> GCCAGGCGTCCTTGGAATCTCGC CAATAACTTTCTTACTGCTCAAACACTCTTGATGG | 2024 |
| | CCATCAAGAGTGTTTGAGCAGTAAGGAAAGTTATTGGCGAGA TTTCCAAGGACGCCTGGC <u>G</u> ATGGTTCCTCACAAGAAATGTGT GACCTTCGAGGAATATTGAGTGCACCTCAGGAGTGGT | 2025 |
| | GGAACCATC <u>G</u> CCAGGCG | 2026 |
| | CGCCTGGC <u>G</u> ATGGTTC | 2027 |
| | | |

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| Haemophilia A Arg282His CGC-CAC | CCACTCCTGAAGTGCACTCAATATTCCTCGAAGGTCACACATT TCTTGTGAGGAACCATC <u>G</u> CCAGGCGTCCTTGAAATCTCGCC AATAACTTTCTTACTGCTCAAACACTCTTGATGGA | 2028 |
| | TCCATCAAGAGTGTGGAGCAGTAAGGAAAGTTATTGGCGAG ATTTCCAAGGACGCCTGG <u>C</u> GATGGTTCCTCACAAGAAATGTG TGACCTTCGAGGAATATTGAGTGCACCTTCAGGAGTGG | 2029 |
| | GAACCATC <u>G</u> CCAGGCGT | 2030 |
| | ACGCCTGG <u>C</u> GATGGTTC | 2031 |
| Haemophilia A Arg282Leu CGC-CTC | CCACTCCTGAAGTGCACTCAATATTCCTCGAAGGTCACACATT TCTTGTGAGGAACCATC <u>G</u> CCAGGCGTCCTTGAAATCTCGCC AATAACTTTCTTACTGCTCAAACACTCTTGATGGA | 2032 |
| | TCCATCAAGAGTGTGGAGCAGTAAGGAAAGTTATTGGCGAG ATTTCCAAGGACGCCTGG <u>C</u> GATGGTTCCTCACAAGAAATGTG TGACCTTCGAGGAATATTGAGTGCACCTTCAGGAGTGG | 2033 |
| | GAACCATC <u>G</u> CCAGGCGT | 2034 |
| | ACGCCTGG <u>C</u> GATGGTTC | 2035 |
| Haemophilia A Ala284Glu GCG-GAG | CTGAAGTGCACTCAATATTCCTCGAAGGTCACACATTTCTTGT GAGGAACCATCGCCAGG <u>G</u> CGTCCTTGAAATCTCGCCAATAAC TTTCCTTACTGCTCAAACACTCTTGATGGACCTTG | 2036 |
| | CCAAGGTCCATCAAGAGTGTGGAGCAGTAAGGAAAGTTATT GGCGAGATTTCCAAGGAC <u>G</u> CCTGGCGATGGTTCCTCACAAG AAATGTGTGACCTTCGAGGAATATTGAGTGCACCTTCAG | 2037 |
| | TCGCCAGG <u>G</u> CGTCCTTG | 2038 |
| | CCAAGGAC <u>G</u> CCTGGCGA | 2039 |
| Haemophilia A Ala284Pro gGCG-CCG | CCTGAAGTGCACTCAATATTCCTCGAAGGTCACACATTTCTTG TGAGGAACCATCGCCAG <u>G</u> CGTCCTTGAAATCTCGCCAATAA CTTTCCTTACTGCTCAAACACTCTTGATGGACCTTG | 2040 |
| | CAAGGTCCATCAAGAGTGTGGAGCAGTAAGGAAAGTTATTG GCGAGATTTCCAAGGAC <u>G</u> CCTGGCGATGGTTCCTCACAAGAA ATGTGTGACCTTCGAGGAATATTGAGTGCACCTTCAGG | 2041 |
| | ATCGCCAG <u>G</u> CGTCCTTG | 2042 |
| | CAAGGAC <u>G</u> CCTGGCGAT | 2043 |
| Haemophilia A Ser289Leu TCG-TTG | TATTCCTCGAAGGTCACACATTTCTTGTGAGGAACCATCGCCA GGCGTCCTTGAAATCT <u>C</u> GCCAATAACTTTCTTACTGCTCAA ACACTCTTGATGGACCTTGACAGTTTCTACTGTT | 2044 |
| | AACAGTAGAACTGTCCAAGGTCCATCAAGAGTGTGGAGCA GTAAGGAAAGTTATTGGC <u>G</u> AGATTTCCAAGGACGCCTGGCGA TGGTTCCTCACAAGAAATGTGTGACCTTCGAGGAATA | 2045 |
| | GGAAATCTC <u>G</u> CCAATAA | 2046 |
| | TTATTGGC <u>G</u> AGATTTCC | 2047 |
| Haemophilia A Phe293Ser TTC-TCC | GTCACACATTTCTTGTGAGGAACCATCGCCAGGCGTCCTTG AAATCTCGCCAATAACTT <u>T</u> CCTTACTGCTCAAACACTCTTGAT GGACCTTGACAGTTTCTACTGTTTTGTCATATCTC | 2048 |

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| | GAGATATGACAAAACAGTAGAACTGTCCAAGGTCCATCAAG AGTGTTTGAGCAGTAAGGA <u>A</u> AGTTATTGGCGAGATTTCCTCAAG GACGCCTGGCGATGGTTCCTCACAAGAAATGTGTGAC | 2049 |
| | AATAACTTTCCTTACTG | 2050 |
| | CAGTAAGGA <u>A</u> AGTTATT | 2051 |
| Haemophilia A Thr295Ala tACT-GCT | ACATTTCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAATC TCGCCAATAACTTTCCTT <u>A</u> CTGCTCAAACACTCTTGATGGACC TTGGACAGTTTCTACTGTTTTGTCATATCTCTTCCC | 2052 |
| | GGGAAGAGATATGACAAAACAGTAGAACTGTCCAAGGTCCA TCAAGAGTGTGAGCAGT <u>A</u> AGGAAAGTTATTGGCGAGATT CCAAGGACGCCTGGCGATGGTTCCTCACAAGAAATGT | 2053 |
| | CTTTCCTT <u>A</u> CTGCTCAA | 2054 |
| | TTGAGCAGT <u>A</u> AGGAAAG | 2055 |
| Haemophilia A Thr295Ile ACT-ATT | CATTTCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAATCT CGCCAATAACTTTCCTT <u>A</u> CTGCTCAAACACTCTTGATGGACCT TGGACAGTTTCTACTGTTTTGTCATATCTCTTCCCA | 2056 |
| | TGGGAAGAGATATGACAAAACAGTAGAACTGTCCAAGGTCC ATCAAGAGTGTGAGCAGT <u>G</u> AAGGAAAGTTATTGGCGAGATT CCAAGGACGCCTGGCGATGGTTCCTCACAAGAAATG | 2057 |
| | TTTCCTT <u>A</u> CTGCTCAA | 2058 |
| | TTTGAGCAGT <u>G</u> AAGGAAA | 2059 |
| Haemophilia A Ala296Val GCT-GTT | TTCTTGTGAGGAACCATCGCCAGGCGTCCTTGGAATCTCGC CAATAACTTTCCTTACTG <u>C</u> TCAAACACTCTTGATGGACCTTG ACAGTTTCTACTGTTTTGTCATATCTCTTCCCACCA | 2060 |
| | TGGTGGGAAGAGATATGACAAAACAGTAGAACTGTCCAAGG TCCATCAAGAGTGTGAGCAGT <u>A</u> AGGAAAGTTATTGGCGAG ATTCCAAGGACGCCTGGCGATGGTTCCTCACAAGAA | 2061 |
| | CCTTACTG <u>C</u> TCAAACAC | 2062 |
| | GTGTTTGAGCAGT <u>A</u> AGG | 2063 |
| Haemophilia A Leu308Pro CTG-CCG | TCTCGCCAATAACTTTCCTTACTGCTCAAACACTCTTGATGGA CCTTGACAGTTTCTACTGTTTTGTCATATCTCTTCCCACCA CATGGTAATATCTTGATCTTTAAATGAATATTA | 2064 |
| | TAATATTCATTTTAAAGATCCAAGATATTACCATGTTGGTGGG AAGAGATATGACAAAAC <u>A</u> GTAGAACTGTCCAAGGTCCATCA AGAGTGTGAGCAGT <u>A</u> AGGAAAGTTATTGGCGAGA | 2065 |
| | GTTTCTACTGTTTTGTC | 2066 |
| | GACAAAAC <u>A</u> GTAGAAAC | 2067 |
| Haemophilia A Glu321Lys gGAA-AAA | ACAGCCTAATATAGCAAGACACTCTGACATTGTTGGTTTGTG TGACTCCAGATGGCATG <u>G</u> AAGCTTATGTCAAAGTAGACAGCT GTCCAGAGGAACCCCACTACGAATGAAAAATAATG | 2068 |
| | CATTATTTTTCATTTCGTAGTTGGGGTTTCTCTGGACAGCTGTC TACTTTGACATAAGCTT <u>C</u> CATGCCATCTGGAGTCAGACAAACC AAACAATGTCAGAGTGTCTTGCTATATTAGGCTGT | 2069 |
| | ATGGCATG <u>G</u> AAGCTTAT | 2070 |

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| | ATAAGCTT <u>C</u> CATGCCAT | 2071 |
| Haemophilia A Tyr323Term TATg-TAA | ATATAGCAAGACACTCTGACATTGTTTGGTTTGTCTGACTCCA GATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGTCCAGAG GAACCCCAACTACGAATGAAAAATAATGAAGAAGCG | 2072 |
| | CGCTTCTTCATTATTTTTTCATTTCGTAGTTGGGGTTCCTCTGGA CAGCTGTCTACTTTGACATAAGCTTCCATGCCATCTGGAGTCA GACAAACCAACAATGTCAGAGTGTCTTGCTATAT | 2073 |
| | GAAGCTTATGTCAAAGT | 2074 |
| | ACTTTGACATAAGCTTC | 2075 |
| | | |
| Haemophilia A Val326Leu aGTA-CTA | AAGACACTCTGACATTGTTTGGTTTGTCTGACTCCAGATGGCA TGGAAGCTTATGTCAAAGTAGACAGCTGTCCAGAGGAACCCC AACTACGAATGAAAAATAATGAAGAAGCGGAAGACT | 2076 |
| | AGTCTTCCGCTTCTTCATTATTTTTTCATTTCGTAGTTGGGGTTC TCTGGACAGCTGTCTACTTTGACATAAGCTTCCATGCCATCTG GAGTCAGACAAACCAACAATGTCAGAGTGTCTT | 2077 |
| | ATGTCAAAGTAGACAGC | 2078 |
| | GCTGTCTACTTTGACAT | 2079 |
| | | |
| Haemophilia A Cys329Arg cTGT-CGT | TGACATTGTTTGGTTTGTCTGACTCCAGATGGCATGGAAGCTT ATGTCAAAGTAGACAGCTGTCCAGAGGAACCCCAACTACGAA TGAAAAATAATGAAGAAGCGGAAGACTATGATGATG | 2080 |
| | CATCATCATAGTCTTCCGCTTCTTCATTATTTTTTCATTTCGTAGT TGGGGTTCCTCTGGACAGCTGTCTACTTTGACATAAGCTTCC ATGCCATCTGGAGTCAGACAAACCAACAATGTCA | 2081 |
| | TAGACAGCIGTCCAGAG | 2082 |
| | CTCTGGACAGCTGTCTA | 2083 |
| | | |
| Haemophilia A Cys329Tyr TGT-TAT | GACATTGTTTGGTTTGTCTGACTCCAGATGGCATGGAAGCTTA TGTCAAAGTAGACAGCTGTCCAGAGGAACCCCAACTACGAAT GAAAAATAATGAAGAAGCGGAAGACTATGATGATGA | 2084 |
| | TCATCATCATAGTCTTCCGCTTCTTCATTATTTTTTCATTTCGTAG TTGGGGTTCCTCTGGACAGCTGTCTACTTTGACATAAGCTTCC ATGCCATCTGGAGTCAGACAAACCAACAATGTC | 2085 |
| | AGACAGCTGTCCAGAGG | 2086 |
| | CCTCTGGACAGCTGTCT | 2087 |
| | | |
| Haemophilia A Arg336Term aCGA-TGA | ACTCCAGATGGCATGGAAGCTTATGTCAAAGTAGACAGCTGT CCAGAGGAACCCCAACTACGAATGAAAAATAATGAAGAAGCG GAAGACTATGATGATGATCTTACTGATTCTGAAATGG | 2088 |
| | CCATTTCAGAATCAGTAAGATCATCATCATAGTCTTCCGCTTC TTCATTATTTTTTCATTCTAGTTGGGGTTCCTCTGGACAGCTG TCTACTTTGACATAAGCTTCCATGCCATCTGGAGT | 2089 |
| | CCCAACTACGAATGAAA | 2090 |
| | TTTCATTCTAGTTGGG | 2091 |
| | | |
| Haemophilia A Arg372Cys tCGC-TGC | GATTCTGAAATGGATGTGGTCAGGTTTGTATGATGACAACTCTC CTTCCTTTATCCAAATTGCTCAGTTGCCAAGAAGCATCCTAA AACTTGGGTACATTACATTGCTGCTGAAGAGGAGG | 2092 |

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| | CCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGATG CTTCTTGGCAACTGAGC <u>G</u> AATTTGGATAAAGGAAGGAGAGTT GTCATCATCAAACCTGACCACATCCATTTCAGAATC | 2093 |
| | TCCAAATT <u>C</u> GCTCAGTT | 2094 |
| | AACTGAGC <u>G</u> AATTTGGA | 2095 |
| Haemophilia A Arg372His CGC-CAC | ATTCTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCC TTCCTTTATCCAAATTC <u>G</u> CTCAGTTGCCAAGAAGCATCCTAAA ACTTGGGTACATTACATTGCTGCTGAAGAGGAGGA | 2096 |
| | TCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGAT GCTTCTTGGCAACTGAGC <u>G</u> AATTTGGATAAAGGAAGGAGAGT TGTCATCATCAAACCTGACCACATCCATTTCAGAAT | 2097 |
| | CCAAATTC <u>G</u> CTCAGTTG | 2098 |
| | CAACTGAGC <u>G</u> AATTTGG | 2099 |
| Haemophilia A Ser373Leu TCA-TTA | CTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCCTTC CTTTATCCAAATTCGCT <u>C</u> AGTTGCCAAGAAGCATCCTAAAAC TGGGTACATTACATTGCTGCTGAAGAGGAGGACTG | 2100 |
| | CAGTCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAG GATGCTTCTTGGCAACT <u>G</u> AGCGAATTTGGATAAAGGAAGGAG AGTTGTCATCATCAAACCTGACCACATCCATTTCAG | 2101 |
| | AATTCGCT <u>C</u> AGTTGCCA | 2102 |
| | TGGCAACT <u>G</u> AGCGAATT | 2103 |
| Haemophilia A Ser373Pro cTCA-CCA | TCTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCCTT CCTTTATCCAAATTCGCT <u>C</u> AGTTGCCAAGAAGCATCCTAAAAC TTGGGTACATTACATTGCTGCTGAAGAGGAGGACT | 2104 |
| | AGTCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGG ATGCTTCTTGGCAACT <u>G</u> AGCGAATTTGGATAAAGGAAGGAGA GTTGTCATCATCAAACCTGACCACATCCATTTCAGA | 2105 |
| | AAATTCGCT <u>C</u> AGTTGCC | 2106 |
| | GGCAACT <u>G</u> AGCGAATT | 2107 |
| Haemophilia A Ser373Term TCA-TAA | CTGAAATGGATGTGGTCAGGTTTGATGATGACAACTCTCCTTC CTTTATCCAAATTCGCT <u>C</u> AGTTGCCAAGAAGCATCCTAAAAC TGGGTACATTACATTGCTGCTGAAGAGGAGGACTG | 2108 |
| | CAGTCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAG GATGCTTCTTGGCAACT <u>G</u> AGCGAATTTGGATAAAGGAAGGAG AGTTGTCATCATCAAACCTGACCACATCCATTTCAG | 2109 |
| | AATTCGCT <u>C</u> AGTTGCCA | 2110 |
| | TGGCAACT <u>G</u> AGCGAATT | 2111 |
| Haemophilia A Ile386Phe cATT-TTT | CCTTCCTTTATCCAAATTCGCTCAGTTGCCAAGAAGCATCCTA AACTTGGGTACATTAC <u>A</u> TTGCTGCTGAAGAGGAGGACTGGG ACTATGCTCCCTTAGTCCTCGCCCCCGATGACAGGT | 2112 |
| | ACCTGTCATCGGGGGCGAGGACTAAGGGAGCATAGTCCCAG TCCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGAT GCTTCTTGGCAACTGAGCGAATTTGGATAAAGGAAGG | 2113 |
| | TACATTAC <u>A</u> TTGCTGCT | 2114 |

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| | AGCAGCAATGTAATGTA | 2115 |
| Haemophilia A Ile386Ser ATT-AGT | CTTCCTTTATCCAAATTCGCTCAGTTGCCAAGAAGCATCCTAA AACTTGGGTACATTACATTGCTGCTGAAGAGGAGGACTGGGA CTATGCTCCCTTAGTCCTCGCCCCCGATGACAGGTA | 2116 |
| | TACCTGTCATCGGGGGCGAGGACTAAGGGAGCATAGTCCCA GTCTCCTCTTCAGCAGCAATGTAATGTACCCAAGTTTTAGGA TGCTTCTTGGCAACTGAGCGAATTTGGATAAAGGAAG | 2117 |
| | ACATTACATTGCTGCTG | 2118 |
| | CAGCAGCAATGTAATGT | 2119 |
| | | |
| Haemophilia A Glu390Gly GAG-GGG | AAATTCGCTCAGTTGCCAAGAAGCATCCTAAAACCTTGGGTACA TTACATTGCTGCTGAAGAGGAGGACTGGGACTATGCTCCCTT AGTCCTCGCCCCCGATGACAGGTAAGCACTTTTTGA | 2120 |
| | TCAAAAAGTGCTTACCTGTCATCGGGGGCGAGGACTAAGGGA GCATAGTCCAGTCCCTCTTCAGCAGCAATGTAATGTACC CAAGTTTTAGGATGCTTCTTGGCAACTGAGCGAATTT | 2121 |
| | TGCTGAAGAGGAGGACT | 2122 |
| | AGTCCTCTCTTCAGCA | 2123 |
| | | |
| Haemophilia A Trp393Gly cTGG-GGG | TCAGTTGCCAAGAAGCATCCTAAAACCTTGGGTACATTACATTG CTGCTGAAGAGGAGGACTGGGACTATGCTCCCTTAGTCCTCG CCCCCGATGACAGGTAAGCACTTTTTGACTATTGGT | 2124 |
| | ACCAATAGTCAAAAAGTGCTTACCTGTCATCGGGGGCGAGGA CTAAGGGAGCATAGTCCCAGTCCTCCTCTTCAGCAGCAATGT AATGTACCCAAGTTTTAGGATGCTTCTTGGCAACTGA | 2125 |
| | AGGAGGACTGGGACTAT | 2126 |
| | ATAGTCCCAGTCCTCCT | 2127 |
| | | |
| Haemophilia A Lys408Ile AAA-ATA | GCCTACCTAGAATTTTTCTTCCCAACCTCTCATCTTTTTTCTC TTATACAGAAGTTATAAAGTCAATATTTGAACAATGGCCCTC AGCGGATTGGTAGGAAGTACAAAAAAGTCCGATT | 2128 |
| | AATCGGACTTTTTTGTACTTCCTACCAATCCGCTGAGGGCCAT TGTTCAAATATTGACTTTATAAATTCTGTATAAGAGAAAAAAA GATGAGAGGTTGGGAAGAAAAATTCTAGGTAGGC | 2129 |
| | AAGTTATAAAGTCAAT | 2130 |
| | ATTGACTTTTATAAATT | 2131 |
| | | |
| Haemophilia A Leu412Phe TTGa-TTT | TTTTCTTCCCAACCTCTCATCTTTTTTCTCTTATACAGAAGTT ATAAAAGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTAG GAAGTACAAAAAAGTCCGATTTATGGCATAACACA | 2132 |
| | TGTGTATGCCATAAATCGGACTTTTTTGTACTTCCTACCAATC CGCTGAGGGCCATTGTTCAAATATTGACTTTTATAAATTCTGT ATAAGAGAAAAAAGATGAGAGGTTGGGAAGAAAA | 2133 |
| | CAATATTTGAACAATGG | 2134 |
| | CCATTGTTCAAATATTG | 2135 |
| | | |

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| Haemophilia A Arg418Trp gCGG-TGG | TCATCTTTTTTCTCTTATACAGAAGTTATAAAAGTCAATATTTG AACAATGGCCCTCAGCGGATTGGTAGGAAGTACAAAAAGTC CGATTTATGGCATAACAGATGAAACCTTTAAGA | 2136 |
| | TCTTAAAGGTTTCATCTGTGTATGCCATAAATCGGACTTTTTTG TACTTCCTACCAATCCGCTGAGGGCCATTGTTCAAATATTGAC TTTTATAACTTCTGTATAAGAGAAAAAAGATGA | 2137 |
| | GCCCTCAGCGGATTGGT | 2138 |
| | ACCAATCCGCTGAGGGC | 2139 |
| Haemophilia A Gly420Val GGT-GTT | TTTTCTCTTATACAGAAGTTATAAAAGTCAATATTTGAACAAT GGCCCTCAGCGGATTGGTAGGAAGTACAAAAAGTCCGATTT ATGGCATAACAGATGAAACCTTTAAGACTCGTGA | 2140 |
| | TCACGAGTCTTAAAGGTTTCATCTGTGTATGCCATAAATCGGA CTTTTTGTACTTCCTACCAATCCGCTGAGGGCCATTGTTCAA ATATTGACTTTTATAACTTCTGTATAAGAGAAAAA | 2141 |
| | GCGGATTGGTAGGAAGT | 2142 |
| | ACTTCCTACCAATCCGC | 2143 |
| Haemophilia A Lys425Arg AAA-AGA | GAAGTTATAAAAGTCAATATTTGAACAATGGCCCTCAGCGGAT TGGTAGGAAGTACAAAAAGTCCGATTTATGGCATAACAGAG TGAAACCTTTAAGACTCGTGAAGCTATTCAGCATGA | 2144 |
| | TCATGCTGAATAGCTTCACGAGTCTTAAAGGTTTCATCTGTGT ATGCCATAAATCGGACTTTTTGTACTTCCTACCAATCCGCTG AGGGCCATTGTTCAAATATTGACTTTTATAACTTC | 2145 |
| | GTACAAAAAGTCCGAT | 2146 |
| | ATCGGACTTTTTGTAC | 2147 |
| Haemophilia A Arg427Term cCGA-TGA | TATAAAAGTCAATATTTGAACAATGGCCCTCAGCGGATTGGTA GGAAGTACAAAAAGTCCGATTTATGGCATAACAGATGAAA CCTTTAAGACTCGTGAAGCTATTCAGCATGAATCAG | 2148 |
| | CTGATTCATGCTGAATAGCTTCACGAGTCTTAAAGGTTTCATC TGTGTATGCCATAAATCGGACTTTTTGTACTTCCTACCAATC CGCTGAGGGCCATTGTTCAAATATTGACTTTTATA | 2149 |
| | AAAAAGTCCGATTTATG | 2150 |
| | CATAAATCGGACTTTTT | 2151 |
| Haemophilia A Tyr431Asn aTAC-AAC | TATTTGAACAATGGCCCTCAGCGGATTGGTAGGAAGTACAAA AAAGTCCGATTTATGGCATACACAGATGAAACCTTTAAGACTC GTGAAGCTATTCAGCATGAATCAGGAATCTTGGGAC | 2152 |
| | GTCCCAAGATTCTGATTCATGCTGAATAGCTTCACGAGTCTT AAAGGTTTCATCTGTGTATGCCATAAATCGGACTTTTTGTAC TTCTACCAATCCGCTGAGGGCCATTGTTCAAATA | 2153 |
| | TTATGGCATACACAGAT | 2154 |
| | ATCTGTGTATGCCATAA | 2155 |
| Haemophilia A Thr435Ile ACC-ATC | GCCCTCAGCGGATTGGTAGGAAGTACAAAAAGTCCGATTTA TGGCATAACAGATGAAACCTTTAAGACTCGTGAAGCTATTCA GCATGAATCAGGAATCTTGGGACCTTTACTTTATGG | 2156 |

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| | CCATAAAGTAAAGGTCCCAAGATTCCTGATTCATGCTGAATAG CTTCACGAGTCTTAAAG <u>G</u> TTTCATCTGTGTATGCCATAAATCG GACTTTTTTGTACTTCCTACCAATCCGCTGAGGGC | 2157 |
| | AGATGAAACCTTTAAGA | 2158 |
| | TCTTAAAG <u>G</u> TTTCATCT | 2159 |
| | | |
| Haemophilia A Pro451Leu CCT-CTT | ACACAGATGAAACCTTTAAGACTCGTGAAGCTATTCAGCATGA ATCAGGAATCTTGGGAC <u>C</u> TTTACTTTATGGGGAAGTTGGAGA CACACTGTTGGTAAGTTGAAGAAAAGATTTAAGGTC | 2160 |
| | GACCTTAAATCTTTTCTTCAACTTACCAACAGTGTGTCTCCAA CTTCCCATAAAGTAAAG <u>G</u> TCCCAAGATTCCTGATTCATGCTG AATAGCTTCACGAGTCTTAAAGGTTTCATCTGTGT | 2161 |
| | CTTGGGAC <u>C</u> TTTACTTT | 2162 |
| | AAAGTAAAG <u>G</u> TCCCAAG | 2163 |
| | | |
| Haemophilia A Pro451Thr aCCT-ACT | TACACAGATGAAACCTTTAAGACTCGTGAAGCTATTCAGCATG AATCAGGAATCTTGGGAC <u>C</u> TTTACTTTATGGGGAAGTTGGAG ACACACTGTTGGTAAGTTGAAGAAAAGATTTAAGGT | 2164 |
| | ACCTTAAATCTTTTCTTCAACTTACCAACAGTGTGTCTCCAACT TCCCATAAAGTAAAG <u>G</u> TCCCAAGATTCCTGATTCATGCTGAA TAGCTTCACGAGTCTTAAAGGTTTCATCTGTGTA | 2165 |
| | TCTTGGGAC <u>C</u> TTTACTT | 2166 |
| | AAGTAAAG <u>G</u> TCCCAAGA | 2167 |
| | | |
| Haemophilia A Gly455Arg tGGG-AGG | ACCTTTAAGACTCGTGAAGCTATTCAGCATGAATCAGGAATCT TGGGACCTTTACTTTAT <u>G</u> GGGAAGTTGGAGACACACTGTTGG TAAGTTGAAGAAAAGATTTAAGGTCAGGTAAGAAGA | 2168 |
| | TCTTCTTACCTGACCTTAAATCTTTTCTTCAACTTACCAACAGT GTGTCTCCAACTTCCC <u>C</u> ATAAAGTAAAGGTCCCAAGATTCCTG ATTCATGCTGAATAGCTTCACGAGTCTTAAAGGT | 2169 |
| | TACTTTAT <u>G</u> GGGAAGTT | 2170 |
| | AACTTCCC <u>C</u> ATAAAGTA | 2171 |
| | | |
| Haemophilia A Gly455Glu GGG-GAG | CCTTTAAGACTCGTGAAGCTATTCAGCATGAATCAGGAATCTT GGGACCTTTACTTTAT <u>G</u> GGGAAGTTGGAGACACACTGTTGGT AAGTTGAAGAAAAGATTTAAGGTCAGGTAAGAAGAA | 2172 |
| | TTCTTCTTACCTGACCTTAAATCTTTTCTTCAACTTACCAACAG TGTGTCTCCAACTTCCC <u>C</u> ATAAAGTAAAGGTCCCAAGATTCCT GATTCATGCTGAATAGCTTCACGAGTCTTAAAGG | 2173 |
| | ACTTTAT <u>G</u> GGGAAGTTG | 2174 |
| | CAACTTCCC <u>C</u> ATAAAGT | 2175 |
| | | |
| Haemophilia A Asp459Asn aGAC-AAC | CGTGAAGCTATTCAGCATGAATCAGGAATCTTGGGACCTTTA CTTTATGGGGAAGTTGGAG <u>G</u> ACACACTGTTGGTAAGTTGAAGA AAAGATTTAAGGTCAGGTAAGAAGAAAAGTCTGGAG | 2176 |
| | CTCCAGACTTTTTCTTCTTACCTGACCTTAAATCTTTTCTTCAA CTTACCAACAGTGTGT <u>C</u> TCCAACTTCCCATAAAGTAAAGGTC CCAAGATTCCTGATTCATGCTGAATAGCTTCACG | 2177 |
| | AAGTTGGAG <u>G</u> ACACACTG | 2178 |
| | | |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | CAGTGTGTCTCCAACCTT | 2179 |
| Haemophilia A Phe465Cys TTT-TGT | TGTTGATCCTAGTCGTTTTAGGATTTGATCTTAGATCTCGCTTA TACTTTTCAGATTATATTTAAGAATCAAGCAAGCAGACCATATAA CATCTACCCTCACGGAATCACTGATGTCCGTCC | 2180 |
| | GGACGGACATCAGTGATTCCGTGAGGGTAGATGTTATATGGT CTGCTTGCTTGATTCTTAATATAATCTGAAAGTATAAGCGAG ATCTAAGATCAAATCCTAAAACGACTAGGATCAACA | 2181 |
| | GATTATATTTAAGAATC | 2182 |
| | GATTCTTAATATAATC | 2183 |
| | | |
| Haemophilia A Ala469Gly GCA-GGA | TCGTTTTAGGATTTGATCTTAGATCTCGCTTATACTTTTCAGATT ATATTTAAGAATCAAGCAAGCAGACCATATAACATCTACCCTC ACGGAATCACTGATGTCCGTCTTTGTATTCAAG | 2184 |
| | CTTGAATACAAAGGACGGACATCAGTGATTCCGTGAGGGTAG ATGTTATATGGTCTGCTTGCTTGATTCTTAAATATAATCTGAAA GTATAAGCGAGATCTAAGATCAAATCCTAAAACGA | 2185 |
| | GAATCAAGCAAGCAGAC | 2186 |
| | GTCTGCTTGCTTGATT | 2187 |
| | | |
| Haemophilia A Arg471Gly cAGA-GGA | TTAGGATTTGATCTTAGATCTCGCTTATACTTTTCAGATTATATT TAAGAATCAAGCAAGCAGACCATATAACATCTACCCTCACGG AATCACTGATGTCCGTCTTTGTATTCAAGGAGAT | 2188 |
| | ATCTCCTTGAATACAAAGGACGGACATCAGTGATTCCGTGAG GGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAAATATAATC TGAAAGTATAAGCGAGATCTAAGATCAAATCCTAA | 2189 |
| | AAGCAAGCAGACCATAT | 2190 |
| | ATATGGTCTGCTTGCTT | 2191 |
| | | |
| Haemophilia A Tyr473Cys TAT-TGT | TTGATCTTAGATCTCGCTTATACTTTTCAGATTATATTTAAGAAT CAAGCAAGCAGACCATATAACATCTACCCTCACGGAATCACT GATGTCCGTCTTTGTATTCAAGGAGATTACCAA | 2192 |
| | TTTGGTAATCTCCTTGAATACAAAGGACGGACATCAGTGATTCC CGTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAAA TATAATCTGAAAGTATAAGCGAGATCTAAGATCAA | 2193 |
| | CAGACCATATAACATCT | 2194 |
| | AGATGTTATATGGTCTG | 2195 |
| | | |
| Haemophilia A Tyr473His aTAT-CAT | TTTGATCTTAGATCTCGCTTATACTTTTCAGATTATATTTAAGAA TCAAGCAAGCAGACCATATAACATCTACCCTCACGGAATCACT GATGTCCGTCTTTGTATTCAAGGAGATTACCAA | 2196 |
| | TTGGTAATCTCCTTGAATACAAAGGACGGACATCAGTGATTCC GTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATTCTTAAAT ATAATCTGAAAGTATAAGCGAGATCTAAGATCAA | 2197 |
| | GCAGACCATATAACATC | 2198 |
| | GATGTTATATGGTCTGC | 2199 |
| | | |
| Haemophilia A Ile475Thr ATC-ACC | TTAGATCTCGCTTATACTTTTCAGATTATATTTAAGAATCAAGCA AGCAGACCATATAACATCTACCCTCACGGAATCACTGATGTCC GTCCTTTGTATTCAAGGAGATTACCAAAGGTAA | 2200 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | TTACCTTTTGGTAATCTCCTTGAATACAAAGGACGGACATCAG TGATTCCGTGAGGGTAGATGTTATATGGTCTGCTTGCTTGATT CTTAAATATAATCTGAAAGTATAAGCGAGATCTAA | 2201 |
| | ATATAACATCTACCCTC | 2202 |
| | GAGGGTAGATGTTATAT | 2203 |
| Haemophilia A Gly479Arg cGGA-AGA | TTATACTTTTCAGATTATATTTAAGAATCAAGCAAGCAGACCATA TAACATCTACCCTCACGGAATCACTGATGTCCGTCCCTTTGTAT TCAAGGAGATTACCAAAGGTAAATATTCCCTCG | 2204 |
| | CGAGGGAATATTTACCTTTTGGTAATCTCCTTGAATACAAAGG ACGGACATCAGTGATTCCGTGAGGGTAGATGTTATATGGTCT GCTTGCTTGATTCTTAAATATAATCTGAAAGTATAA | 2205 |
| | ACCCTCACGGAATCACT | 2206 |
| | AGTGATTCCGTGAGGGT | 2207 |
| Haemophilia A Thr522Ser aACT-TCT | CCAATTCTGCCAGGAGAAATATTCAAATATAAATGGACAGTGA CTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGA CCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAG | 2208 |
| | CTCTCTCCATATTAACGAACTAGAGTAATAGCGGGTCAGGC ACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCACTGT CCATTTATATTTGAATATTTCTCCTGGCAGAATTGG | 2209 |
| | ATGGGCCAACTAAATCA | 2210 |
| | TGATTTAGTTGGCCCAT | 2211 |
| Haemophilia A Asp525Asn aGAT-AAT | CCAGGAGAAATATTCAAATATAAATGGACAGTGACTGTAGAAG ATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATT ACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTT | 2212 |
| | AAGCTAGATCTCTCCATATTAACGAACTAGAGTAATAGCG GGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTAC AGTCACTGTCCATTTATATTTGAATATTTCTCCTGG | 2213 |
| | CTAAATCAGATCCTCGG | 2214 |
| | CCGAGGATCTGATTTAG | 2215 |
| Haemophilia A Arg527Trp tCGG-TGG | GAAATATTCAAATATAAATGGACAGTGACTGTAGAAGATGGGC CAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAG TTTCGTTAATATGGAGAGAGATCTAGCTTCAGGAC | 2216 |
| | GTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAGAGTA ATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATC TTCTACAGTCACTGTCCATTTATATTTGAATATTTT | 2217 |
| | CAGATCCTCGGTGCCTG | 2218 |
| | CAGGCACCGAGGATCTG | 2219 |
| Haemophilia A Arg531Cys cCGC-TGC | TATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCA GATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATA TGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC | 2220 |
| | GAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAA CGAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATT TAGTTGGCCCATCTTCTACAGTCACTGTCCATTTATA | 2221 |
| | GCCTGACCCGCTATTAC | 2222 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | GTAATAGC <u>G</u> GGTCAGGC | 2223 |
| Haemophilia A Arg531Gly cCGC-GGC | TATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC | 2224 |
| | GAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAACGAACTAGAGTAATAGC <u>G</u> GGTCAGGCACCGAGGATCTGATTAGTTGGCCCATCTTCTACAGTCACTGTCCATTATA | 2225 |
| | GCCTGACCCGCTATTAC | 2226 |
| | GTAATAGC <u>G</u> GGTCAGGC | 2227 |
| | | |
| Haemophilia A Arg531His CGC-CAC | ATAAATGGACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTC | 2228 |
| | AGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAACGAACTAGAGTAATAGC <u>G</u> GGTCAGGCACCGAGGATCTGATTAGTTGGCCCATCTTCTACAGTCACTGTCCATTAT | 2229 |
| | CCTGACCCGCTATTACT | 2230 |
| | AGTAATAGC <u>G</u> GGTCAGG | 2231 |
| | | |
| Haemophilia A Ser534Pro cTCT-CCT | ACAGTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCT | 2232 |
| | AGATGAGGAGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAACGAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCACTGT | 2233 |
| | GCTATTACTCTAGTTTC | 2234 |
| | GAACTAGAGTAATAGC | 2235 |
| | | |
| Haemophilia A Ser535Gly tAGT-GGT | GTGACTGTAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCTGCT | 2236 |
| | AGCAGATGAGGAGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAACGAACTAGAGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTGGCCCATCTTCTACAGTCAC | 2237 |
| | ATTACTCTAGTTTCGTT | 2238 |
| | AACGAACTAGAGTAAT | 2239 |
| | | |
| Haemophilia A Val537Asp GTT-GAT | TAGAAGATGGGCCAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCTGCTACAAAGA | 2240 |
| | TCTTTGTAGCAGATGAGGAGAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAACGAACTAGAGTAATAGCGGGTCAAGCACCAGAGGATCTGATTTAGTTGGCCCATCTTCTA | 2241 |
| | TAGTTTCGTTAATATGG | 2242 |
| | CCATATTAAACGAACTA | 2243 |
| | | |
| Haemophilia A Arg541Thr AGA-ACA | CAACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTTCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCATCTGCTACAAAGAATCTGTAGATCA | 2244 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | TGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCAATG AGTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAGAGT AATAGCGGGTCAGGCACCGAGGATCTGATTTAGTTG | 2245 |
| | TATGGAGAGAGATCTAG | 2246 |
| | CTAGATCTCTCTCCATA | 2247 |
| | | |
| Haemophilia A Asp542Gly GAT-GGT | CTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTTT CGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCC TCTCCTCATCTGCTACAAAGAATCTGTAGATCAAA | 2248 |
| | CTTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCA ATGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAG AGTAATAGCGGGTCAGGCACCGAGGATCTGATTTAG | 2249 |
| | GGAGAGAGATCTAGCTT | 2250 |
| | AAGCTAGATCTCTCTCC | 2251 |
| Haemophilia A Asp542His aGAT-CAT | ACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTT TCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCC CTCTCCTCATCTGCTACAAAGAATCTGTAGATCAAA | 2252 |
| | TTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCAA TGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAGA GTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGT | 2253 |
| | TGGAGAGAGATCTAGCT | 2254 |
| | AGCTAGATCTCTCTCCA | 2255 |
| Haemophilia A Asp542Tyr aGAT-TAT | ACTAAATCAGATCCTCGGTGCCTGACCCGCTATTACTCTAGTT TCGTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCC CTCTCCTCATCTGCTACAAAGAATCTGTAGATCAAA | 2256 |
| | TTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGCCAA TGAGTCCTGAAGCTAGATCTCTCTCCATATTAACGAACTAGA GTAATAGCGGGTCAGGCACCGAGGATCTGATTTAGT | 2257 |
| | TGGAGAGAGATCTAGCT | 2258 |
| | AGCTAGATCTCTCTCCA | 2259 |
| Haemophilia A Glu557Term aGAA-TAA | GTTAATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCT CTCCTCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACC AGGTGAGTTCTTGCCTTTCCAAGTGCTGGGTTTCAT | 2260 |
| | ATGAAACCCAGCACTTGAAAGGCAAGAACTCACCTGGTTTC CTCTTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAGGGC CAATGAGTCCTGAAGCTAGATCTCTCTCCATATTAAC | 2261 |
| | GCTACAAAGAATCTGTA | 2262 |
| | TACAGATTCTTTGTAGC | 2263 |
| Haemophilia A Ser558Phe TCT-TTT | ATATGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCC TCATCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACCAGG TGAGTTCTTGCCTTTCCAAGTGCTGGGTTTCATTCTC | 2264 |
| | GAGAATGAAACCCAGCACTTGAAAGGCAAGAACTCACCTGG TTTCCTCTTTGATCTACAGATTCTTTGTAGCAGATGAGGAGAG GGCCAATGAGTCCTGAAGCTAGATCTCTCTCCATAT | 2265 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---------------------------------------|---|------------|
| Haemophilia A Val559Ala GTA-GCA | CAAAGAATCTGTAGATC | 2266 |
| | GATCTACAGATTCTTTG | 2267 |
| | TGGAGAGAGATCTAGCTTCAGGACTCATTGGCCCTCTCCTCA TCTGCTACAAAGAATCTGTAGATCAAAGAGGAAACCAGGTGA GTTCTTGCCTTTCCAAGTGCTGGGTTTCATTCTCAGT | 2268 |
| | ACTGAGAATGAAACCCAGCACTTGGAAAGGCAAGAACTCACC TGGTTTCCTCTTTGATCTACAGATTCTTTGTAGCAGATGAGGA GAGGGCCAATGAGTCCTGAAGCTAGATCTCTCTCCA | 2269 |
| | AGAATCTGTAGATCAAA | 2270 |
| | TTTGATCTACAGATTCT | 2271 |

EXAMPLE 15

Hemophilia – Factor IX Deficiency

[0227] The attached table discloses the correcting oligonucleotide base sequences for the Factor IX oligonucleotides of the invention.

5

Table 17

Factor IX Mutations And Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--------------------------------------|---|------------|
| Haemophilia B Asn2Asp tAAT-GAT | ATTTAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAA TCGGCCAAAGAGGTATAATTAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAA | 2272 |
| | TTTCTTCCATACATTCTCTCAAGGTTCCCTTGAACAACTCT TCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTT GTTGGCGTTTTTCATGATCAAGAAAACTGAAAT | 2273 |
| | AGAGGTATAATTAGGT | 2274 |
| | ACCTGAATTATACCTCT | 2275 |
| | | |
| Haemophilia B Asn2Ile AAT-ATT | TTTCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAAT CGGCCAAAGAGGTATAATTAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAA | 2276 |
| | TTTTCTTCCATACATTCTCTCAAGGTTCCCTTGAACAACTC TTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCAGAATTT TGTTGGCGTTTTTCATGATCAAGAAAACTGAAA | 2277 |
| | GAGGTATAATTAGGT | 2278 |
| | TACCTGAATTATACCTC | 2279 |
| | | |
| Haemophilia B Asn2Tyr tAAT-TAT | ATTTAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAA TCGGCCAAAGAGGTATAATTAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAA | 2280 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--------------------------------------|--|------------|
| | TTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTCT TCCAATTTACCTGAATTATACCTCTTTGGCCGATTGAGAATTTT GTTGGCGTTTTTCATGATCAAGAAAACTGAAAT | 2281 |
| | AGAGGTAT <u>A</u> ATTGAGT | 2282 |
| | ACCTGAATTATACCTCT | 2283 |
| Haemophilia B Ser3Pro tTCA-CCA | TCAGTTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATC GGCCAAAGAGGTATAATT <u>C</u> AGGTAAATTGGAAGAGTTTGTTT AAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGT | 2284 |
| | ACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAAC TCTTCCAATTTACCTG <u>A</u> ATTATACCTCTTTGGCCGATTGAGAAT TTTGTTGGCGTTTTTCATGATCAAGAAAACTGA | 2285 |
| | GGTATAATT <u>C</u> AGGTAAA | 2286 |
| | TTTACCTG <u>A</u> ATTATACC | 2287 |
| Haemophilia B Gly4Asp GGT-GAT | TTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCC AAAGAGGTATAATTGAGTAAATTGGAAGAGTTTGTTCAAGG GAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAG | 2288 |
| | CTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAAC AACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCA GAATTTTGTTGGCGTTTTTCATGATCAAGAAAA | 2289 |
| | TAATTCAGGTAATTGG | 2290 |
| | CCAATTTACCTGAATTA | 2291 |
| Haemophilia B Gly4Ser aGGT-AGT | GTTTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCC CAAAGAGGTATAATTGAGTAAATTGGAAGAGTTTGTTCAAGG GAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAG | 2292 |
| | TACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACA AACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATTCA GAATTTTGTTGGCGTTTTTCATGATCAAGAAAAAC | 2293 |
| | ATAATTCAGGTAATTG | 2294 |
| | CAATTTACCTGAATTAT | 2295 |
| Haemophilia B LysSGlu tAAA-GAA | TTTCTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAA AGAGGTATAATTGAGGTAAATTGGAAGAGTTTGTTCAAGGGA ACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTT | 2296 |
| | AACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGA ACAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCGATT CAGAATTTTGTTGGCGTTTTTCATGATCAAGAAA | 2297 |
| | ATTCAGGTAAATTGGAA | 2298 |
| | TTCCAATTTACCTGAAT | 2299 |
| Haemophilia B Glu7Ala GAA-GCA | ATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGT ATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTGA GAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGA | 2300 |
| | TCTTCAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTT CCCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCTTTG GCCGATTGAGAATTTTGTTGGCGTTTTTCATGAT | 2301 |
| | TAAATTGGAAGAGTTTG | 2302 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--------------------------------------|---|------------|
| | CAA <u>A</u> CTCTTCCMTTTA | 2303 |
| Haemophilia B Glu7Lys gGAA-AAA | GATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGG TATAATTCAGGTAAATTGGAAGAGTTTGTTCAGGGAAACCTTG AGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAG | 2304 |
| | CTTCAAACTACACTTTTTCTTCCATACATTCTCTCTCAAGGTT CCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCTTTGG CCGATTCAGAATTTTGTGGCGTTTTCATGATC | 2305 |
| | GTAAATTGGAAGAGTTT | 2306 |
| | AACTCTTCCAATTTAC | 2307 |
| | | |
| Haemophilia B Glu7Val GAA-GTA | ATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGT ATAATTCAGGTAAATTGGAAGAGTTTGTTCAGGGAAACCTTGA GAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGA | 2308 |
| | TCTTCAAACTACACTTTTTCTTCCATACATTCTCTCTCAAGGTT CCCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCTTTG GCCGATTCAGAATTTTGTGGCGTTTTCATGAT | 2309 |
| | TAAATTGGAAGAGTTTG | 2310 |
| | CAA <u>A</u> CTCTTCCAATTTA | 2311 |
| | | |
| Haemophilia B Glu8Ala GAG-GCG | ATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATA ATTCAGGTAAATTGGAAGAGTTTGTTCAGGGAAACCTTGAGA GAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGC | 2312 |
| | GCTTCTTCAAACTACACTTTTTCTTCCATACATTCTCTCTCAAG GTTCCCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCT TTGGCCGATTCAGAATTTTGTGGCGTTTTCAT | 2313 |
| | ATTGGAAGAGTTTGTTC | 2314 |
| | GAACAACTCTTCCAAT | 2315 |
| | | |
| Haemophilia B Glu8Gly GAG-GGG | ATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATA ATTCAGGTAAATTGGAAGAGTTTGTTCAGGGAAACCTTGAGA GAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGC | 2316 |
| | GCTTCTTCAAACTACACTTTTTCTTCCATACATTCTCTCTCAAG GTTCCCTTGAACAACTCTTCCAATTTACCTGAATTATACCTCT TTGGCCGATTCAGAATTTTGTGGCGTTTTCAT | 2317 |
| | ATTGGAAGAGTTTGTTC | 2318 |
| | GAACAACTCTTCCAAT | 2319 |
| | | |
| Haemophilia B Phe9Cys TTT-TGT | AAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTC AGGTAAATTGGAAGAGTTTGTTCAGGGAAACCTTGAGAGAGA ATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACG | 2320 |
| | CGTGCTTCTTCAAACTACACTTTTTCTTCCATACATTCTCTCTC AAGGTTCCCTTGAACA <u>A</u> ACTCTTCCAATTTACCTGAATTATAC CTCTTTGGCCGATTCAGAATTTTGTGGCGTTTT | 2321 |
| | GGAAGAGTTTGTTCAG | 2322 |
| | CTTGAACA <u>A</u> ACTCTTCC | 2323 |
| | | |
| Haemophilia B Phe9Ile ATT-ATT | GAAAACGCCAACAAAATTCTGAATCGGCCAAAGAGGTATAAT TCAGGTAAATTGGAAGAGTTTGTTCAGGGAAACCTTGAGAGA GAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCAC | 2324 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| gTTT-ATT | GTGCTTCTTCAAACTACACTTTTCTTCCATACATTCTCTCTCA AGGTTCCCTTGAACAA <u>ACT</u> CTTCCAATTTACCTGAATTATACC TCTTTGGCCGATTCAGAATTTTGTGGCGTTTTT | 2325 |
| | TGGAAGAGTTTGTTC | 2326 |
| | TTGAACAA <u>ACT</u> CTTCCA | 2327 |
| Haemophilia B Arg(-1)Ser AGGt-AGC | TTACATTTTCAGTTTTCTTGATCATGAAAACGCCAACAAAATTC TGAATCGGCCAAAGAG <u>G</u> TATAATTCAGGTAAATTGGAAGAGT TTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAA | 2328 |
| | TTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTCTTCC AATTTACCTGAATTATAC <u>C</u> CTCTTTGGCCGATTCAGAATTTTGT GGCGTTTTCATGATCAAGAAAACTGAAATGTAA | 2329 |
| | CCAAAGAG <u>G</u> TATAATTC | 2330 |
| | GAATTATAC <u>C</u> CTTTGG | 2331 |
| Haemophilia B Arg(-1)Thr AGG-ACG | TTTACATTTTCAGTTTTCTTGATCATGAAAACGCCAACAAAATT CTGAATCGGCCAAAGAG <u>G</u> TATAATTCAGGTAAATTGGAAGAG TTTGTTCAGGGAACCTTGAGAGAGAATGTATGGA | 2332 |
| | TCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCA ATTTACCTGAATTATAC <u>C</u> CTTTGGCCGATTCAGAATTTTGTG GCGTTTTCATGATCAAGAAAACTGAAATGTAA | 2333 |
| | GCCAAAGAG <u>G</u> TATAATT | 2334 |
| | AATTATAC <u>C</u> CTTTGGC | 2335 |
| Haemophilia B Lys(-2)Asn AAGa-AAT | CTTTTACATTTTCAGTTTTCTTGATCATGAAAACGCCAACAAAA TTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATTGGAAG AGTTTGTTCAGGGAACCTTGAGAGAGAATGTATG | 2336 |
| | CATACATTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATT TACCTGAATTATACCT <u>C</u> TTTGGCCGATTCAGAATTTTGTGGC GTTTTCATGATCAAGAAAACTGAAATGTAAAAG | 2337 |
| | CGGCCAAAGAGGTATAA | 2338 |
| | TTATACCT <u>C</u> TTTGGCCG | 2339 |
| Haemophilia B Arg(-4)Gln CGG-CAG | AATTATTCTTTTACATTTTCAGTTTTCTTGATCATGAAAACGCC AACAAAATTCTGAATC <u>G</u> GCCAAAGAGGTATAATTCAGGTAAAT TGGAAGAGTTTGTTCAGGGAACCTTGAGAGAGA | 2340 |
| | TCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTG AATTATACCTCTTTGGC <u>C</u> GATTCAGAATTTTGTGGCGTTTTC ATGATCAAGAAAACTGAAATGTAAAAGAATAATT | 2341 |
| | TCTGAATC <u>G</u> GCCAAAGA | 2342 |
| | TCTTTGGC <u>C</u> GATTCAGA | 2343 |
| Haemophilia B Arg(-4)Leu CGG-CTG | AATTATTCTTTTACATTTTCAGTTTTCTTGATCATGAAAACGCC AACAAAATTCTGAATC <u>G</u> GCCAAAGAGGTATAATTCAGGTAAAT TGGAAGAGTTTGTTCAGGGAACCTTGAGAGAGA | 2344 |
| | TCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTG AATTATACCTCTTTGGC <u>C</u> GATTCAGAATTTTGTGGCGTTTTC ATGATCAAGAAAACTGAAATGTAAAAGAATAATT | 2345 |
| | TCTGAATC <u>G</u> GCCAAAGA | 2346 |
| | TCTTTGGC <u>C</u> GATTCAGA | 2347 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Haemophilia B Arg(-4)Trp tCGG-TGG | GAATTATTCTTTTACATTTTCAGTTTTCTTGATCATGAAAACGC CAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAA TTGGAAGAGTTTGTTCAGGGAACCTTGAGAGAG | 2348 |
| | CTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTGA ATTATACCTCTTTGGCCGATTGAGAATTTTGTGGCGTTTTTCAT GATCAAGAAAACTGAAATGTAAAAGAATAATTC | 2349 |
| | TTCTGAATCGGCCAAAG | 2350 |
| | CTTTGGCCGATTGAGAA | 2351 |
| Haemophilia B GinII Term tCAA-TAA | GCCAACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGT AAATTGGAAGAGTTTGTTCAGGGAACCTTGAGAGAGAATGT ATGGAAGAAAAGTGTAGTTTGAAGAAGCACGAGAAG | 2352 |
| | CTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATACATTCT CTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTGAAT TATACCTCTTTGGCCGATTGAGAATTTTGTGGC | 2353 |
| | AGTTTGTTCAGGGAAC | 2354 |
| | GTTCCCTTGAACAACT | 2355 |
| Haemophilia B Gly12Ala GGG-GCG | ACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATT GGAAGAGTTTGTTCAGGGAACCTTGAGAGAGAATGTATGGA AGAAAAGTGTAGTTTGAAGAAGCACGAGAAGTTT | 2356 |
| | AAAATTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATACA TTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCT GAATTATACCTCTTTGGCCGATTGAGAATTTTGT | 2357 |
| | TGTTCAAGGGAACCTTG | 2358 |
| | CAAGGTTCCCTTGAACA | 2359 |
| Haemophilia B Gly12Arg aGGG-AGG | AACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAAT TGGAAGAGTTTGTTCAGGGAACCTTGAGAGAGAATGTATGG AAGAAAAGTGTAGTTTGAAGAAGCACGAGAAGTTT | 2360 |
| | AACTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATACAT TCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCTG AATTATACCTCTTTGGCCGATTGAGAATTTTGT | 2361 |
| | TTGTTCAAGGGAACCTT | 2362 |
| | AAGGTTCCCTTGAACAA | 2363 |
| Haemophilia B Gly12Glu GGG-GAG | ACAAAATTCTGAATCGGCCAAAGAGGTATAATTCAGGTAAATT GGAAGAGTTTGTTCAGGGAACCTTGAGAGAGAATGTATGGA AGAAAAGTGTAGTTTGAAGAAGCACGAGAAGTTT | 2364 |
| | AAAATTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATACA TTCTCTCTCAAGGTTCCCTTGAACAACTCTTCCAATTTACCT GAATTATACCTCTTTGGCCGATTGAGAATTTTGT | 2365 |
| | TGTTCAAGGGAACCTTG | 2366 |
| | CAAGGTTCCCTTGAACA | 2367 |
| Haemophilia B Glu17Gln aGAA-CAA | CGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGT TTTGAAGAAGCACGAGAAGTTTTTGAACAACTGAAA | 2368 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
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| | TTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAACTACAC TTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTC TTCCAATTTACCTGAATTATACCTCTTTGGCCG | 2369 |
| | TTGAGAGAGAATGTATG | 2370 |
| | CATACATTCTCTCTCAA | 2371 |
| | | |
| Haemophilia B Glu17Lys aGAA-AAA | CGGCCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTT CAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGT TTTGAAGAAGCACGAGAAGTTTTTGAAAACACTGAAA | 2372 |
| | TTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAACTACAC TTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAACTC TTCCAATTTACCTGAATTATACCTCTTTGGCCG | 2373 |
| | TTGAGAGAGAATGTATG | 2374 |
| | CATACATTCTCTCTCAA | 2375 |
| Haemophilia B Cys18Arg aTGT-CGT | CCAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAG GGAACCTTGAGAGAGAAATGTATGGAAGAAAAGTGTAGTTTTG AAGAAGCACGAGAAGTTTTTGAAAACACTGAAAGAA | 2376 |
| | TTCTTTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAACTA CACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAAA CTCTTCCAATTTACCTGAATTATACCTCTTTGG | 2377 |
| | AGAGAGAATGTATGGAA | 2378 |
| | TTCCATACATTCTCTCT | 2379 |
| Haemophilia B Cys18Tyr TGT-TAT | CAAAGAGGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGG GAACCTTGAGAGAGAAATGTATGGAAGAAAAGTGTAGTTTTGA AGAAGCACGAGAAGTTTTTGAAAACACTGAAAGAAC | 2380 |
| | GTTCTTTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAACT ACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTTGAACAA ACTCTTCCAATTTACCTGAATTATACCTCTTTG | 2381 |
| | GAGAGAATGTATGGAA | 2382 |
| | CTTCCATACATTCTCTCT | 2383 |
| Haemophilia B Glu20Val GAA-GTA | GGTATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCT TGAGAGAGAAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGC ACGAGAAGTTTTTGAAAACACTGAAAGAACAGTGAG | 2384 |
| | CTCACTGTTCTTTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTT AAAACCTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCCTT GAACAACTCTTCCAATTTACCTGAATTATACC | 2385 |
| | ATGTATGGAAGAAAAGT | 2386 |
| | ACTTTTCTTCCATACAT | 2387 |
| Haemophilia B Glu21Lys aGAA-AAA | TATAATTCAGGTAAATTGGAAGAGTTTGTTCAAGGGAACCTTG AGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCAC GAGAAGTTTTTGAAAACACTGAAAGAACAGTGAGTA | 2388 |
| | TACTCACTGTTCTTTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCT TCAAACTACACTTTTCTTCCATACATTCTCTCTCAAGGTTCCC TTGAACAACTCTTCCAATTTACCTGAATTATA | 2389 |
| | GTATGGAAGAAAAGTGT | 2390 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---------------------------------------|---|------------|
| | ACACTTTT <u>C</u> TTCCATAC | 2391 |
| Haemophilia B Cys23Arg gTGT-CGT | TCAGGTAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGA GAATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAA GTTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCA | 2392 |
| | TGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAAACCTTCTCGT GCTTCTTCAAACTAC <u>A</u> CTTTTCTTCCATACATTCTCTCTCAAG GTTCCCTTGAACAAACTCTTCCAATTTACCTGA | 2393 |
| | AAGAAAAGTGTAGTTTT | 2394 |
| | AAAACCTAC <u>A</u> CTTTTCTT | 2395 |
| Haemophilia B Cys23Tyr TGT-TAT | CAGGTAAATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAG AATGTATGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAG TTTTTGAAAACACTGAAAGAACAGTGAGTATTTCCAC | 2396 |
| | GTGGAAATACTCACTGTTCTTTCAGTGTTTTCAAAAACCTTCTC GTGCTTCTTCAAACTAC <u>A</u> CTTTTCTTCCATACATTCTCTCTCA AGGTTCCCTTGAACAAACTCTTCCAATTTACCTG | 2397 |
| | AGAAAAGTGTAGTTTTG | 2398 |
| | CAAACTAC <u>A</u> CTTTTCTT | 2399 |
| Haemophilia B Phe25Ser TTT-TCT | AATTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAATGTA TGGAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTG AAAACACTGAAAGAACAGTGAGTATTTCCACATAATA | 2400 |
| | TATTATGTGGAATACTCACTGTTCTTTCAGTGTTTTCAAAAAC TTCTCGTGCTTCTTCA <u>A</u> AACTACACTTTTCTTCCATACATTCTC TCTCAAGGTTCCCTTGAACAAACTCTTCCAATT | 2401 |
| | GTGTAGTTTTGAAGAAG | 2402 |
| | CTTCTTCA <u>A</u> AACTACAC | 2403 |
| Haemophilia B Glu26Gln tGAA-CAA | TTGGAAGAGTTTGTTC AAGGGAACCTTGAGAGAGAATGTATG GAAGAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAA ACACTGAAAGAACAGTGAGTATTTCCACATAATACC | 2404 |
| | GGTATTATGTGGAATACTCACTGTTCTTTCAGTGTTTTCAAAA ACTTCTCGTGCTTCTTCA <u>A</u> AACTACACTTTTCTTCCATACATTCTC TCTCTCAAGGTTCCCTTGAACAAACTCTTCCAA | 2405 |
| | GTAGTTTTGAAGAAGCA | 2406 |
| | TGCTTCTTCA <u>A</u> AACTAC | 2407 |
| Haemophilia B Glu27Ala GAA-GCA | AAGAGTTTGTTC AAGGGAACCTTGAGAGAGAATGTATGGAAG AAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACAC TGAAAGAACAGTGAGTATTTCCACATAATACCCTTC | 2408 |
| | GAAGGGTATTATGTGGAATACTCACTGTTCTTTCAGTGTTTT CAAAAACCTTCTCGTGCTTCTTCA <u>A</u> AACTACACTTTTCTTCCATA CATTCTCTCTCAAGGTTCCCTTGAACAAACTCTT | 2409 |
| | TTTTGAAGAAGCACGAG | 2410 |
| | CTCGTGCTTCTTCAAAA | 2411 |
| Haemophilia B Glu27Asp GAAg-GAC | AGAGTTTGTTC AAGGGAACCTTGAGAGAGAATGTATGGAAGA AAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAAAACACT GAAAGAACAGTGAGTATTTCCACATAATACCCTTCA | 2412 |
| | TGAAGGGTATTATGTGGAATACTCACTGTTCTTTCAGTGTTT | 2413 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
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| | TCAAAACTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCAT ACATTCTCTCTCAAGGTTCCCTTGAACAACTCT | |
| | TTTGAAGAAGCACGAGA | 2414 |
| | TCTCGTGCTTCTTCAAA | 2415 |
| Haemophilia B Glu27Lys aGAA-AAA | GAAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAA GAAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAACA CTGAAAGAACAGTGAGTATTTCCACATAATACCCTT | 2416 |
| | AAGGGTATTATGTGGAAATACTCACTGTTCTTTCACTGTTTT AAAACTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATAC ATTCTCTCTCAAGGTTCCCTTGAACAACTCTT | 2417 |
| | GTTTTGAAGAAGCACGA | 2418 |
| | TCGTGCTTCTTCAAAAC | 2419 |
| Haemophilia B Glu27Val GAA-GTA | AAGAGTTTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAG AAAAGTGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAACAC TGAAAGAACAGTGAGTATTTCCACATAATACCCTTC | 2420 |
| | GAAGGGTATTATGTGGAAATACTCACTGTTCTTTCACTGTTTT CAAAACTTCTCGTGCTTCTTCAAACTACACTTTTCTTCCATA CATTCTCTCTCAAGGTTCCCTTGAACAACTCTT | 2421 |
| | TTTTGAAGAAGCACGAG | 2422 |
| | CTCGTGCTTCTTCAAAA | 2423 |
| Haemophilia B Arg29Gln CGA-CAA | TTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGT GTAGTTTTGAAGAAGCACGAGAAGTTTTTGAACAACTGAAAG AACAGTGAGTATTTCCACATAATACCCTTCAGATGC | 2424 |
| | GCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTTCT TGTTTTCAAAACTTCTCGTGCTTCTTCAAACTACACTTTTCT TCCATACATTCTCTCTCAAGGTTCCCTTGAACAA | 2425 |
| | AGAAGCACGAGAAGTTT | 2426 |
| | AACTTCTCGTGCTTCT | 2427 |
| Haemophilia B Arg29Pro CGA-CCA | TTGTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGT GTAGTTTTGAAGAAGCACGAGAAGTTTTTGAACAACTGAAAG AACAGTGAGTATTTCCACATAATACCCTTCAGATGC | 2428 |
| | GCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTTCT TGTTTTCAAAACTTCTCGTGCTTCTTCAAACTACACTTTTCT TCCATACATTCTCTCTCAAGGTTCCCTTGAACAA | 2429 |
| | AGAAGCACGAGAAGTTT | 2430 |
| | AACTTCTCGTGCTTCT | 2431 |
| Haemophilia B Arg29Term aCGA-TGA | TTTGTTCAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAG TGTAGTTTTGAAGAAGCACGAGAAGTTTTTGAACAACTGAAA GAACAGTGAGTATTTCCACATAATACCCTTCAGATG | 2432 |
| | CATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTTCT GTTTTCAAAACTTCTCGTGCTTCTTCAAACTACACTTTTCT CCATACATTCTCTCTCAAGGTTCCCTTGAACAA | 2433 |
| | AAGAAGCACGAGAAGTT | 2434 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
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| | AACTTCTC <u>G</u> TGCTTCTT | 2435 |
| Haemophilia B Glu30Lys aGAA-AAA | GTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGT AGTTTTGAAGAAGCACGAGAAAGTTTTTGAAAACACTGAAAGAA CAGTGAGTATTTCCACATAATACCCTTCAGATGCAG | 2436 |
| | CTGCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTC AGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAACTACACTTTT CTTCCATACATTCTCTCTCAAGGTTCCCTTGAAC | 2437 |
| | AAGCACGAGAAAGTTTTT | 2438 |
| | AAAAACTTCTCGTGCTT | 2439 |
| | | |
| Haemophilia B Glu30Term aGAA-TAA | GTTCAAGGGAACCTTGAGAGAGAATGTATGGAAGAAAAGTGT AGTTTTGAAGAAGCACGAGAAAGTTTTTGAAAACACTGAAAGAA CAGTGAGTATTTCCACATAATACCCTTCAGATGCAG | 2440 |
| | CTGCATCTGAAGGGTATTATGTGGAAATACTCACTGTTCTTTC AGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAACTACACTTTT CTTCCATACATTCTCTCTCAAGGTTCCCTTGAAC | 2441 |
| | AAGCACGAGAAAGTTTTT | 2442 |
| | AAAAACTTCTCGTGCTT | 2443 |
| | | |
| Haemophilia B Glu33Asp GAAa-GAC | CCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAAGA AGCACGAGAAGTTTTTGAAACACTGAAAGAACAGTGAGTAT TTCCACATAATACCCTTCAGATGCAGAGCATAGAATA | 2444 |
| | TATTCTATGCTCTGCATCTGAAGGGTATTATGTGGAAATACTC ACTGTTCTTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAA ACTACACTTTTCTTCCATACATTCTCTCTCAAGG | 2445 |
| | GTTTTTGAAACACTGA | 2446 |
| | TCAGTGTTTTCAAAAAC | 2447 |
| | | |
| Haemophilia B Glu33Term tGAA-TAA | AACCTTGAGAGAGAATGTATGGAAGAAAAGTGTAGTTTTGAA GAAGCACGAGAAGTTTTGAAAACACTGAAAGAACAGTGAGT ATTTCCACATAATACCCTTCAGATGCAGAGCATAGAA | 2448 |
| | TTCTATGCTCTGCATCTGAAGGGTATTATGTGGAAATACTCAC TGTTCTTTCAGTGTTTTCAAAAACCTTCTCGTGCTTCTTCAAAC TACACTTTTCTTCCATACATTCTCTCTCAAGGTT | 2449 |
| | AAGTTTTTGAAAACACT | 2450 |
| | AGTGTTTTCAAAAACCTT | 2451 |
| | | |
| Haemophilia B Trp42Term TGG-TAG | CAAAACACTTTAGATATTACCGTTAATTTGTCTTCTTTTATTCTT TATAGACTGAATTTTGAAGCAGTATGTTGGTAAGCAATTCAT TTTATCCTCTAGCTAATATATGAAACATATGAG | 2452 |
| | CTCATATGTTTCATATATTAGCTAGAGGATAAAATGAATTGCTT ACCAACATACTGCTTCCAAAATTCAAGTCTATAAAGAATAAAAG AAGACAAATTAACGGTAATATCTAAAGTGTTTTG | 2453 |
| | TGAATTTTGAAGCAGT | 2454 |
| | ACTGCTTCCAAAATTCA | 2455 |
| | | |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Haemophilia B Lys43Glu gAAG-GAG | AAACACTTTAGATATTACCGTTAATTTGTCTTCTTTTATTCTTTA TAGACTGAATTTTGGAGCAGTATGTTGGTAAGCAATTCATTT TATCCTCTAGCTAATATATGAAACATATGAGAA | 2456 |
| | TTCTCATATGTTTCATATATTAGCTAGAGGATAAAATGAATTGC TTACCAACATACTGCTTCCAAAATTCAGTCTATAAAGAATAAAA GAAGACAAATTAACGGTAATATCTAAAGTGTTT | 2457 |
| | AATTTTGGAGCAGTAT | 2458 |
| | ATACTGCTTCCAAAATT | 2459 |
| Haemophilia B Gln44Term gCAG-TAG | CACTTTAGATATTACCGTTAATTTGTCTTCTTTTATTCTTTATAG ACTGAATTTTGGAGCAGTATGTTGGTAAGCAATTCATTTTAT CCTCTAGCTAATATATGAAACATATGAGAATTA | 2460 |
| | TAATTCTCATATGTTTCATATATTAGCTAGAGGATAAAATGAAT TGCTTACCAACATACTGCTTCCAAAATTCAGTCTATAAAGAAT AAAAGAAGACAAATTAACGGTAATATCTAAAGTG | 2461 |
| | TTTGGAGCAGTATGTT | 2462 |
| | AACATACTGCTTCCAAA | 2463 |
| Haemophilia B Asp49Gly GAT-GGT | CCGGGCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAAC CTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTA AATGGCGGCAGTTGCAAGGATGACATTAATTCCTA | 2464 |
| | TAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATG GATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAGAA ATTGAATTGGCACGTAAACTGCTTAGAATGCCCGG | 2465 |
| | AGATGGAGATCAGTGTG | 2466 |
| | CACACTGATCTCCATCT | 2467 |
| Haemophilia B Gln50His CAGt-CAC | GCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTAT CTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATG GCGGCAGTTGCAAGGATGACATTAATTCCTATGAA | 2468 |
| | TTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAA CATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTA AGAAATTGAATTGGCACGTAAACTGCTTAGAATGC | 2469 |
| | GGAGATCAGTGTGAGTC | 2470 |
| | GACTCACACTGATCTCC | 2471 |
| Haemophilia B Gln50Pro CAG-CCG | GGCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTA TCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAAT GGCGGCAGTTGCAAGGATGACATTAATTCCTATGA | 2472 |
| | TCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAAC ATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAA GAAATTGAATTGGCACGTAAACTGCTTAGAATGCC | 2473 |
| | TGGAGATCAGTGTGAGT | 2474 |
| | ACTCACACTGATCTCCA | 2475 |
| Haemophilia B Gln50Term gCAG-TAG | GGGCATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCT ATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAA TGGCGGCAGTTGCAAGGATGACATTAATTCCTATG | 2476 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| tCAG-TAG | CATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACA TGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTTAAG AAATTGAATTGGCACGTAACTGCTTAGAATGCCC | 2477 |
| | ATGGAGATCAGTGTGAG | 2478 |
| | CTCACACTGATCTCCAT | 2479 |
| Haemophilia B Cys51Arg gTGT-CGT | CATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCT CAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGG CGGCAGTTGCAAGGATGACATTAATTCCTATGAAT | 2480 |
| | ATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAA ACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTT AAGAAATTGAATTGGCACGTAACTGCTTAGAATG | 2481 |
| | GAGATCAGTGTGAGTCC | 2482 |
| | GGACTCACACTGATCTC | 2483 |
| Haemophilia B Cys51Ser gTGT-AGT | CATTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCT CAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGG CGGCAGTTGCAAGGATGACATTAATTCCTATGAAT | 2484 |
| | ATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAA ACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGGTT AAGAAATTGAATTGGCACGTAACTGCTTAGAATG | 2485 |
| | GAGATCAGTGTGAGTCC | 2486 |
| | GGACTCACACTGATCTC | 2487 |
| Haemophilia B Cys51Trp TGTg-TGG | TTCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCA AAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCG GCAGTTGCAAGGATGACATTAATTCCTATGAATGT | 2488 |
| | ACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTT AAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAGG TTAAGAAATTGAATTGGCACGTAACTGCTTAGAA | 2489 |
| | GATCAGTGTGAGTCCAA | 2490 |
| | TTGGACTCACACTGATC | 2491 |
| Haemophilia B Glu52Term tGAG-TAG | TCTAAGCAGTTTACGTGCCAATTCAATTTCTTAACCTATCTCAA AGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGG CAGTTGCAAGGATGACATTAATTCCTATGAATGTT | 2492 |
| | AACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATT TAAACATGGATTGGACTCACACTGATCTCCATCTTTGAGATAG GTTAAGAAATTGAATTGGCACGTAACTGCTTAGA | 2493 |
| | ATCAGTGTGAGTCCAAT | 2494 |
| | ATTGGACTCACACTGAT | 2495 |
| Haemophilia B Pro55Ala tCCA-GCA | TTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAG ATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCA AGGATGACATTAATTCCTATGAATGTTGGTGTCCCT | 2496 |
| | AGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACT GCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCT TTGAGATAGGTTAAGAAATTGAATTGGCACGTAAA | 2497 |
| | AGTCCAATCCATGTTTA | 2498 |

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|---------------------------------------|--|------------|
| | TAAACATGGATTGGACT | 2499 |
| Haemophilia B Pro55Arg CCA-CGA | TTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGA TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAA GGATGACATTAATTCCTATGAATGTTGGTGTCCCTT | 2500 |
| | AAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAAC TGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATC TTTGAGATAGGTTAAGAAATTGAATTGGCACGTAA | 2501 |
| | GTCCAATCCATGTTTAA | 2502 |
| | TTAAACATGGATTGGAC | 2503 |
| | | |
| Haemophilia B Pro55Gln CCA-CAA | TTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGA TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAA GGATGACATTAATTCCTATGAATGTTGGTGTCCCTT | 2504 |
| | AAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAAC TGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATC TTTGAGATAGGTTAAGAAATTGAATTGGCACGTAA | 2505 |
| | GTCCAATCCATGTTTAA | 2506 |
| | TTAAACATGGATTGGAC | 2507 |
| | | |
| Haemophilia B Pro55Leu CCA-CTA | TTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGA TCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAA GGATGACATTAATTCCTATGAATGTTGGTGTCCCTT | 2508 |
| | AAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAAC TGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATC TTTGAGATAGGTTAAGAAATTGAATTGGCACGTAA | 2509 |
| | GTCCAATCCATGTTTAA | 2510 |
| | TTAAACATGGATTGGAC | 2511 |
| | | |
| Haemophilia B Pro55Ser tCCA-TCA | TTTACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAG ATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCA AGGATGACATTAATTCCTATGAATGTTGGTGTCCCTT | 2512 |
| | AGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACT GCCGCCATTTAAACATGGATTGGACTCACACTGATCTCCATCT TTGAGATAGGTTAAGAAATTGAATTGGCACGTAA | 2513 |
| | AGTCCAATCCATGTTTAA | 2514 |
| | TAAACATGGATTGGACT | 2515 |
| | | |
| Haemophilia B Cys56Arg aTGT-CGT | ACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATC AGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGG ATGACATTAATTCCTATGAATGTTGGTGTCCCTTTG | 2516 |
| | CAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCA ACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCC ATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGT | 2517 |
| | CCAATCCATGTTTAAAT | 2518 |
| | ATTTAAACATGGATTGG | 2519 |
| | | |
| Haemophilia B Cys56Ser aTGT-AGT | ACGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATC AGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGG ATGACATTAATTCCTATGAATGTTGGTGTCCCTTTG | 2520 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---------------------------------------|---|------------|
| | CAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGCA ACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCC ATCTTTGAGATAGGTTAAGAAATTGAATTGGCACGT | 2521 |
| | CCAATCCATGTTTAAAT | 2522 |
| | ATTTAAACATGGATTGG | 2523 |
| Haemophilia B Cys56Ser TGT-TCT | CGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCA GTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGA TGACATTAATTCCTATGAATGTTGGTGTCCCTTTGG | 2524 |
| | CAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGC AACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCC ATCTTTGAGATAGGTTAAGAAATTGAATTGGCACG | 2525 |
| | CAATCCATGTTTAAATG | 2526 |
| | CATTTAAACATGGATTG | 2527 |
| Haemophilia B Cys56Tyr TGT-TAT | CGTGCCAATTCAATTTCTTAACCTATCTCAAAGATGGAGATCA GTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGA TGACATTAATTCCTATGAATGTTGGTGTCCCTTTGG | 2528 |
| | CAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTTGC AACTGCCGCCATTTAAACATGGATTGGACTCACACTGATCTCC ATCTTTGAGATAGGTTAAGAAATTGAATTGGCACG | 2529 |
| | CAATCCATGTTTAAATG | 2530 |
| | CATTTAAACATGGATTG | 2531 |
| Haemophilia B Asn58Lys AATg-AAG | ATTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAG TCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTA ATTCCTATGAATGTTGGTGTCCCTTTGGATTTGAA | 2532 |
| | TTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCA TCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACACT GATCTCCATCTTTGAGATAGGTTAAGAAATTGAAT | 2533 |
| | TGTTTAAATGGCGGCAG | 2534 |
| | CTGCCGCCATTTAAACA | 2535 |
| Haemophilia B Gly59Asp GGC-GAC | TCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTC CAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAT TCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGG | 2536 |
| | CCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGT CATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACA CTGATCTCCATCTTTGAGATAGGTTAAGAAATTGA | 2537 |
| | TTTAAATGGCGGCAGTT | 2538 |
| | AACTGCCGCCATTTAAA | 2539 |
| Haemophilia B Gly59Val GGC-GTC | TCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTC CAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAT TCCTATGAATGTTGGTGTCCCTTTGGATTTGAAGG | 2540 |
| | CCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGT CATCCTTGCAACTGCCGCCATTTAAACATGGATTGGACTCACA CTGATCTCCATCTTTGAGATAGGTTAAGAAATTGA | 2541 |
| | TTTAAATGGCGGCAGTT | 2542 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---------------------------------------|---|------------|
| | AACTGCCGCCATTAAA | 2543 |
| Haemophilia B Gly59Ser tGGC-AGC | TTCAATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGT CCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTA ATTCCATGAATGTTGGTGTCCCTTTGGATTTGAAG | 2544 |
| | CTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTC ATCCTTGCAACTGCCGCCATTAAACATGGATTGGACTCACAC TGATCTCCATCTTTGAGATAGGTTAAGAAATTGAA | 2545 |
| | GTTTAAATGGCGGCAGT | 2546 |
| | ACTGCCGCCATTAAAC | 2547 |
| Haemophilia B Gly60Ser cGGC-AGC | AATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCA ATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTC CTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAA | 2548 |
| | TTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAAT GTCATCCTTGCAACTGCCGCCATTAAACATGGATTGGACTCA CACTGATCTCCATCTTTGAGATAGGTTAAGAAATT | 2549 |
| | TAAATGGCGGCAGTTGC | 2550 |
| | GCAACTGCCGCCATTAA | 2551 |
| Haemophilia B Gly60Cys cGGC-TGC | AATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCA ATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTC CTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAA | 2552 |
| | TTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAAT GTCATCCTTGCAACTGCCGCCATTAAACATGGATTGGACTCA CACTGATCTCCATCTTTGAGATAGGTTAAGAAATT | 2553 |
| | TAAATGGCGGCAGTTGC | 2554 |
| | GCAACTGCCGCCATTAA | 2555 |
| Haemophilia B Gly60Asp GGC-GAC | ATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAA TCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCC TATGAATGTTGGTGTCCCTTTGGATTTGAAGGAAA | 2556 |
| | TTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAAT TGTCATCCTTGCAACTGCCGCCATTAAACATGGATTGGACTC AACTGATCTCCATCTTTGAGATAGGTTAAGAAAT | 2557 |
| | AAATGGCGGCAGTTGCA | 2558 |
| | TGCAACTGCCGCCATT | 2559 |
| Haemophilia B Gly60Arg cGGC-CGC | AATTTCTTAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCA ATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTC CTATGAATGTTGGTGTCCCTTTGGATTTGAAGGAA | 2560 |
| | TTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAAT GTCATCCTTGCAACTGCCGCCATTAAACATGGATTGGACTCA CACTGATCTCCATCTTTGAGATAGGTTAAGAAATT | 2561 |
| | TAAATGGCGGCAGTTGC | 2562 |
| | GCAACTGCCGCCATTAA | 2563 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---------------------------------------|---|------------|
| Haemophilia B Cys62Tyr TGC-TAC | TAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATG TTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAA TGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTG | 2564 |
| | CAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGG AATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATT GGACTCACACTGATCTCCATCTTTGAGATAGGTTA | 2565 |
| | CGGCAGTTGCAAGGATG | 2566 |
| | CATCCTTGCAACTGCCG | 2567 |
| Haemophilia B Cys62Ser TGC-TCC | TAACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATG TTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAA TGTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTG | 2568 |
| | CAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGG AATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGATT GGACTCACACTGATCTCCATCTTTGAGATAGGTTA | 2569 |
| | CGGCAGTTGCAAGGATG | 2570 |
| | CATCCTTGCAACTGCCG | 2571 |
| Haemophilia B Cys62Term TGC-TGA | AACCTATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGT TTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAAT GTTGGTGTCCCTTTGGATTTGAAGGAAAGAACTGT | 2572 |
| | ACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAG GAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACATGGAT TGGACTCACACTGATCTCCATCTTTGAGATAGGTT | 2573 |
| | GGCAGTTGCAAGGATGA | 2574 |
| | TCATCCTTGCAACTGCC | 2575 |
| Haemophilia B Asp64Glu GATg-GAG | TCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAAT GGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGG TGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTA | 2576 |
| | TAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACAT TCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAAC ATGGATTGGACTCACACTGATCTCCATCTTTGAGA | 2577 |
| | TGCAAGGATGACATTAA | 2578 |
| | TTAATGTCATCCTTGCA | 2579 |
| Haemophilia B Asp64Gly GAT-GGT | ATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAA TGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTG GTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATT | 2580 |
| | AATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACAT CATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACA TGGATTGGACTCACACTGATCTCCATCTTTGAGAT | 2581 |
| | TTGCAAGGATGACATTAA | 2582 |
| | TAATGTCATCCTTGCAA | 2583 |
| Haemophilia B Asp64Asn gGAT-AAT | TATCTCAAAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAA ATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTT GGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAAT | 2584 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | ATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACATTC ATAGGAATTAATGTCATCCTTGCAACTGCCGCCATTTAAACAT GGATTGGACTCACACTGATCTCCATCTTTGAGATA | 2585 |
| | GTTGCAAGGATGACATT | 2586 |
| | AATGTCATCCTTGCAAC | 2587 |
| Haemophilia B Ile66Ser ATT-AGT | AAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCG GCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCC CTTTGGATTGAAGGAAAGAACTGTGAATTAGGTAA | 2588 |
| | TTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACC AACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATT TAAACATGGATTGGACTCACACTGATCTCCATCTT | 2589 |
| | GGATGACATTAATTCCT | 2590 |
| | AGGAATTAATGTCATCC | 2591 |
| Haemophilia B Ile66Thr ATT-ACT | AAGATGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCG GCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCC CTTTGGATTGAAGGAAAGAACTGTGAATTAGGTAA | 2592 |
| | TTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACC AACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGCCATT TAAACATGGATTGGACTCACACTGATCTCCATCTT | 2593 |
| | GGATGACATTAATTCCT | 2594 |
| | AGGAATTAATGTCATCC | 2595 |
| Haemophilia B Asn67Lys AATt-AAA | TGGAGATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAG TTGCAAGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTT GGATTGAAGGAAAGAACTGTGAATTAGGTAAGTAA | 2596 |
| | TTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGA CACCAACATTCATAGGAATTAATGTCATCCTTGCAACTGCCGC CATTTAAACATGGATTGGACTCACACTGATCTCCA | 2597 |
| | GACATTAATTCCTATGA | 2598 |
| Haemophilia B Tyr69Cys TAT-TGT | TCATAGGAATTAATGTC | 2599 |
| | ATCAGTGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCA AGGATGACATTAATTCCTATGAATGTTGGTGTCCCTTTGGATT TGAAGGAAAGAACTGTGAATTAGGTAAGTAACTATT | 2600 |
| | AATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAATCCAAA GGGACACCAACATTCATAGGAATTAATGTCATCCTTGCAACTG CCGCCATTTAAACATGGATTGGACTCACACTGAT | 2601 |
| | TAATTCCTATGAATGTT | 2602 |
| Haemophilia B Cys71Term TGTt-TGA | AACATTCATAGGAATTA | 2603 |
| | TGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGA CATTAAATTCCTATGAATGTTGGTGTCCCTTTGGATTGAAGGA AAGAACTGTGAATTAGGTAAGTAACTATTTTTTGA | 2604 |
| | TTCAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAA ATCCAAAGGGACACCAACATTCATAGGAATTAATGTCATCCTT GCAACTGCCGCCATTTAAACATGGATTGGACTCA | 2605 |
| | TATGAATGTTGGTGTCC | 2606 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
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| | GGACACCA <u>A</u> CATTCATA | 2607 |
| Haemophilia B Cys71Ser TGT-TCT | GTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG ACATTAATTCCTATGAAT <u>G</u> TTGGTGTCCCTTTGGATTGAAGG AAAGAACTGTGAATTAGGTAAGTAACTATTTTTTTGA | 2608 |
| | TCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAA TCCAAAGGGACACCA <u>A</u> CATTCATAGGAATTAATGTCATCCTTG CAACTGCCGCCATTTAAACATGGATTGGACTCAC | 2609 |
| | CTATGAAT <u>G</u> TTGGTGTG | 2610 |
| | GACACCA <u>A</u> CATTCATAG | 2611 |
| | | |
| Haemophilia B Cys71Tyr TGT-TAT | GTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATG ACATTAATTCCTATGAAT <u>G</u> TTGGTGTCCCTTTGGATTGAAGG AAAGAACTGTGAATTAGGTAAGTAACTATTTTTTTGA | 2612 |
| | TCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAA TCCAAAGGGACACCA <u>A</u> CATTCATAGGAATTAATGTCATCCTTG CAACTGCCGCCATTTAAACATGGATTGGACTCAC | 2613 |
| | CTATGAAT <u>G</u> TTGGTGTG | 2614 |
| | GACACCA <u>A</u> CATTCATAG | 2615 |
| | | |
| Haemophilia B Cys71Ser aTGT-AGT | TGTGAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGAT GACATTAATTCCTATGAAT <u>G</u> TTGGTGTCCCTTTGGATTGAAG GAAAGAACTGTGAATTAGGTAAGTAACTATTTTTTTG | 2616 |
| | CAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCAAAT CCAAAGGGACACCA <u>A</u> ATTCATAGGAATTAATGTCATCCTTGC AACTGCCGCCATTTAAACATGGATTGGACTCACA | 2617 |
| | CCTATGAAT <u>G</u> TTGGTGT | 2618 |
| | ACACCA <u>A</u> CATTCATAGG | 2619 |
| | | |
| Haemophilia B Trp72Arg tTGG-AGG | GAGTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGAC ATTAATTCCTATGAATG <u>T</u> GGTGTCCCTTTGGATTGAAGGAA AGAACTGTGAATTAGGTAAGTAACTATTTTTTTGAAT | 2620 |
| | ATTCAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTTCA AATCCAAAGGGACACCA <u>A</u> CATTCATAGGAATTAATGTCATCCT TGCAACTGCCGCCATTTAAACATGGATTGGACTC | 2621 |
| | ATGAATG <u>T</u> GGTGTCCC | 2622 |
| | GGGACACCA <u>A</u> CATTCAT | 2623 |
| | | |
| Haemophilia B Trp72Term TGGt-TGA | GTCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACAT TAATTCCTATGAATGTT <u>G</u> GTGTCCCTTTGGATTGAAGGAAAG AACTGTGAATTAGGTAAGTAACTATTTTTTTGAATAC | 2624 |
| | GTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCTT CAAATCCAAAGGGACAC <u>C</u> CAATTCATAGGAATTAATGTCATC CTTGCAACTGCCGCCATTTAAACATGGATTGGAC | 2625 |
| | GAATGTTG <u>G</u> GTGTCCCTT | 2626 |
| | AAGGGACAC <u>C</u> CAATTC | 2627 |
| | | |
| Haemophilia B Cys73Tyr TGT-TAT | CCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTA ATTCCTATGAATGTTGGT <u>G</u> TCCCTTTGGATTGAAGGAAAGAA CTGTGAATTAGGTAAGTAACTATTTTTTTGAATACTC | 2628 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | GAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCC TTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCA TCCTTGCAACTGCCGCCATTTAAACATGGATTGG | 2629 |
| | ATGTTGGTGTCCCTTTG | 2630 |
| | CAAAGGGACACCAACAT | 2631 |
| Haemophilia B Cys73Arg gTGT-CGT | TCCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTA ATTCCTATGAATGTTGGTGTCCCTTTGGATTGGAAGGAAAGAA CTGTGAATTAGGTAAGTAACTATTTTTTGAATACT | 2632 |
| | AGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCCT TCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCA CCTTGCAACTGCCGCCATTTAAACATGGATTGGA | 2633 |
| | AATGTTGGTGTCCCTTT | 2634 |
| | AAAGGGACACCAACATT | 2635 |
| Haemophilia B Cys73Phe TGT-TTT | CCAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTA ATTCCTATGAATGTTGGTGTCCCTTTGGATTGGAAGGAAAGAA CTGTGAATTAGGTAAGTAACTATTTTTTGAATACTC | 2636 |
| | GAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTCC TTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTCA TCCTTGCAACTGCCGCCATTTAAACATGGATTGG | 2637 |
| | ATGTTGGTGTCCCTTTG | 2638 |
| | CAAAGGGACACCAACAT | 2639 |
| Haemophilia B Cys73Term TGTc-TGA | CAATCCATGTTTAAATGGCGGCAGTTGCAAGGATGACATTAAT TCCTATGAATGTTGGTGTCCCTTTGGATTGGAAGGAAAGAACT GTGAATTAGGTAAGTAACTATTTTTTGAATACTCA | 2640 |
| | TGAGTATTCAAAAAATAGTTACTTACCTAATTCACAGTTCTTTC CTTCAAATCCAAAGGGACACCAACATTCATAGGAATTAATGTC ATCCTTGCAACTGCCGCCATTTAAACATGGATTG | 2641 |
| | TGTTGGTGTCCCTTTGG | 2642 |
| | CCAAAGGGACACCAACA | 2643 |
| Haemophilia B Gly76Val GGA-GTA | GTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGA ATGTTGGTGTCCCTTTGGATTGGAAGGAAAGAACTGTGAATTA GGTAAGTAACTATTTTTTGAATACTCATGGTTCAA | 2644 |
| | TTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTCACA GTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAA TTAATGTCATCCTTGCAACTGCCGCCATTTAAAC | 2645 |
| | TCCCTTTGGATTGGAAG | 2646 |
| | CTTCAAATCCAAAGGGA | 2647 |
| Haemophilia B Gly76Arg tGGA-AGA | TGTTTAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATG AATGTTGGTGTCCCTTTGGATTGGAAGGAAAGAACTGTGAATT AGGTAAGTAACTATTTTTTGAATACTCATGGTTCA | 2648 |
| | TGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTCACA GTTCTTTCCTTCAAATCCAAAGGGACACCAACATTCATAGGAA TTAATGTCATCCTTGCAACTGCCGCCATTTAAACA | 2649 |
| | GTCCCTTTGGATTGAA | 2650 |

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|---------------------------------------|--|------------|
| | TTCAAATCCAAAGGGAC | 2651 |
| Haemophilia B Phe77Cys TTT-TGT | TAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATG TTGGTGTCCCTTTGGATTGAAGGAAAGAACTGTGAATTAGGT AAGTAACTATTTTTGAATACTCATGGTTCAAAGT | 2652 |
| | ACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTC ACAGTTCTTTCCCTTCAATCCAAAGGGACACCAACATTCATAG GAATTAATGTCATCCTTGCAACTGCCGCCATTTA | 2653 |
| | CTTTGGATTGAAGGAA | 2654 |
| | TTCTTCAATCCAAAG | 2655 |
| Haemophilia B Phe77Ser TTT-TCT | TAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATG TTGGTGTCCCTTTGGATTGAAGGAAAGAACTGTGAATTAGGT AAGTAACTATTTTTGAATACTCATGGTTCAAAGT | 2656 |
| | ACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTC ACAGTTCTTTCCCTTCAATCCAAAGGGACACCAACATTCATAG GAATTAATGTCATCCTTGCAACTGCCGCCATTTA | 2657 |
| | CTTTGGATTGAAGGAA | 2658 |
| | TTCTTCAATCCAAAG | 2659 |
| Haemophilia B Phe77Tyr TTT-TAT | TAAATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATG TTGGTGTCCCTTTGGATTGAAGGAAAGAACTGTGAATTAGGT AAGTAACTATTTTTGAATACTCATGGTTCAAAGT | 2660 |
| | ACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAATTC ACAGTTCTTTCCCTTCAATCCAAAGGGACACCAACATTCATAG GAATTAATGTCATCCTTGCAACTGCCGCCATTTA | 2661 |
| | CTTTGGATTGAAGGAA | 2662 |
| | TTCTTCAATCCAAAG | 2663 |
| Haemophilia B Glu78Lys tGAA-AAA | AATGGCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTT GGTGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTA AGTAACTATTTTTGAATACTCATGGTTCAAAGTTT | 2664 |
| | AAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACCTAAT TCACAGTTCTTTCCCTTCAAATCCAAAGGGACACCAACATTCAT AGGAATTAATGTCATCCTTGCAACTGCCGCCATT | 2665 |
| | TTGGATTTGAAGGAAAG | 2666 |
| | CTTTCCTTCAAATCCAA | 2667 |
| Haemophilia B Gly79Val GGA-GTA | GCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGT GTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTA ACTATTTTTGAATACTCATGGTTCAAAGTTTCCCT | 2668 |
| | AGGGAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTAC CTAATTCACAGTTCTTTCCTTCAAATCCAAAGGGACACCAACA TTCATAGGAATTAATGTCATCCTTGCAACTGCCGC | 2669 |
| | ATTTGAAGGAAAGAACT | 2670 |
| | AGTTCTTTCCTTCAAAT | 2671 |
| Haemophilia B Gly79Arg GGA-AGA | GCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGG TGTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGT AACTATTTTTGAATACTCATGGTTCAAAGTTTCCC | 2672 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---------------------------------------|---|------------|
| aGGA-AGA | GGGAAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTACC TAATTCACAGTTCTTTCTTCAAATCCAAAGGGACACCAACAT TCATAGGAATTAATGTCATCCTTGCAACTGCCGCC | 2673 |
| | GATTTGAAGGAAAGAAC | 2674 |
| | GTTCTTTCTTCAAATC | 2675 |
| Haemophilia B Gly79Glu GGA-GAA | GCGGCAGTTGCAAGGATGACATTAATTCCTATGAATGTTGGT GTCCCTTTGGATTTGAAGGAAAGAACTGTGAATTAGGTAAGTA ACTATTTTTGAATACTCATGGTTCAAAGTTTCCCT | 2676 |
| | AGGGAAACTTTGAACCATGAGTATTCAAAAAATAGTTACTTAC CTAATTCACAGTTCTTTCTTCAAATCCAAAGGGACACCAACA TTCATAGGAATTAATGTCATCCTTGCAACTGCCGC | 2677 |
| | ATTTGAAGGAAAGAAC | 2678 |
| | AGTTCTTTCTTCAAAT | 2679 |
| Haemophilia B Cys88Ser TGT-TCT | TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTT CTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAGC AGTTTTGTAAAAATAGTGCTGATAACAAGGTGGT | 2680 |
| | ACCACCTTGTTATCAGCACTATTTTTACAAAAGTCTCGCATC TGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAAATA GACAGTAACAGCATCATTTAACATGCATTTCTAA | 2681 |
| | TGTAACATGTAACATTA | 2682 |
| | TAATGTTACATGTTACA | 2683 |
| Haemophilia B Cys88Phe TGT-TTT | TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTT CTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAGC AGTTTTGTAAAAATAGTGCTGATAACAAGGTGGT | 2684 |
| | ACCACCTTGTTATCAGCACTATTTTTACAAAAGTCTCGCATC TGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAAATA GACAGTAACAGCATCATTTAACATGCATTTCTAA | 2685 |
| | TGTAACATGTAACATTA | 2686 |
| | TAATGTTACATGTTACA | 2687 |
| Haemophilia B Cys88Arg aTGT-CGT | TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTT TCTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAG CAGTTTTGTAAAAATAGTGCTGATAACAAGGTGG | 2688 |
| | CCACCTTGTTATCAGCACTATTTTTACAAAAGTCTCGCATCT GCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAAATA GACAGTAACAGCATCATTTAACATGCATTTCTAAA | 2689 |
| | ATGTAACATGTAACATT | 2690 |
| | AATGTTACATGTTACAT | 2691 |
| Haemophilia B Cys88Tyr TGT-TAT | TTAGAAATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTT CTTTTAGATGTAACATGTAACATTAAGAATGGCAGATGCGAGC AGTTTTGTAAAAATAGTGCTGATAACAAGGTGGT | 2692 |
| | ACCACCTTGTTATCAGCACTATTTTTACAAAAGTCTCGCATC TGCCATTCTTAATGTTACATGTTACATCTAAAAGAAGCAAAAATA GACAGTAACAGCATCATTTAACATGCATTTCTAA | 2693 |
| | TGTAACATGTAACATTA | 2694 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---------------------------------------|--|------------|
| | TAATGTTACATGTTACA | 2695 |
| Haemophilia B Ile90Thr ATT-ACT | ATGCATGTTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTA GATGTAACATGTAACATTAAGAATGGCAGATGCGAGCAGTTTT GTAAAAATAGTGCTGATAACAAGGTGGTTTGCTC | 2696 |
| | GAGCAAACCACCTTGTTATCAGCACTATTTTACAAAACCTGCT CGCATCTGCCATTCTTAATGTTACATGTTACATCTAAAAGAAG CAAAATAGACAGTAACAGCATCATTTAACATGCAT | 2697 |
| | ATGTAACATTAAGAATG | 2698 |
| | CATTCTTAATGTTACAT | 2699 |
| Haemophilia B Asn92His gAAT-CAT | TGTTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGT AACATGTAACATTAAGAAATGGCAGATGCGAGCAGTTTTGTAAA AATAGTGCTGATAACAAGGTGGTTTGCTCCTGTA | 2700 |
| | TACAGGAGCAAACCACCTTGTTATCAGCACTATTTTACAAAA CTGCTCGCATCTGCCATTCTTAATGTTACATGTTACATCTAAA AGAAGCAAAATAGACAGTAACAGCATCATTTAACA | 2701 |
| | ACATTAAGAAATGGCAGA | 2702 |
| | TCTGCCATTCTTAATGT | 2703 |
| Haemophilia B Asn92Lys AATg-AAA | TTAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAA CATGTAACATTAAGAAATGGCAGATGCGAGCAGTTTTGTAAAAA TAGTGCTGATAACAAGGTGGTTTGCTCCTGTACT | 2704 |
| | AGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTACAA AACTGCTCGCATCTGCCATTCTTAATGTTACATGTTACATCTA AAAGAAGCAAAATAGACAGTAACAGCATCATTTAA | 2705 |
| | ATTAAGAATGGCAGATG | 2706 |
| | CATCTGCCATTCTTAAT | 2707 |
| Haemophilia B Gly93Asp GGC-GAC | AAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACA TGTAACATTAAGAAATGGCAGATGCGAGCAGTTTTGTAAAAATA GTGCTGATAACAAGGTGGTTTGCTCCTGTACTGA | 2708 |
| | TCAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTAC AAACTGCTCGCATCTGCCATTCTTAATGTTACATGTTACATC TAAAAGAAGCAAAATAGACAGTAACAGCATCATTT | 2709 |
| | TAAGAATGGCAGATGCG | 2710 |
| | CGCATCTGCCATTCTTA | 2711 |
| Haemophilia B Gly93Ser tGGC-AGC | TAAATGATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAAC ATGTAACATTAAGAAATGGCAGATGCGAGCAGTTTTGTAAAAAT AGTGCTGATAACAAGGTGGTTTGCTCCTGTACTG | 2712 |
| | CAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTTTACA AAACTGCTCGCATCTGCCATTCTTAATGTTACATGTTACATCT AAAAGAAGCAAAATAGACAGTAACAGCATCATTTA | 2713 |
| | TTAAGAATGGCAGATGC | 2714 |
| | GCATCTGCCATTCTTA | 2715 |
| Haemophilia B Arg94Ser AGAt-AGT | GATGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTA ACATTAAGAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTG CTGATAACAAGGTGGTTTGCTCCTGTACTGAGGGA | 2716 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | TCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTATTT TTACAAAACCTGCTCGCATCTGCCATTCTTAATGTTACATGTTA CATCTAAAAGAAGCAAAATAGACAGTAACAGCATC | 2717 |
| | AATGGCAGATGCGAGCA | 2718 |
| | TGCTCGCATCTGCCATT | 2719 |
| | | |
| Haemophilia B Cys95Tyr TGC-TAC | TGCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAAC ATTAAGAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCT GATAACAAGGTGGTTTGCTCCTGTACTGAGGGATA | 2720 |
| | TATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTAT TTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTTACATGTT ACATCTAAAAGAAGCAAAATAGACAGTAACAGCA | 2721 |
| | TGGCAGATGCGAGCAGT | 2722 |
| | ACTGCTCGCATCTGCCA | 2723 |
| Haemophilia B Cys95Trp TGCg-TGG | GCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACA TTAAGAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTG ATAACAAGGTGGTTTGCTCCTGTACTGAGGGATAT | 2724 |
| | ATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTA TTTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTTACATGT TACATCTAAAAGAAGCAAAATAGACAGTAACAGC | 2725 |
| | GGCAGATGCGAGCAGTT | 2726 |
| | AACTGCTCGCATCTGCC | 2727 |
| Haemophilia B Cys95Term TGCg-TGA | GCTGTTACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACA TTAAGAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTG ATAACAAGGTGGTTTGCTCCTGTACTGAGGGATAT | 2728 |
| | ATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAGCACTA TTTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTTACATGT TACATCTAAAAGAAGCAAAATAGACAGTAACAGC | 2729 |
| | GGCAGATGCGAGCAGTT | 2730 |
| | AACTGCTCGCATCTGCC | 2731 |
| Haemophilia B Gln97Pro CAG-CCG | TACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAG AATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAAC AAGGTGGTTTGCTCCTGTACTGAGGGATATCGACT | 2732 |
| | AGTCGATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCA GCACTATTTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTT ACATGTTACATCTAAAAGAAGCAAAATAGACAGTA | 2733 |
| | ATGCGAGCAGTTTTGTA | 2734 |
| | TACAAAACCTGCTCGCAT | 2735 |
| Haemophilia B Gln97Glu gCAG-GAG | TACTGTCTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAG GAATGGCAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAA CAAGGTGGTTTGCTCCTGTACTGAGGGATATCGAC | 2736 |
| | GTCGATATCCCTCAGTACAGGAGCAAACCACCTTGTTATCAG CACTATTTTTACAAAACCTGCTCGCATCTGCCATTCTTAATGTTA CATGTTACATCTAAAAGAAGCAAAATAGACAGTAA | 2737 |
| | GATGCGAGCAGTTTTGT | 2738 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | ACAAA <u>A</u> CTGCTCGCATC | 2739 |
| Haemophilia B Cys99Arg tTGT-CGT | TCTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAGAATGG CAGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGT GGTTTGCTCCTGTACTGAGGGATATCGACTTGCA | 2740 |
| | CTGCAAGTCGATATCCCTCAGTACAGGAGCAAACCACCTTGT TATCAGCACTATTTTTACAAA <u>A</u> CTGCTCGCATCTGCCATTCTTA ATGTTACATGTTACATCTAAAAGAAGCAAATAGA | 2741 |
| | AGCAGTTTTGTAAAAAT | 2742 |
| | ATTTTACAAA <u>A</u> CTGCT | 2743 |
| Haemophilia B Cys99Tyr TGT-TAT | CTATTTTGCTTCTTTTAGATGTAACATGTAACATTAAGAATGGC AGATGCGAGCAGTTTTGTAAAAATAGTGCTGATAACAAGGTG GTTTGCTCCTGTACTGAGGGATATCGACTTGCA | 2744 |
| | TCTGCAAGTCGATATCCCTCAGTACAGGAGCAAACCACCTTG TTATCAGCACTATTTTTACAAA <u>A</u> CTGCTCGCATCTGCCATTCTT AATGTTACATGTTACATCTAAAAGAAGCAAATAGA | 2745 |
| | GCAGTTTTGTAAAAATA | 2746 |
| | TATTTTACAAA <u>A</u> CTGC | 2747 |
| Warfarin sensitivity Ala(-10)Thr cGCC-ACC | TTTTTGCTAAA <u>A</u> CTAAAGAATTATTCTTTACATTTTCAGTTTTT CTTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGA GGTATAATTCAGGTAAATTGGAAGAGTTTGTT | 2748 |
| | GAACAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCCG ATTCAGAATTTTGTGGCGTTTTTCATGATCAAGAAAACTGAA ATGTAAAAGAATAATTCTTTAGTTTTAGCAAAAA | 2749 |
| | ATGAAAACGCCAACAAA | 2750 |
| | TTTGTTGGCGTTTTTCAT | 2751 |
| Warfarin sensitivity Ala(-10)Val GCC-GTC | TTTTTGCTAAA <u>A</u> CTAAAGAATTATTCTTTACATTTTCAGTTTTT TTGATCATGAAAACGCCAACAAAATTCTGAATCGGCCAAAGA GGTATAATTCAGGTAAATTGGAAGAGTTTGTTCA | 2752 |
| | TGAACAACTCTTCCAATTTACCTGAATTATACCTCTTTGGCC GATTCAGAATTTTGTGGCGTTTTTCATGATCAAGAAAACTGA AATGTAAAAGAATAATTCTTTAGTTTTAGCAAAAA | 2753 |
| | TGAAAACGCCAACAAA | 2754 |
| | TTTTGTTGGCGTTTTCA | 2755 |
| Haemophilia B Gly(-26)Val GGA-GTA | TGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCCTCA TCACCATCTGCCTTTTAGGATATCTACTCAGTGCTGAATGTAC AGGTTTGTTTCCTTTTTTAAATACATTGAGTATGC | 2756 |
| | GCATACTCAATGTATTTTAAAAAGGAAACAAACCTGTACATT CAGCACTGAGTAGATATCTAAAAGGCAGATGGTGATGAGGC CTGGTGATTCTGCCATGATCATGTTACGCGCTGCA | 2757 |
| | CCTTTTAGGATATCTAC | 2758 |
| | GATGATATCTAAAAGG | 2759 |
| Haemophilia B Leu(-27)Term TTΔ-TΔΔ | TTATGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCC TCATCACCATCTGCCTTTTAGGATATCTACTCAGTGCTGAATG TACAGGTTTGTTTCCTTTTTTAAATACATTGAGTA | 2760 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| TTA-TAA | TACTCAATGTATTTTAAAAAAGGAAACAAACCTGTACATTCAG CACTGAGTAGATATCCTAAAAGGCAGATGGTGATGAGGCCTG GTGATTCTGCCATGATCATGTTACGCGCTGCATAA | 2761 |
| | CTGCCTTTTAGGATATC | 2762 |
| | GATATCCTAAAAGGCAG | 2763 |
| Haemophilia B Ile(-30)Asn ATC-AAC | TAGCAAAGGTTATGCAGCGCGTGAACATGATCATGGCAGAAT CACCAGGCCTCATCACCATCTGCCTTTTAGGATATCTACTCAG TGCTGAATGTACAGGTTTGTTCCTTTTTTAAATA | 2764 |
| | TATTTTAAAAAAGGAAACAAACCTGTACATTCAGCACTGAGTA GATATCCTAAAAGGCAGATGGTGATGAGGCCTGGTGATTCTG CCATGATCATGTTACGCGCTGCATAACCTTTGCTA | 2765 |
| | CATCACCATCTGCCTTT | 2766 |
| | AAAGGCAGATGGTGATG | 2767 |
| Haemophilia B Ile(-40)Phe gATC-TTC | ACTAATCGACCTTACCACTTTCACAATCTGCTAGCAAAGGTTA TGCAGCGCGTGAACATGATCATGGCAGAATCACCAGGCCTCA TCACCATCTGCCTTTTAGGATATCTACTCAGTGCTG | 2768 |
| | CAGCACTGAGTAGATATCCTAAAAGGCAGATGGTGATGAGGC CTGGTGATTCTGCCATGATCATGTTACGCGCTGCATAACCTT TGCTAGCAGATTGTGAAAGTGGTAAGGTCGATTAGT | 2769 |
| | TGAACATGATCATGGCA | 2770 |
| | TGCCATGATCATGTTCA | 2771 |
| Haemophilia B Arg(-44)His CGC-CAC | ACTTTGGTACAACCTAATCGACCTTACCACTTTCACAATCTGCT AGCAAAGGTTATGCAGCGCGTGAACATGATCATGGCAGAATC ACCAGGCCTCATCACCATCTGCCTTTTAGGATATCT | 2772 |
| | AGATATCCTAAAAGGCAGATGGTGATGAGGCCTGGTGATTCT GCCATGATCATGTTACGCGCTGCATAACCTTTGCTAGCAGA TTGTGAAAGTGGTAAGGTCGATTAGTTGTACCAAAGT | 2773 |
| | TATGCAGCGCGTGAACA | 2774 |
| | TGTTACGCGCTGCATA | 2775 |

EXAMPLE 16

Alpha thalassemia - Hemoglobin alpha locus 1

[0228] The thalassemia syndromes are a heterogeneous group of inherited anemias characterized by defects in the synthesis of one or more globin chain subunits. For example, beta-thalassemia discussed in Example 6, is caused by a decrease in beta-chain production relative to alpha-chain production; the converse is the case for alpha-thalassemia. The attached table discloses the correcting oligonucleotide base sequences for the hemoglobin alpha locus 1 oligonucleotides of the invention.

Table 18

HBA1 Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Thalassaemia alpha Met(-1)Val cATG-GTG | CCCTGGCGCGCTCGCGGCCCGGCACTCTTCTGGTCCCCACA GACTCAGAGAGAACCCACC <u>A</u> TGGTGCTGTCTCCTGCCGACAA GACCAACGTCAAGGCCCGCTGGGGTAAGGTCGGCGCGC | 2776 |
| | GCGCGCCGACCTTACCCAGGGCGCCTTGACGTTGGTCTTG TCGGCAGGAGACAGCACC <u>A</u> TGGTGGGTTCTCTCTGAGTCTGT GGGGACCAGAAGAGTGCCGGGCCGCGAGCGCGCCAGGG | 2777 |
| | AACCCACC <u>A</u> TGGTGCTG | 2778 |
| | CAGCACC <u>A</u> TGGTGGGT | 2779 |
| Haemoglobin variant Ala12Asp GCC-GAC | CACAGACTCAGAGAGAACCCACCATGGTGCTGTCTCCTGCCG ACAAGACCAACGTCAAGG <u>C</u> CGCCTGGGGTAAGGTCGGCGCG CACGCTGGCGAGTATGGTGCGGAGGCCCTGGAGAGGTG | 2780 |
| | CACCTCTCCAGGGCCTCCGCACCATACTCGCCAGCGTGCGC GCCGACCTTACCCAGGGCG <u>G</u> CCTTGACGTTGGTCTTGTCGG CAGGAGACAGCACCATGGTGGGTTCTCTCTGAGTCTGTG | 2781 |
| | CGTCAAGG <u>C</u> CGCCTGGG | 2782 |
| | CCCAGGCG <u>G</u> CCTTGACG | 2783 |
| Haemoglobin variant Gly15Asp GGT-GAT | AGAGAGAACCCACCATGGTGCTGTCTCCTGCCGACAAGACCA ACGTCAAGGCCCGCCTGGG <u>G</u> TAAGGTCGGCGCGCACGCTGG CGAGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCTCCCT | 2784 |
| | AGGGAGCCTCACCTCTCCAGGGCCTCCGCACCATACTCGCC AGCGTGCGCGCCGACCTT <u>A</u> CCCCAGGCGGCCTTGACGTTGG TCTTGTCGGCAGGAGACAGCACCATGGTGGGTTCTCTCT | 2785 |
| | CGCCTGGG <u>G</u> TAAGGTCG | 2786 |
| | CGACCTT <u>A</u> CCCCAGGCG | 2787 |
| Haemoglobin variant Tyr24Cys TAT-TGT | CTGCCGACAAGACCAACGTCAAGGCCCGCCTGGGGTAAGGTC GGCGCGCACGCTGGCGAGT <u>A</u> TGGTGCGGAGGCCCTGGAGA GGTGAGGCTCCCTCCCCTGCTCCGACCCGGGCTCCTCGCC | 2788 |
| | GGCGAGGAGCCCGGGTCGGAGCAGGGGAGGGAGCCTCACC TCTCCAGGGCCTCCGCACC <u>A</u> CTCGCCAGCGTGCGCGCCG ACCTTACCCAGGCGGCCTTGACGTTGGTCTTGTCGGCAG | 2789 |
| | TGGCGAGT <u>A</u> TGGTGCGG | 2790 |
| | CCGCACC <u>A</u> CTCGCCA | 2791 |
| Haemoglobin variant Glu27Asp GAGg-GAT | GACCAACGTCAAGGCCCGCCTGGGGTAAGGTCGGCGCGCAC GCTGGCGAGTATGGTGCGGAG <u>G</u> CCCTGGAGAGGTGAGGCT CCCTCCCCTGCTCCGACCCGGGCTCCTCGCCCCGCCGGACC | 2792 |
| | GGTCCGGGCGGGCGAGGAGCCCGGGTCGGAGCAGGGGAG GGAGCCTCACCTCTCCAGGGC <u>C</u> TCCGCACCATACTCGCCAG CGTGCGCGCCGACCTTACCCAGGCGGCCTTGACGTTGGTC | 2793 |
| | GGTGCGGAG <u>G</u> CCCTGGA | 2794 |
| | TCCAGGGC <u>C</u> TCCGCACC | 2795 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| Haemoglobin variant Asn68Lys AACg-AAG | GAGCCACGGCTCTGCCCAGGTTAAGGGCCACGGCAAGAAGG TGGCCGACGCGCTGACCAACGCCGTGGCGCACGTGGACGA CATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG | 2796 |
| | CGCGTGACAGGTGCTCAGGGCGGACAGCGCGTTGGGCATGT CGTCCACGTGCGCCACGGCGTTGGTCAGCGCGTCGGCCACC TTCTTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTC | 2797 |
| | CTGACCAACGCCGTGGC | 2798 |
| | GCCACGGCGTTGGTCAG | 2799 |
| Haemoglobin variant Asp74Gly GAC-GGC | AGGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTGACC AACGCCGTGGCGCACGTGGACGACATGCCCAACGCGCTGTC CGCCCTGAGCGACCTGCACGCGCACAAGCTTCGGGTGGA | 2800 |
| | TCCACCCGAAGCTTGTGCGCGTGCAGGTCGCTCAGGGCGGA CAGCGCGTTGGGCATGTCGTCACGTGCGCCACGGCGTTGG TCAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACCT | 2801 |
| | GCACGTGGACGACATGC | 2802 |
| | GCATGTCGTCCACGTGC | 2803 |
| Haemoglobin variant Asp74His gGAC-CAC | CAGGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTGAC CAACGCCGTGGCGCACGTGGACGACATGCCCAACGCGCTGT CCGCCCTGAGCGACCTGCACGCGCACAAGCTTCGGGTGG | 2804 |
| | CCACCCGAAGCTTGTGCGCGTGCAGGTCGCTCAGGGCGGAC AGCGCGTTGGGCATGTCGTCCACGTGCGCCACGGCGTTGGT CAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACCTG | 2805 |
| | CGCACGTGGACGACATG | 2806 |
| | CATGTCGTCCACGTGCG | 2807 |
| Haemoglobin variant Asn78His cAAC-CAC | CACGGCAAGAAGGTGGCCGACGCGCTGACCAACGCCGTGG CGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGAGC GACCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAACT | 2808 |
| | AGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTCG CTCAGGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGC CACGGCGTTGGTCAGCGCGTCGGCCACCTTCTTGCCGTG | 2809 |
| | ACATGCCCACGCGCTG | 2810 |
| | CAGCGCGTTGGGCATGT | 2811 |
| Haemoglobin variant His87Tyr gCAC-TAC | ACCAACGCCGTGGCGCACGTGGACGACATGCCCAACGCGCT GTCCGCCCTGAGCGACCTGCACGCGCACAAGCTTCGGGTGG ACCCGGTCAACTTCAAGGTGAGCGGCGGGCCGGGAGCGA | 2812 |
| | TCGCTCCCGGCCCGCCGCTCACCTTGAAGTTGACCGGGTCC ACCCGAAGCTTGTGCGCGTGCAGGTCGCTCAGGGCGGACAG CGCGTTGGGCATGTCGTCCACGTGCGCCACGGCGTTGGT | 2813 |
| | GCGACCTGCACGCGCAC | 2814 |
| | GTGCGCGTGCAGGTCGC | 2815 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| Haemoglobin variant Lys90Asn AAGc-AAC | GGCGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGA GCGACCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAAC TTCAAGGTGAGCGGCGGGCCGGGAGCGATCTGGGTCGAG | 2816 |
| | CTCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTTGAAGT TGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTGCTC AGGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGCC | 2817 |
| | GCGCACAAGCTTCGGGT | 2818 |
| | ACCCGAAGCTTGTGCGC | 2819 |
| Haemoglobin variant Lys90Thr AAG-ACG | TGGCGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTG AGCGACCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAA CTTCAAGGTGAGCGGCGGGCCGGGAGCGATCTGGGTCGA | 2820 |
| | TCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTTGAAGTT GACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTGCTCA GGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGCCA | 2821 |
| | CGCGCACAAGCTTCGGG | 2822 |
| | CCCGAAGCTTGTGCGCG | 2823 |
| Haemoglobin variant Arg92Gln CGG-CAG | ACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGAGCGAC CTGCACGCGCACAAGCTTCCGGGTGGACCCGGTCAACTTCAA GGTGAGCGGCGGGCCGGGAGCGATCTGGGTGAGGGGCG | 2824 |
| | CGCCCCTCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTT GAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGT CGCTCAGGGCGGACAGCGCGTTGGGCATGTCGTCCACGT | 2825 |
| | CAAGCTTCCGGGTGGACC | 2826 |
| | GGTCCACCCGAAGCTTG | 2827 |
| Haemoglobin variant Asp94Gly GAC-GGC | ACGACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCAC GCGCACAAGCTTCGGGTGGACCCGGTCAACTTCAAGGTGAG CGGCGGGCCGGGAGCGATCTGGGTGAGGGGCGAGATGG | 2828 |
| | CCATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCCGCT CACCTTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGT GCAGGTGCTCAGGGCGGACAGCGCGTTGGGCATGTCGT | 2829 |
| | TCGGGTGGACCCGGTCA | 2830 |
| | TGACCGGGTCCACCCGA | 2831 |
| Haemoglobin variant Pro95Arg CCG-CGG | ACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG CACAAGCTTCGGGTGGACCCGGTCAACTTCAAGGTGAGCGG CGGGCCGGGAGCGATCTGGGTGAGGGGCGAGATGGCGC | 2832 |
| | GCGCCATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCC GCTCACCTTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCG CGTGCAGGTGCTCAGGGCGGACAGCGCGTTGGGCATGT | 2833 |
| | GGTGGACCCGGTCAACT | 2834 |
| | AGTTGACCGGGTCCACC | 2835 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Haemoglobin variant Ser102Arg AGCc-AGA | CGGCGGCTGCGGGCCTGGGCCCTCGGCCCACTGACCCTC TTCTCTGCACAGCTCCTAAGCCACTGCCTGCTGGTGACCCTG GCCGCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCAC | 2836 |
| | GTGCACCGCAGGGGTGAACTCGGCGGGGAGGTGGGCGGGCC AGGGTCACCAGCAGGCAGTGCTTAGGAGCTGTGCAGAGAA GAGGGTCAGTGGGGCCGAGGGCCCAGGCCCGCAGCCGCCG | 2837 |
| | CTCCTAAGCCACTGCCT | 2838 |
| | AGGCAGTGCTTAGGAG | 2839 |
| Haemoglobin variant Glu116Lys cGAG-AAG | TTCTCTGCACAGCTCCTAAGCCACTGCCTGCTGGTGACCCTG GCCGCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCACGC CTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGC | 2840 |
| | GCACGGTGCTCACAGAAGCCAGGAAGTTGTCCAGGGAGGCG TGACCCGCAGGGGTGAACTCGGCGGGGAGGTGGGCGGGCA GGGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCAGAGAA | 2841 |
| | TCCCCGCCGAGTTCACC | 2842 |
| | GGTGAAGTCGGCGGGGA | 2843 |
| Haemoglobin variant Ala120Glu GCG-GAG | TCCTAAGCCACTGCCTGCTGGTGACCCTGGCCGCCACCTC CCCGCCGAGTTCACCCCTGCGGTGCACGCCTCCCTGGACAA GTTCTTGGCTTCTGTGAGCACCGTGTGACCTCCAATA | 2844 |
| | TATTTGGAGGTCAGCACGGTGCTCACAGAAGCCAGGAAGTTG TCCAGGGAGGCGTGACCGCAGGGGTGAACTCGGCGGGGA GGTGGGCGGCCAGGGTCACCAGCAGGCAGTGGCTTAGGA | 2845 |
| | CACCCCTGCGGTGCACG | 2846 |
| | CGTGCACCGCAGGGGTG | 2847 |
| Thalassaemia alpha Leu129Pro CTG-CCG | TGGCCGCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCAC GCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGTG ACCTCAAATACCGTTAAGCTGGAGCCTCGGTGGCCAT | 2848 |
| | ATGGCCACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGC ACGGTGCTCACAGAAGCCAGGAAGTTGTCCAGGGAGGCGTG CACCGCAGGGGTGAACTCGGCGGGGAGGTGGGCGGGCA | 2849 |
| | CAAGTTCCTGGCTTCTG | 2850 |
| | CAGAAGCCAGGAAGTTG | 2851 |
| Haemoglobin variant Arg141Leu CGT-CTT | TGCACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCG TGCTGACCTCAAATACCGTTAAGCTGGAGCCTCGGTGGCCA TGCTTCTTGCCCTTGGGCCTCCCCCAGCCCTCCT | 2852 |
| | AGGAGGGGCTGGGGGGAGGCCCAAGGGGCAAGAAGCATGG CCACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGCACG GTGCTCACAGAAGCCAGGAAGTTGTCCAGGGAGGCGTGCA | 2853 |
| | CAAATACCGTTAAGCTG | 2854 |
| | CAGCTTAACGGTATTTG | 2855 |

EXAMPLE 17

Alpha-thalassemia - Hemoglobin alpha locus 2

[0229] The attached table discloses the correcting oligonucleotide base sequences for the hemoglobin alpha locus 2 oligonucleotides of the invention.

Table 19

HBA2 Mutations and Genome-Correcting Oligos

5

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Thalassaemia alpha Met(-1)Thr ATG-ACG | CCTGGCGCGCTCGCGGGCCGGCACTCTTCTGGTCCCCACAG ACTCAGAGAGAACCACCATGGTGCTGTCTCCTGCCGACAAG ACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCA | 2856 |
| | TGCGCGCCGACCTTACCCCAGGCGGCCTTGACGTTGGTCTT GTCGGCAGGAGACAGCACCATGGTGCGGTTCTCTCTGAGTCT GTGGGGACCAGAAGAGTGCCGGCCCGCAGCGCGCCAGG | 2857 |
| | ACCCACCATGGTGCTGT | 2858 |
| | ACAGCACCATGGTGCGG | 2859 |
| Haemoglobin variant Ala12Asp GCC-GAC | CACAGACTCAGAGAGAACCACCATGGTGCTGTCTCCTGCCG ACAAGACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCG CACGCTGGCGAGTATGGTGCGGAGGCCCTGGAGAGGTG | 2860 |
| | CACCTCTCCAGGGCCTCCGCACCATACTCGCCAGCGTGCGC GCCGACCTTACCCCAGGCGGCCTTGACGTTGGTCTTGTGCG CAGGAGACAGCACCATGGTGCGGTTCTCTCTGAGTCTGTG | 2861 |
| | CGTCAAGGCCGCCTGGG | 2862 |
| | CCCAGGCGGCCTTGACG | 2863 |
| Haemoglobin variant Lys16Glu TAAG-GAG | AGAGAACCCACCATGGTGCTGTCTCCTGCCGACAAGACCAAC GTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCACGCTGGCG AGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCTCCCTCC | 2864 |
| | GGAGGGAGCCTCACCTCTCCAGGGCCTCCGCACCATACTCG CCAGCGTGCGCGCCGACCTTACCCCAGGCGGCCTTGACGTT GGTCTTGTGCGCAGGAGACAGCACCATGGTGCGGTTCTCT | 2865 |
| | CCTGGGGTAAGGTCGGC | 2866 |
| | GCCGACCTTACCCCAGG | 2867 |
| Haemoglobin variant His20Gln CACg-CAA | GGTGCTGTCTCCTGCCGACAAGACCAACGTCAAGGCCGCCT GGGGTAAGGTCGGCGCGCACGCTGGCGAGTATGGTGCGGA GGCCCTGGAGAGGTGAGGCTCCCTCCCCTGCTCCGACCCG | 2868 |
| | CGGGTCGGAGCAGGGGAGGGAGCCTCACCTCTCCAGGGCC TCCGCACCATACTCGCCAGCGTGCGCGCCGACCTTACCCA GGCGGCCTTGACGTTGGTCTTGTGCGCAGGAGACAGCACC | 2869 |
| | GGCGCGCACGCTGGCGA | 2870 |
| | TCGCCAGCGTGCGCGCC | 2871 |
| Haemoglobin variant Glu27Asp GAGg-GAC | GACCAACGTCAAGGCCGCCTGGGGTAAGGTCGGCGCGCAC GCTGGCGAGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCT CCCTCCCCTGCTCCGACCCGGGCTCCTCGCCCGCCCGGACC | 2872 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | GGTCCGGGCGGGCGAGGAGCCCGGGTCGGAGCAGGGGAG GGAGCCTCACCTCTCCAGGGCCTCCGCACCATACTCGCCAG CGTGCGCGCCGACCTTACCCAGGCGGCCTTGACGTTGGTC | 2873 |
| | GGTGCGGAGGCCCTGGA | 2874 |
| | TCCAGGGCCTCCGCACC | 2875 |
| Thalassaemia alpha Leu29Pro CTG-CCG | ACGTCAAGGCCGCTGGGGTAAGGTCGGCGCGCACGCTGG CGAGTATGGTGCGGAGGCCCTGGAGAGGTGAGGCTCCCTCC CCTGCTCCGACCCGGGCTCCTCGCCCGCCCGACCCACAG | 2876 |
| | CTGTGGGTCCGGGCGGGCGAGGAGCCCGGGTCGGAGCAGG GGAGGGAGCCTCACCTCTCCAGGGCCTCCGCACCATACTCG CCAGCGTGCGCGCCGACCTTACCCAGGCGGCCTTGACGT | 2877 |
| | GGAGGCCCTGGAGAGGT | 2878 |
| | ACCTCTCCAGGGCCTCC | 2879 |
| Haemoglobin variant Asp47His cGAC-CAC | GCTTCTCCCCGCAGGATGTTCTGTCTTCCCCACCACCAAG ACCTACTTCCCGCACTTCGACCTGAGCCACGGCTCTGCCCAG GTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTGA | 2880 |
| | TCAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACCTGG GCAGAGCCGTGGCTCAGGTGGAAGTGCGGGAAGTAGGTCTT GGTGGTGGGGAAGGACAGGAACATCCTGCGGGGAGAAGC | 2881 |
| | CGCACTTCGACCTGAGC | 2882 |
| | GCTCAGGTGGAAGTGCG | 2883 |
| Haemoglobin variant Leu48Arg CTG-CGG | CTCCCCGCAGGATGTTCTGTCTTCCCCACCACCAAGACCT ACTTCCCGCACTTCGACCTGAGCCACGGCTCTGCCCAGGTTA AGGGCCACGGCAAGAAGGTGGCCGACGCGCTGACCAA | 2884 |
| | TTGGTCAGCGCGTCGGCCACCTTCTTGCCGTGGCCCTTAACC TGGGCAGAGCCGTGGCTCAGGTGGAAGTGCGGGAAGTAGGT CTTGGTGGTGGGGAAGGACAGGAACATCCTGCGGGGAG | 2885 |
| | CTTCGACCTGAGCCACG | 2886 |
| | CGTGGCTCAGGTGGAAG | 2887 |
| Haemoglobin variant Gln54Glu cCAG-GAG | CTGTCCTTCCCCACCACCAAGACCTACTTCCCGCACTTCGAC CTGAGCCACGGCTCTGCCAGGTTAAGGGCCACGGCAAGAA GGTGGCCGACGCGCTGACCAACGCCGTGGCGCACGTGG | 2888 |
| | CCACGTGCGCCACGGCGTTGGTCAGCGCGTCGGCCACCTTC TTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTCAGGTC GAAGTGCGGGAAGTAGGTCTTGGTGGTGGGGAAGGACAG | 2889 |
| | GCTCTGCCAGGTTAAG | 2890 |
| | CTTAACCTGGGCAGAGC | 2891 |
| Haemoglobin variant Gly59Asp GGC-GAC | CCAAGACCTACTTCCCGCACTTCGACCTGAGCCACGGCTCTG CCCAGGTTAAGGGCCACGGCAAGAAGGTGGCCGACGCGCTG ACCAACGCCGTGGCGCACGTGGACGACATGCCCAACGC | 2892 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | GCGTTGGGCATGTCGTCCACGTGCGCCACGGCGTTGGTCAG CGCGTCGGCCACCTTCTTG <u>C</u> CGTGGCCCTTAACCTGGGCAG AGCCGTGGCTCAGGTCTGAAGTGCGGGAAGTAGGTCTTGG | 2893 |
| | GGGCCACGGCAAGAAGG | 2894 |
| | CCTTCTTG <u>C</u> CGTGGCCC | 2895 |
| Haemoglobin variant Asn68Lys AACg-AAG | GAGCCACGGCTCTGCCCAGGTTAAGGGCCACGGCAAGAAGG TGGCCGACGCGCTGACCAA <u>C</u> GCCGTGGCGCACGTGGACGA CATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG | 2896 |
| | CGCGTGCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATGT CGTCCACGTGCGCCACGGC <u>G</u> TTGGTCAGCGCGTCGGCCACC TTCTTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTC | 2897 |
| | CTGACCAA <u>C</u> GCCGTGGC | 2898 |
| | GCCACGGC <u>G</u> TTGGTCAG | 2899 |
| Haemoglobin variant Asn68Lys AACg-AAA | GAGCCACGGCTCTGCCCAGGTTAAGGGCCACGGCAAGAAGG TGGCCGACGCGCTGACCAA <u>C</u> GCCGTGGCGCACGTGGACGA CATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG | 2900 |
| | CGCGTGCAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATGT CGTCCACGTGCGCCACGGC <u>G</u> TTGGTCAGCGCGTCGGCCACC TTCTTGCCGTGGCCCTTAACCTGGGCAGAGCCGTGGCTC | 2901 |
| | CTGACCAA <u>C</u> GCCGTGGC | 2902 |
| | GCCACGGC <u>G</u> TTGGTCAG | 2903 |
| Haemoglobin variant Asn78Lys AACg-AAA | CGGCAAGAAGGTGGCCGACGCGCTGACCAACGCCGTGGCG CACGTGGACGACATGCCCAA <u>C</u> GCGCTGTCCGCCCTGAGCGA CCTGCACGCGCACAAGCTTCGGGTGGACCCGGTCAACTTC | 2904 |
| | GAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGT CGCTCAGGGCGGACAGCGC <u>G</u> TTGGGCATGTCGTCCACGTGC GCCACGGCGTTGGTCAGCGCGTCGGCCACCTTCTTGCCG | 2905 |
| | ATGCCCAA <u>C</u> GCGCTGTC | 2906 |
| | GACAGCGC <u>G</u> TTGGGCAT | 2907 |
| Haemoglobin variant Asp85Val GAC-GTC | CGCTGACCAACGCCGTGGCGCACGTGGACGACATGCCAAC GCGCTGTCCGCCCTGAGCGA <u>C</u> CTGCACGCGCACAAGCTTCG GGTGGACCCGGTCAACTTCAAGGTGAGCGGCGGGCCGGG | 2908 |
| | CCCGGCCCGCCGCTACCTTGAAGTTGACCGGGTCCACCCG AAGCTTGTGCGCGTGCAGG <u>T</u> CGCTCAGGGCGGACAGCGCGT TGGGCATGTCGTCCACGTGCGCCACGGCGTTGGTCAGCG | 2909 |
| | CCTGAGCGA <u>C</u> CTGCACG | 2910 |
| | CGTGCAGG <u>T</u> CGCTCAGG | 2911 |
| Haemoglobin variant Lys90Asn AAGc-AAT | GGCGCACGTGGACGACATGCCCAACGCGCTGTCCGCCCTGA GCGACCTGCACGCGCACAAG <u>C</u> TTCCGGTGGACCCGGTCAAC TTCAAGGTGAGCGGCGGGCCGGGAGCGATCTGGGTCGAG | 2912 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | CTCGACCCAGATCGCTCCCGGCCCGCCGCTCACCTTGAAGT TGACCGGGTCCACCCGAAGCTTGTGCGCGTGCAGGTGCGTC AGGGCGGACAGCGCGTTGGGCATGTCGTCCACGTGCGCC | 2913 |
| | GCGCACAAGCTTCGGGT | 2914 |
| | ACCCGAAGCTTGTGCGC | 2915 |
| | | |
| Haemoglobin variant Asp94His gGAC-CAC | GACGACATGCCAACGCGCTGTCCGCCCTGAGCGACCTGCA CGCGCACAAGCTTCGGGTGGACCCGGTCAACTTCAAGGTGA GCGGCGGGGCCGGGAGCGATCTGGGTGAGGGGCGAGATG | 2916 |
| | CATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCCGCTC ACCTTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCGCGTG CAGGTCGCTCAGGGCGGACAGCGCGTTGGGCATGTCGTC | 2917 |
| | TTCGGGTGGACCCGGTC | 2918 |
| | GACCGGGTCCACCCGAA | 2919 |
| Haemoglobin variant Pro95Leu CCG-CTG | ACATGCCCAACGCGCTGTCCGCCCTGAGCGACCTGCACGCG CACAAGCTTCGGGTGGACCCGGTCAACTTCAAGGTGAGCGG CGGGCCGGGAGCGATCTGGGTGAGGGGCGAGATGGCGC | 2920 |
| | GCGCCATCTCGCCCCTCGACCCAGATCGCTCCCGGCCCGCC GCTCACCTTGAAGTTGACCGGGTCCACCCGAAGCTTGTGCG CGTGCAAGTCGCTCAGGGCGGACAGCGCGTTGGGCATGT | 2921 |
| | GGTGGACCCGGTCAACT | 2922 |
| | AGTTGACCGGGTCCACC | 2923 |
| Haemoglobin variant Ser102Arg aAGC-CGC | TAGCGCAGGCGGCGGCTGCGGGCCTGGGCGCACTGACCC TCTTCTCTGCACAGCTCCTAAGCCACTGCCTGCTGGTGACCC TGGCCGCCACCTCCCCGCCGAGTTCACCCCTGCGGTGC | 2924 |
| | GCACCGCAGGGGTGAAGTTCGGCGGGGAGGTGGGCGGCCAG GGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCAGAGAAGA GGGTCAGTGCGGCCAGGCCCGCAGCCGCCGCTGCGCTA | 2925 |
| | AGCTCCTAAGCCACTGC | 2926 |
| | GCAGTGGCTTAGGAGCT | 2927 |
| Haemoglobin H disease Cys104Tyr TGC-TAC | GGCGGCGGCTGCGGGCCTGGGCGCACTGACCCTCTTCTCT GCACAGCTCCTAAGCCACTGCCTGCTGGTGACCCTGGCCGC CCACCTCCCCGCCGAGTTCACCCCTGCGGTGCACGCCTC | 2928 |
| | GAGGCGTGACCCGAGGGGTGAAGTTCGGCGGGGAGGTGGG CGGCCAGGGTCACCAGCAGGCAGTGGCTTAGGAGCTGTGCA GAGAAGAGGGTCAGTGCGGCCAGGCCCGCAGCCGCCGCC | 2929 |
| | AAGCCACTGCCTGCTGG | 2930 |
| | CCAGCAGGCAGTGGCTT | 2931 |
| Haemoglobin variant Ala111Val GCC-GTC | CCGCACTGACCCTCTTCTCTGCACAGCTCCTAAGCCACTGCC TGCTGGTGACCCTGGCCGCCACCTCCCCGCCGAGTTCACC CCTGCGGTGCACGCCTCCCTGGACAAGTTCCTGGCTTC | 2932 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | GAAGCCAGGAACTTGTCCAGGGAGGCGTGCACCGCAGGGGT GAACTCGGCGGGGAGGTGGGCGGCCAGGGTCACCAGCAGG CAGTGGCTTAGGAGCTGTGCAGAGAAGAGGGTCAGTGC GG | 2933 |
| | CCTGGCCGCCCACCTCC | 2934 |
| | GGAGGTGGGCGGCCAGG | 2935 |
| | | |
| Haemoglobin variant Ala120Glu GCG-GAG | TCCTAAGCCACTGCCTGCTGGTGACCCTGGCCGCCACCTC CCCGCCGAGTTCACCCCTGCGGTGCACGCCTCCCTGGACAA GTTCTTGCTTCTGTGAGCACCGTGTGACCTCCAAATA | 2936 |
| | TATTTGGAGGTCAGCACGGTGCTCACAGAAGCCAGGAACTTG TCCAGGGAGGCGTGCACCGCAGGGGTGAACTCGGCGGGGA GGTGGGCGGCCAGGGTCACCAGCAGGCAGTGGCTTAGGA | 2937 |
| | CACCCCTGCGGTGCACG | 2938 |
| | CGTGCACCGCAGGGGTG | 2939 |
| Haemoglobin variant His122Gln CACg-CAG | CCACTGCCTGCTGGTGACCCTGGCCGCCACCTCCCCGCCG AGTTCACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCTG GCTTCTGTGAGCACCGTGTGACCTCCAAATACCGTTAA | 2940 |
| | TTAACGGTATTTGGAGGTCAGCACGGTGCTCACAGAAGCCAG GAACTTGTCCAGGGAGGCGTGCACCGCAGGGGTGAACTCGG CGGGGAGGTGGGCGGCCAGGGTCACCAGCAGGCAGTGG | 2941 |
| | GCGGTGCACGCCTCCCT | 2942 |
| | AGGGAGGCGTGCACCGC | 2943 |
| Haemoglobin variant Ala123Ser cGCC-TCC | CACTGCCTGCTGGTGACCCTGGCCGCCACCTCCCCGCCGA GTTACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCTGG CTTCTGTGAGCACCGTGTGACCTCCAAATACCGTTAAG | 2944 |
| | CTTAACGGTATTTGGAGGTCAGCACGGTGCTCACAGAAGCCA GGA ACTTGTCCAGGGAGGCGTGCACCGCAGGGGTGAACTCG GCGGGGAGGTGGGCGGCCAGGGTCACCAGCAGGCAGTGTG | 2945 |
| | CGGTGCACGCCTCCCTG | 2946 |
| | CAGGGAGGCGTGCACCG | 2947 |
| Thalassaemia alpha Leu125Pro CTG-CCG | TGCTGGTGACCCTGGCCGCCACCTCCCCGCCGAGTTCACC CCTGCGGTGCACGCCTCCCTGGACAAGTTCCTGGCTTCTGTG AGCACCGTGTGACCTCCAAATACCGTTAAGCTGGAGC | 2948 |
| | GCTCCAGCTTAACGGTATTTGGAGGTCAGCACGGTGCTCACA GAAGCCAGGAACTTGTCCAGGGAGGCGTGCACCGCAGGGGT GAACTCGGCGGGGAGGTGGGCGGCCAGGGTCACCAGCA | 2949 |
| | CGCCTCCCTGGACAAGT | 2950 |
| | ACTTGTCCAGGGAGGCG | 2951 |
| Haemoglobin variant Ser131Pro tTCT-CCT | GCCCCACCTCCCCGCCGAGTTCACCCCTGCGGTGCACGCCTC CCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGTGACCTC CAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTTCTC | 2952 |
| | GAGGAACGGCTACCGAGGCTCCAGCTTAACGGTATTTGGAG GTCAGCACGGTGCTCACAGAGCCAGGAACTTGTCCAGGGA GGCGTGCACCGCAGGGGTGAACTCGGCGGGGAGGTGGGC | 2953 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | TCCTGGCTTCTGTGAGC | 2954 |
| | GCTCACAGAAAGCCAGGA | 2955 |
| Haemoglobin variant Leu136Met gCTG-ATG | GAGTTCACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCT GGCTTCTGTGAGCACCGTGCTGACCTCCAAATACCGTTAAGC TGGAGCCTCGGTAGCCGTTCTCCTGCCCGCTGGGCCT | 2956 |
| | AGGCCCAGCGGGCAGGAGGAACGGCTACCGAGGCTCCAGC TTAACGGTATTTGGAGGTCAGCACGGTGCTCACAGAAGCCAG GAACTTGTCCAGGGAGGCGTGACCGCAGGGGTGAACTC | 2957 |
| | GCACCGTGCTGACCTCC | 2958 |
| | GGAGGTCAGCACGGTG | 2959 |
| Haemoglobin variant Leu136Pro CTG-CCG | AGTTCACCCCTGCGGTGCACGCCTCCCTGGACAAGTTCCTG GCTTCTGTGAGCACCGTGCTGACCTCCAAATACCGTTAAGCT GGAGCCTCGGTAGCCGTTCTCCTGCCCGCTGGGCCTC | 2960 |
| | GAGGCCAGCGGGCAGGAGGAACGGCTACCGAGGCTCCAG CTTAACGGTATTTGGAGGTCAGCACGGTGCTCACAGAAGCCA GGAATTGTCCAGGGAGGCGTGACCGCAGGGGTGAACT | 2961 |
| | CACCGTGCTGACCTCCA | 2962 |
| | TGGAGGTCAGCACGGTG | 2963 |
| Haemoglobin variant Arg141Cys cCGT-TGT | GTGCACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACC GTGCTGACCTCCAAATACCGTTAAGCTGGAGCCTCGGTAGCC GTTCTCCTGCCCGCTGGGCCTCCCAACGGGGCCCTCC | 2964 |
| | GGAGGGCCCGTTGGGAGGCCAGCGGGCAGGAGGAACGGC TACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGCACGGT GCTCACAGAAGCCAGGAACTTGTCCAGGGAGGCGTGAC | 2965 |
| | CCAAATACCGTTAAGCT | 2966 |
| | AGCTTAACGGTATTTGG | 2967 |
| Haemoglobin variant Term142Gln tTAA-CAA | CACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTG CTGACCTCCAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTT CCTCCTGCCCGCTGGGCCTCCCAACGGGGCCCTCCTCC | 2968 |
| | GGAGGAGGGCCCGTTGGGAGGCCAGCGGGCAGGAGGAAC GGCTACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGCA CGGTGCTCACAGAAGCCAGGAACTTGTCCAGGGAGGCGTG | 2969 |
| | AATACCGTTAAGCTGGA | 2970 |
| | TCCAGCTTAACGGTATT | 2971 |
| Haemoglobin variant Term142Lys tTAA-AAA | CACGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTG CTGACCTCCAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTT CCTCCTGCCCGCTGGGCCTCCCAACGGGGCCCTCCTCC | 2972 |
| | GGAGGAGGGCCCGTTGGGAGGCCAGCGGGCAGGAGGAAC GGCTACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGCA CGGTGCTCACAGAAGCCAGGAACTTGTCCAGGGAGGCGTG | 2973 |
| | AATACCGTTAAGCTGGA | 2974 |
| | TCCAGCTTAACGGTATT | 2975 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Haemoglobin variant Term142Tyr TAAg-TAT | CGCCTCCCTGGACAAGTTCCTGGCTTCTGTGAGCACCGTGCT GACCTCCAAATACCGTTAAGCTGGAGCCTCGGTAGCCGTTCC TCCTGCCCCGCTGGGCCTCCCAACGGGCCCTCCTCCCC | 2976 |
| | GGGGAGGAGGGCCCGTTGGGAGGCCAGCGGGCAGGAGGA ACGGCTACCGAGGCTCCAGCTTAACGGTATTTGGAGGTCAGC ACGGTGCTCACAGAAGCCAGGAACCTTGTCAGGGAGGCG | 2977 |
| | TACCGTTAAGCTGGAGC | 2978 |
| | GCTCCAGCTTAACGGTA | 2979 |

EXAMPLE 18

Human mismatch repair - MLH1

[0230] The human MLH1 gene is homologous to the bacterial *mutL* gene, which is involved in mismatch repair. Mutations in the MLH1 gene have been identified in many individuals with hereditary nonpolyposis colorectal cancer (HNPCC). Mutations in the MLH1 gene are also implicated in predisposition to a variety of cancers associated with, for example, Muir-Torre syndrome and Turcot syndrome. The attached table discloses the correcting oligonucleotide base sequences for the MLH1 oligonucleotides of the invention.

Table 20

MLH1 Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Non-polyposis colorectal cancer Met1Arg ATG-AGG | TTGGCTGAAGGCACTTCCGTTGAGCATCTAGACGTTTCCTTG GCTCTTCTGGCGCCAAAATGTCGTTTCGTGGCAGGGGTTATTC GGCGGCTGGACGAGACAGTGGTGAACCGCATCGCGGC | 2980 |
| | GCCGCGATGCGGTTCACTACTGTCTCGTCCAGCCGCCGAAT AACCCCTGCCACGAACGACATTTTGGCGCCAGAAGAGCCAA GGAAACGTCTAGATGCTCAACGGAAGTGCCTTCAGCCAA | 2981 |
| | CGCCAAAATGTCGTTTCG | 2982 |
| | CGAACGACATTTTGGCG | 2983 |
| Non-polyposis colorectal cancer Met1Lys ATG-AAG | TTGGCTGAAGGCACTTCCGTTGAGCATCTAGACGTTTCCTTG GCTCTTCTGGCGCCAAAATGTCGTTTCGTGGCAGGGGTTATTC GGCGGCTGGACGAGACAGTGGTGAACCGCATCGCGGC | 2984 |
| | GCCGCGATGCGGTTCACTACTGTCTCGTCCAGCCGCCGAAT AACCCCTGCCACGAACGACATTTTGGCGCCAGAAGAGCCAA GGAAACGTCTAGATGCTCAACGGAAGTGCCTTCAGCCAA | 2985 |
| | CGCCAAAATGTCGTTTCG | 2986 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | CGAACGAC <u>A</u> TTTTGGCG | 2987 |
| Non-polyposis colorectal cancer Met35Arg ATG-AGG | TGGTGAACCGCATCGCGGCGGGGGAAGTTATCCAGCGGCCA GCTAATGCTATCAAAGAGAT <u>T</u> GATTGAGAACTGGTACGGAGGG AGTCGAGCCGGGCTCACTTAAGGGCTACGACTTAACGG | 2988 |
| | CCGTTAAGTCGTAGCCCTTAAGTGAGCCCGGCTCGACTCCCT CCGTACCAGTTCTCAATC <u>A</u> TCTCTTTGATAGCATTAGCTGGCC GCTGGATAACTCCCCCGCCGCGATGCGGTTACCA | 2989 |
| | CAAAGAGATGATTGAGA | 2990 |
| | TCTCAATC <u>A</u> TCTCTTTG | 2991 |
| Non-polyposis colorectal cancer Ser44Phe TCC-TTC | TAGAGTAGTTGCAGACTGATAAATTATTTTCTGTTTGATTGGC AGTTTAGATGCAAAAT <u>C</u> CACAAGTATTCAAGTGATTGTTAAAG AGGGAGGCCTGAAGTTGATTGAGATCCAAGACAA | 2992 |
| | TTGTCTTGGATCTGAATCAACTTCAGGCCTCCCTCTTTAACAA TCACTTGAATACTTGTG <u>G</u> ATTTTGCATCTAACTGGCAAATCA AACAGAAAATAATTTATCAGTCTGCAACTACTCTA | 2993 |
| | TGCAAAAT <u>C</u> CACAAGTA | 2994 |
| | TACTTGTG <u>G</u> ATTTTGCA | 2995 |
| Non-polyposis colorectal cancer Gln62Lys CAA-AAA | GCAAAATCCACAAGTATTCAAGTGATTGTTAAAGAGGGAGGC CTGAAGTTGATTGAGATC <u>C</u> AAGACAATGGCACC ^{GG} GATCAGG GTAAGTAAACCTCAAAGTAGCAGGATGTTTGTGCGC | 2996 |
| | GCGCACAAACATCCTGCTACTTTGAGGTTTTACTTACCCTGAT CCCGGTGCCATTGTCTT <u>G</u> GATCTGAATCAACTTCAGGCCTCC CTCTTTAACAATCACTTGAATACTTGTGGATTTTGC | 2997 |
| | TTCAGATC <u>C</u> AAGACAAT | 2998 |
| | ATTGTCTT <u>G</u> GATCTGAA | 2999 |
| Non-polyposis colorectal cancer Gln62Term CAA-TAA | GCAAAATCCACAAGTATTCAAGTGATTGTTAAAGAGGGAGGC CTGAAGTTGATTGAGATC <u>C</u> AAGACAATGGCACC ^{GG} GATCAGG GTAAGTAAACCTCAAAGTAGCAGGATGTTTGTGCGC | 3000 |
| | GCGCACAAACATCCTGCTACTTTGAGGTTTTACTTACCCTGAT CCCGGTGCCATTGTCTT <u>G</u> GATCTGAATCAACTTCAGGCCTCC CTCTTTAACAATCACTTGAATACTTGTGGATTTTGC | 3001 |
| | TTCAGATC <u>C</u> AAGACAAT | 3002 |
| | ATTGTCTT <u>G</u> GATCTGAA | 3003 |
| Non-polyposis colorectal cancer Asn64Ser AAT-AGT | CCACAAGTATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGT TGATTGAGATCCAAGACA <u>A</u> TGGCACC ^{GG} GATCAGGGTAAGTA AAACCTCAAAGTAGCAGGATGTTTGTGCGCTTCATGG | 3004 |
| | CCATGAAGCGCACAAACATCCTGCTACTTTGAGGTTTTACTTA CCCTGATCCCGGTGCCA <u>T</u> TGTCTTGGATCTGAATCAACTTCA GGCCTCCCTCTTTAACAATCACTTGAATACTTGTGG | 3005 |
| | CCAAGACA <u>A</u> TGGCACCG | 3006 |
| | CGGTGCCA <u>T</u> TGTCTTGG | 3007 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Non-polypoidis colorectal cancer Gly67Arg GGG-AGG | ATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTGAG ATCCAAGACAATGGCACC <u>GGG</u> ATCAGGGTAAGTAAACCTCA AAGTAGCAGGATGTTTGTGCGCTTCATGGAAGAGTCA | 3008 |
| | TGACTCTTCCATGAAGCGCACAAACATCCTGCTACTTTGAGGT TTTACTTACCCTGATCC <u>CGG</u> TGCCATTGTCTTGGATCTGAATC AACTTCAGGCCTCCCTCTTTAACAATCACTTGAAT | 3009 |
| | ATGGCACCC <u>GGG</u> ATCAGG | 3010 |
| | CCTGATCC <u>CGG</u> TGCCAT | 3011 |
| Non-polypoidis colorectal cancer Gly67Arg GGG-CGG | ATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTGAG ATCCAAGACAATGGCACC <u>GGG</u> ATCAGGGTAAGTAAACCTCA AAGTAGCAGGATGTTTGTGCGCTTCATGGAAGAGTCA | 3012 |
| | TGACTCTTCCATGAAGCGCACAAACATCCTGCTACTTTGAGGT TTTACTTACCCTGATCC <u>CGG</u> TGCCATTGTCTTGGATCTGAATC AACTTCAGGCCTCCCTCTTTAACAATCACTTGAAT | 3013 |
| | ATGGCACCC <u>GGG</u> ATCAGG | 3014 |
| | CCTGATCC <u>CGG</u> TGCCAT | 3015 |
| Non-polypoidis colorectal cancer Gly67Trp GGG-TGG | ATTCAAGTGATTGTTAAAGAGGGAGGCCTGAAGTTGATTGAG ATCCAAGACAATGGCACC <u>GGG</u> ATCAGGGTAAGTAAACCTCA AAGTAGCAGGATGTTTGTGCGCTTCATGGAAGAGTCA | 3016 |
| | TGACTCTTCCATGAAGCGCACAAACATCCTGCTACTTTGAGGT TTTACTTACCCTGATCC <u>CGG</u> TGCCATTGTCTTGGATCTGAATC AACTTCAGGCCTCCCTCTTTAACAATCACTTGAAT | 3017 |
| | ATGGCACCC <u>GGG</u> ATCAGG | 3018 |
| | CCTGATCC <u>CGG</u> TGCCAT | 3019 |
| Non-polypoidis colorectal cancer Cys77Arg TGT-CGT | GTAACATGATTATTTACTCATCTTTTTGGTATCTAACAGAAAGA AGATCTGGATATTGTAT <u>GTG</u> AAAGGTTCACTACTAGTAAACTG CAGTCCTTTGAGGATTTAGCCAGTATTTCTACCT | 3020 |
| | AGGTAGAAATACTGGCTAAATCCTCAAAGGACTGCAGTTTACT AGTAGTGAACCTTTAC <u>A</u> TACAATATCCAGATCTTCTTTCTGTT AGATACCAAAAAGATGAGTAAATAATCATGTTAC | 3021 |
| | ATATTGTAT <u>GTG</u> AAAGG | 3022 |
| | CCTTTCAC <u>A</u> TACAATAT | 3023 |
| Non-polypoidis colorectal cancer Cys77Tyr TGT-TAT | TAACATGATTATTTACTCATCTTTTTGGTATCTAACAGAAAGAA GATCTGGATATTGTAT <u>GTG</u> AAAGGTTCACTACTAGTAAACTGC AGTCCTTTGAGGATTTAGCCAGTATTTCTACCTA | 3024 |
| | TAGGTAGAAATACTGGCTAAATCCTCAAAGGACTGCAGTTTAC TAGTAGTGAACCTTTCA <u>C</u> ATACAATATCCAGATCTTCTTTCTGT TAGATACCAAAAAGATGAGTAAATAATCATGTTA | 3025 |
| | TATTGTAT <u>GTG</u> AAAGG | 3026 |
| | ACCTTTCAC <u>A</u> TACAATA | 3027 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Non-polyposis colorectal cancer Ser93Gly AGT-GGT | CTGGATATTGTATGTGAAAGGTTCACTACTAGTAAACTGCAGT CCTTTGAGGATTTAGCC <u>A</u> GTATTTCTACCTATGGCTTTGAGG TGAGGTAAGCTAAAGATTCAAGAAATGTGTAAAAT | 3028 |
| | ATTTTACACATTTCTTGAATCTTTAGCTTACCTCACCTCGAAAG CCATAGGTAGAAATACTGGCTAAATCCTCAAAGGACTGCAGT TACTAGTAGTGAACCTTTACATACAATATCCAG | 3029 |
| | ATTTAGCC <u>A</u> GTATTTCT | 3030 |
| | AGAAATACTGGCTAAAT | 3031 |
| Non-polyposis colorectal cancer Arg100Term CGA-TGA | TTCCTACTAGTAAACTGCAGTCCTTTGAGGATTTAGCCAGTA TTTCTACCTATGGCTTT <u>C</u> GAGGTGAGGTAAGCTAAAGATTCAA GAAATGTGTAAAATATCCTCCTGTGATGACATTGT | 3032 |
| | ACAATGTCATCACAGGAGGATATTTTACACATTTCTTGAATCTT TAGCTTACCTCACCTC <u>G</u> AAAGCCATAGGTAGAAATACTGGCT AAATCCTCAAAGGACTGCAGTTTACTAGTAGTGAA | 3033 |
| | ATGGCTTT <u>C</u> GAGGTGAG | 3034 |
| | CTCACCTC <u>G</u> AAAGCCAT | 3035 |
| Non-polyposis colorectal cancer Ile107Arg ATA-AGA | ACCCAGCAGTGAGTTTTCTTTCAGTCTATTTTCTTTCTTCCT TAGGCTTTGGCCAGCATAAGCCATGTGGCTCATGTTACTATTA CAACGAAAACAGCTGATGGAAAGTGTGCATACAG | 3036 |
| | CTGTATGCACACTTTCCATCAGCTGTTTTCGTTGTAATAGTAA CATGAGCCACATGGCTT <u>A</u> TGCTGGCCAAAGCCTAAGGAAGAA AAGAAAATAGACTGAAAGAAAAACTCACTGCTGGGT | 3037 |
| | GGCCAGCATAAGCCATG | 3038 |
| | CATGGCTT <u>A</u> TGCTGGCC | 3039 |
| Non-polyposis colorectal cancer Thr117Arg ACG-AGG | TTTCTTTTCTTCCTTAGGCTTTGGCCAGCATAAGCCATGTGGC TCATGTTACTATTACAACGAAAACAGCTGATGGAAAGTGTGCA TACAGGTATAGTGCTGACTTCTTTTACTCATATAT | 3040 |
| | ATATATGAGTAAAAGAAGTCAGCACTATACCTGTATGCACACT TTCCATCAGCTGTTTTC <u>G</u> TTGTAATAGTAACATGAGCCACATG GCTTATGCTGGCCAAAGCCTAAGGAAGAAAAGAAA | 3041 |
| | TATTACAACGAAAACAG | 3042 |
| | CTGTTTTC <u>G</u> TTGTAATA | 3043 |
| Non-polyposis colorectal cancer Thr117Met ACG-ATG | TTTCTTTTCTTCCTTAGGCTTTGGCCAGCATAAGCCATGTGGC TCATGTTACTATTACAACGAAAACAGCTGATGGAAAGTGTGCA TACAGGTATAGTGCTGACTTCTTTTACTCATATAT | 3044 |
| | ATATATGAGTAAAAGAAGTCAGCACTATACCTGTATGCACACT TTCCATCAGCTGTTTTC <u>G</u> TTGTAATAGTAACATGAGCCACATG GCTTATGCTGGCCAAAGCCTAAGGAAGAAAAGAAA | 3045 |
| | TATTACAACGAAAACAG | 3046 |
| | CTGTTTTC <u>G</u> TTGTAATA | 3047 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|--------------|
| Non-polyposis colorectal cancer Gly133Term GGA-TGA | TCTATCTCTCTACTGGATATTAATTTGTTATATTTCTCATTAGA GCAAGTTACTCAGATGGA ^{AA} ACTGAAAGCCCCTCCTAAACCA TGTGCTGGCAATCAAGGGACCCAGATCACGGTAA | 3048 |
| | TTACCGTGATCTGGGTCCCTTGATTGCCAGCACATGGTTTAG GAGGGGCTTTTCAGTTTTCCATCTGAGTAACTTGCTCTAATGAG AAAATATAACAAATTAATATCCAGTAGAGAGATAGA | 3049 |
| | ACTCAGATGGA ^{AA} ACTG | 3050 |
| | CAGTTTTCCATCTGAGT | 3051 |
| Non-polyposis colorectal cancer Val185Gly GTA-GGA | TAGTGTGTGTTTTGGCAACTCTTTCTTACTCTTTGTTTTTC TTTTCCAGGTATTCAGTACACAATGCAGGCATTAGTTTCTCAG TTAAAAAGTAAGTTCTTGGTTTATGGGGGATGG | 3052 |
| | CCATCCCCCATAAACCAAGAACTTACTTTTTTAAGTGAAGAAC TAATGCCTGCATTGTGTACTGAATACCTGGAAAAGAAAAACAA AAGAGTAAGAAAAGAGTTGCCAAAAACACACACTA | 3053 |
| | GTATTCAGTACACAATG CATTGTGTACTGAATAC | 3054 3055 |
| Non-polyposis colorectal cancer Ser193Pro TCA-CCA | TTTCTTACTCTTTTGTTTTCTTTTCCAGGTATTCAGTACACAA TGCAGGCATTAGTTTCTCAGTTAAAAAGTAAGTTCTTGGTTT ATGGGGGATGGTTTTGTTTTATGAAAAGAAAAAA | 3056 |
| | TTTTTTCTTTTCATAAAACAAAACCATCCCCCATAAACCAAGAA CTTACTTTTTTAACTGAGAAACTAATGCCTGCATTGTGTACTG AATACCTGGAAGAAAAGAAAACAAAAGAGTAAGAAA | 3057 |
| | TTAGTTTCTCAGTTAAA | 3058 |
| | TTTAACTGAGAAACTAA | 3059 |
| Non-polyposis colorectal cancer Val213Met GTG-ATG | TTTGTTTATCAGCAAGGAGAGACAGTAGCTGATGTTAGGACA CTACCCAATGCCTCAACCGTGGACAATATTCGCTCCATCTTTG GAAATGCTGTTAGTCGGTATGTCGATAACCTATATA | 3060 |
| | TATATAGGTTATCGACATACCGACTAACAGCATTTCCAAAGAT GGAGCGAATATTGTCCACGGTTGAGGCATTGGGTAGTGTCTT AACATCAGCTACTGTCTCTCCTTGCTGATAAACAAA | 3061 |
| | CCTCAACCGTGGACAAT | 3062 |
| | ATTGTCCACGGTTGAGG | 3063 |
| Non-polyposis colorectal cancer Arg217Cys CGC-TGC | CAAGGAGAGACAGTAGCTGATGTTAGGACACTACCCAATGCC TCAACCGTGGACAATATTGCTCCATCTTTGGAAATGCTGTTA GTCGGTATGTCGATAACCTATATAAAAAAATCTTTT | 3064 |
| | AAAAGATTTTTTTATATAGGTTATCGACATACCGACTAACAGC ATTTCCAAAGATGGAGCGAATATTGTCCACGGTTGAGGCATT GGGTAGTGTCTAACATCAGCTACTGTCTCTCCTTG | 3065 |
| | ACAATATTGCTCCATC | 3066 |
| | GATGGAGCGAATATTGT | 3067 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Non-polyposis colorectal cancer Ile219Val ATC-GTC | GAGACAGTAGCTGATGTTAGGACACTACCCAATGCCTCAACC GTGGACAATATTCGCTCCATCTTTGGAAATGCTGTTAGTCGGT ATGTCGATAACCTATATAAAAAAATCTTTTACATTT | 3068 |
| | AAATGTAAAAGATTTTTTATATAGGTTATCGACATACCGACTA ACAGCATTTCCAAAGATGGAGCGAATATTGTCCACGGTTGAG GCATTGGGTAGTGTCTAACATCAGCTACTGTCTC | 3069 |
| | TTCGCTCCATCTTTGGA | 3070 |
| | TCCAAAGATGGAGCGAA | 3071 |
| Non-polyposis colorectal cancer Gly244Asp GGT-GAT | CTAATAGAGAACTGATAGAAATTGGATGTGAGGATAAAACCTT AGCCTTCAAATGAATGGTTACATATCCAATGCAAACACTACTCA GTGAAGAAGTGCATCTTCTTACTCTTCATCAACCG | 3072 |
| | CGGTTGATGAAGAGTAAGAAGATGCACTTCTTCACTGAGTAG TTTGCATTGGATATGTAACCATTCATTTTGAAGGCTAGGGTTT TATCCTCACATCCAATTTCTATCAGTTCTCTATTAG | 3073 |
| | AATGAATGGTTACATAT | 3074 |
| | ATATGTAACCATTCATT | 3075 |
| Non-polyposis colorectal cancer Ser252Term TCA-TAA | GATGTGAGGATAAAACCCTAGCCTTCAAATGAATGGTTACAT ATCCAATGCAAACACTACTCAGTGAAGAAGTGCATCTTCTTACTC TTCATCAACCGTAAGTTAAAAAGAACCACATGGGA | 3076 |
| | TCCCATGTGGTTCTTTTAACTTACGGTTGATGAAGAGTAAGA AGATGCACTTCTTCACTGAGTAGTTTGCATTGGATATGTAACC ATTCATTTTGAAGGCTAGGGTTTTATCCTCACATC | 3077 |
| | AACTACTCAGTGAAGA | 3078 |
| | TCTTCACTGAGTAGTTT | 3079 |
| Non-polyposis colorectal cancer Glu268Gly GAA-GGA | CACCCCTCAGGACAGTTTTGAACTGGTTGCTTTCTTTTATTG TTTAGATCGTCTGGTAGAATCAACTTCCTTGAGAAAAGCCATA GAAACAGTGTATGCAGCCTATTTGCCCAAAACAC | 3080 |
| | GTGTTTTTGGGCAAATAGGCTGCATACACTGTTTCTATGGCTT TTCTCAAGGAAGTTGATTCTACCAGACGATCTAAACAATAAAA AGAAAGCAACCAGTTCAAACCTGTCCTGAGGGGTG | 3081 |
| | TCTGGTAGAATCAACTT | 3082 |
| | AAGTTGATTCTACCAGA | 3083 |
| Non-polyposis colorectal cancer Ser269Term TCA-TGA | CCCTCAGGACAGTTTTGAACTGGTTGCTTTCTTTTATTGTTTA GATCGTCTGGTAGAATCAACTTCCTTGAGAAAAGCCATAGAAA CAGTGTATGCAGCCTATTTGCCCAAAACACACA | 3084 |
| | TGTGTGTTTTTGGGCAAATAGGCTGCATACACTGTTTCTATGG CTTTTCTCAAGGAAGTTGATTCTACCAGACGATCTAAACAATA AAAAGAAAGCAACCAGTTCAAACCTGTCCTGAGGG | 3085 |
| | GGTAGAATCAACTTCCT | 3086 |
| | AGGAAGTTGATTCTACC | 3087 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Non-polyposis colorectal cancer Glu297Term GAA-TAA | CTTTTCTCCCCCTCCCACTATCTAAGGTAATTGTTCTCTCTTA TTTCCTGACAGTTTAA <u>G</u> AAATCAGTCCCCAGAATGTGGATGTT AATGTGCACCCCACAAAGCATGAAGTTCACCTCC | 3088 |
| | GGAAGTGA <u>A</u> CTTCATGCTTTGTGGGGTGCACATTAACATCCA CATTCTGGGGACTGATTT <u>C</u> TAAACTGTCAGGAAAATAAGAGA GAACAATTACCTTAGATAGTGGGAGGGGGAGAAAAAG | 3089 |
| | ACAGTTTAA <u>G</u> AAATCAGT | 3090 |
| | ACTGATTT <u>C</u> TAAACTGT | 3091 |
| Non-polyposis colorectal cancer Gln301Term CAG-TAG | CTCCCACTATCTAAGGTAATTGTTCTCTCTTATTTTCTGACAG TTTAGAAATCAGTCCCC <u>A</u> GAATGTGGATGTTAATGTGCACCCC ACAAAGCATGAAGTTCACCTTCCTGCACGAGGAGA | 3092 |
| | TCTCCTCGTGCAGGAAGTGA <u>A</u> CTTCATGCTTTGTGGGGTGC CATTAAACATCCACATTCT <u>G</u> GGGACTGATTTCTAAACTGTCAGG AAAATAAGAGAGAACAATTACCTTAGATAGTGGGAG | 3093 |
| | TCAGTCCCC <u>A</u> GAATGTG | 3094 |
| | CACATTCT <u>G</u> GGGACTGA | 3095 |
| Non-polyposis colorectal cancer Val326Ala GTG-GCG | ATGTGCACCCCACAAAGCATGAAGTTCACCTCCTGCACGAGG AGAGCATCCTGGAGCGGGTGCAGCAGCACATCGAGAGCAAG CTCCTGGGCTCCAATTCCTCCAGGATGTACTTCACCCA | 3096 |
| | TGGGTGAAGTACATCCTGGAGGAATTGGAGCCCAGGAGCTT GCTCTCGATGTGCTGCTGC <u>A</u> CCCGCTCCAGGATGCTCTCCTC GTGCAGGAAGTGA <u>A</u> CTTCATGCTTTGTGGGGTGCACAT | 3097 |
| | GGAGCGGGTGCAGCAGC | 3098 |
| | GCTGCTGC <u>A</u> CCCGCTCC | 3099 |
| Non-polyposis colorectal cancer His329Pro CAC-CCC | CCACAAAGCATGAAGTTCACCTCCTGCACGAGGAGAGCATCC TGGAGCGGGTGCAGCAGC <u>A</u> CATCGAGAGCAAGCTCCTGGGC TCCAATTCCTCCAGGATGTACTTCACCCAGGTCAGGGC | 3100 |
| | GCCCTGACCTGGGTGAAGTACATCCTGGAGGAATTGGAGCC CAGGAGCTTGCTCTCGATGT <u>G</u> GCTGCTGCACCCGCTCCAGGAT GCTCTCCTCGTGCAGGAAGTGA <u>A</u> CTTCATGCTTTGTGG | 3101 |
| | GCAGCAGC <u>A</u> CATCGAGA | 3102 |
| | TCTCGATGT <u>G</u> GCTGCTGC | 3103 |
| Non-polyposis colorectal cancer Val384Asp GTT-GAT | CAAGTCTGACCTCGTCTTCTACTTCTGGAAGTAGTGATAAGGT CTATGCCACCAGATGGT <u>T</u> TCGTACAGATTCCCGGGAACAGAA GCTTGATGCATTTCTGCAGCCTCTGAGCAAACCCCT | 3104 |
| | AGGGGTTTGCTCAGAGGCTGCAGAAATGCATCAAGCTTCTGT TCCCGGGAATCTGTACGA <u>A</u> CCATCTGGTGGGCATAGACCTTA TCACTACTTCCAGAAAGTAGAAGACGAGGTCAGACTTG | 3105 |
| | CCAGATGGT <u>T</u> TCGTACAG | 3106 |
| | CTGTACGA <u>A</u> CCATCTGG | 3107 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Non-polyposis colorectal cancer Ala441Thr GCT-ACT | AGTGGCAGGGCTAGGCAGCAAGATGAGGAGATGCTTGAAC CCCAGCCCCTGCTGAAGTG <u>G</u> CTGCCAAAAATCAGAGCTTGA GGGGGATACAACAAAGGGGACTTCAGAAATGTCAGAGA | 3108 |
| | TCTCTGACATTTCTGAAGTCCCCTTTGTTGTATCCCCCTCAA GCTCTGATTTTTGGCAG <u>C</u> CACTTCAGCAGGGGCTGGGAGTTC AAGCATCTCCTCATCTTGCTGCCTAGCCCTGCCACT | 3109 |
| | CTGAAGTG <u>G</u> CTGCCAAA | 3110 |
| | TTTGGCAG <u>C</u> CACTTCAG | 3111 |
| Non-polyposis colorectal cancer Arg487Term CGA-TGA | CTTCATTGCAGAAAGAGACATCGGGAAGATTCTGATGTGGAA ATGGTGGAAGATGATTCC <u>C</u> GAAAGGAAATGACTGCAGCTTGT ACCCCCCGGAGAAGGATCATTAACTCACTAGTGT | 3112 |
| | AAACACTAGTGAGGTTAATGATCCTTCTCCGGGGGGTACAAG CTGCAGTCATTTCTTT <u>C</u> GGAATCATCTTCCACCATTTCAC ATCAGAATCTTCCCGATGTCTTTCTGCAATGAAG | 3113 |
| | ATGATTCC <u>C</u> GAAAGGAA | 3114 |
| | TTCCTTT <u>C</u> GGAATCAT | 3115 |
| Non-polyposis colorectal cancer Ala492Thr GCA-ACA | AGACATCGGGAAGATTCTGATGTGGAAATGGTGGAAGATGAT TCCCGAAAGGAAATGACT <u>G</u> CAGCTTGTACCCCCCGGAGAAG GATCATTAACTCACTAGTGTTTTGAGTCTCCAGGAAG | 3116 |
| | CTTCCTGGAGACTCAAAACACTAGTGAGGTTAATGATCCTTCT CCGGGGGGTACAAGCTG <u>C</u> AGTCATTTCTTTCCGGGAATCATC TTCCACCATTTCACATCAGAATCTTCCCGATGTCT | 3117 |
| | AAATGACT <u>G</u> CAGCTTGT | 3118 |
| | ACAAGCTG <u>C</u> AGTCATT | 3119 |
| Non-polyposis colorectal cancer Val506Ala GTT-GCT | CCCGAAAGGAAATGACTGCAGCTTGTACCCCCCGGAGAAGG ATCATTAACTCACTAGTG <u>T</u> TTTGAGTCTCCAGGAAGAAATTA ATGAGCAGGGACATGAGGGTACGTAAACGCTGTGGCC | 3120 |
| | GGCCACAGCGTTTACGTACCCTCATGTCCCTGCTCATTATTT CTTCCTGGAGACTCAAA <u>A</u> CACTAGTGAGGTTAATGATCCTTCT CCGGGGGGTACAAGCTGCAGTCATTTCTTTCCGGG | 3121 |
| | CACTAGTG <u>T</u> TTTGAGTC | 3122 |
| | GACTCAAA <u>A</u> CACTAGTG | 3123 |
| Non-polyposis colorectal cancer Gln542Leu CAG-CTG | GGGAGATGTTGCATAACCACTCCTTCGTGGGCTGTGTGAATC CTCAGTGGGCCTTGGCAC <u>A</u> GCATCAAACCAAGTTATACCTTC TCAACACCACCAAGCTTAGGTAAATCAGCTGAGTGTG | 3124 |
| | CACACTCAGCTGATTACCTAAGCTTGGTGGTGTGAGAAGG TATACTTGTTTTGATGCT <u>I</u> GTGCCAAGGCCCACTGAGGATTC ACACAGCCCACGAAGGAGTGGTTATGCAACATCTCCC | 3125 |
| | CTTGGCAC <u>A</u> GCATCAAA | 3126 |
| | TTTGATGCT <u>I</u> GTGCCAAG | 3127 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Non-polyposis colorectal cancer Leu549Pro CTT-CCT | CCTTCGTGGGCTGTGTGAATCCTCAGTGGGCCTTGGCACAG CATCAAACCAAGTTATACCTTCTCAACACCACCAAGCTTAGGT AAATCAGCTGAGTGTGTGAACAAGCAGAGCTACTACA | 3128 |
| | TGTAGTAGCTCTGCTTGTTACACACTCAGCTGATTTACCTAA GCTTGGTGGTGGTGGAGAAGGTATAACTTGGTTTGATGCTGTG CCAAGGCCCACTGAGGATTCACACAGCCCACGAAGG | 3129 |
| | GTTATACCTTCTCAACA | 3130 |
| | TGTTGAGAAGGTATAAC | 3131 |
| Non-polyposis colorectal cancer Asn551Thr AAC-ACC | TGGGCTGTGTGAATCCTCAGTGGGCCTTGGCACAGCATCAA CCAAGTTATACCTTCTCAACACCACCAAGCTTAGGTAAATCAG CTGAGTGTGTGAACAAGCAGAGCTACTACAACAATG | 3132 |
| | CATTGTTGTAGTAGCTCTGCTTGTTACACACTCAGCTGATTT ACCTAAGCTTGGTGGTGTGAGAAGGTATAACTTGGTTTGAT GCTGTGCCAAGGCCCACTGAGGATTCACACAGCCCA | 3133 |
| | CCTTCTCAACACCACCA | 3134 |
| | TGGTGGTGTGAGAAGG | 3135 |
| Non-polyposis colorectal cancer Gln562Term CAG-TAG | ATGAATTCAGCTTTTCCTTAAAGTCACTTCATTTTTATTTTCAG TGAAGAACTGTTCTACCAGATACTCATTTATGATTTTGCCAATT TTGGTGTTCAGGTTATCGGTAAGTTTAGATC | 3136 |
| | GATCTAACTTACCGATAACCTGAGAACACCAAAATTGGCAAA ATCATAAATGAGTATCTGGTAGAACAGTTCTTCACTGAAAATA AAAATGAAGTGACTTTAAGGAAAAGCTGAATTCAT | 3137 |
| | TGTTCTACCAGATACTC | 3138 |
| | GAGTATCTGGTAGAACA | 3139 |
| Non-polyposis colorectal cancer Ile565Phe ATT-TTT | GCTTTTCCTTAAAGTCACTTCATTTTTATTTTCAGTGAAGAACT GTTCTACCAGATACTCATTTATGATTTTGCCAATTTGGTGTTC TCAGGTTATCGGTAAGTTTAGATCCTTTTCACT | 3140 |
| | AGTGAAAAGGATCTAACTTACCGATAACCTGAGAACACCAAA ATTGGCAAAATCATAAATGAGTATCTGGTAGAACAGTTCTTCA CTGAAAATAAAATGAAGTGACTTTAAGGAAAAGC | 3141 |
| | AGATACTCATTTATGAT | 3142 |
| | ATCATAAATGAGTATCT | 3143 |
| Non-polyposis colorectal cancer Leu574Pro CTC-CCC | TTTTCAGTGAAGAACTGTTCTACCAGATACTCATTTATGATTTT GCCAATTTTGGTGTTCACAGGTTATCGGTAAGTTTAGATCCTT TTCACCTCTGAAATTTCAACTGATCGTTTCTGAA | 3144 |
| | TTCAGAAACGATCAGTTGAAATTTCAGAAGTGAAAAGGATCTA AACTTACCGATAACCTGAGAACACCAAAATTGGCAAAATCATA AATGAGTATCTGGTAGAACAGTTCTTCACTGAAAA | 3145 |
| | TGGTGTTCACAGTTAT | 3146 |
| | ATAACCTGAGAACACCA | 3147 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Non-polyposis colorectal cancer Leu582Val CTC-GTC | TGGATGCTCCGTTAAAGCTTGCTCCTTCATGTTCTTGCTTCTT CCTAGGAGCCAGCACCGCTCTTTGACCTTGCCATGCTTGCCT TAGATAGTCCAGAGAGTGGCTGGACAGAGGAAGATG | 3148 |
| | CATCTTCCTCTGTCCAGCCACTCTCTGGACTATCTAAGGCAA GCATGGCAAGGTCAAAGAAGCGGTGCTGGCTCCTAGGAAGAA GCAAGAACATGAAGGAGCAAGCTTTAACGGAGCATCCA | 3149 |
| | CAGCACCGCTCTTTGAC | 3150 |
| | GTCAAAGAAGCGGTGCTG | 3151 |
| Non-polyposis colorectal cancer Leu607His CTT-CAT | TGCTTGCCTTAGATAGTCCAGAGAGTGGCTGGACAGAGGAAG ATGGTCCCAAAGAAGGACTTGCTGAATACATTGTTGAGTTTCT GAAGAAGAAGGCTGAGATGCTTGCAGACTATTTCTC | 3152 |
| | GAGAAATAGTCTGCAAGCATCTCAGCCTTCTTCTTCAGAACT CAACAATGTATTAGCAAGTCCTTCTTTGGGACCATCTTCCTC TGTCAGCCACTCTCTGGACTATCTAAGGCAAGCA | 3153 |
| | AGAAGGACTTGCTGAAT | 3154 |
| | ATTCAGCAAGTCCTTCT | 3155 |
| Non-polyposis colorectal cancer Lys618Term AAG-TAG | ACAGAGGAAGATGGTCCCAAAGAAGGACTTGCTGAATACATT GTTGAGTTTCTGAAGAAGAAGGCTGAGATGCTTGCAGACTAT TTCTCTTTGGAAATTGATGAGGTGTGACAGCCATTCT | 3156 |
| | AGAATGGCTGTCACACCTCATCAATTTCCAAAGAGAAATAGTC TGCAAGCATCTCAGCCTTCTTCTTCAGAACTCAACAATGTAT TCAGCAAGTCCTTCTTTGGGACCATCTTCCTCTGT | 3157 |
| | TGAAGAAGAAGGCTGAG | 3158 |
| | CTCAGCCTTCTTCTTCA | 3159 |
| Non-polyposis colorectal cancer Lys618Thr AAG-ACG | CAGAGGAAGATGGTCCCAAAGAAGGACTTGCTGAATACATTG TTGAGTTTCTGAAGAAGAAGGCTGAGATGCTTGCAGACTATTT CTCTTTGGAAATTGATGAGGTGTGACAGCCATTCTT | 3160 |
| | AAGAATGGCTGTCACACCTCATCAATTTCCAAAGAGAAATAGT CTGCAAGCATCTCAGCCTTCTTCTTCAGAACTCAACAATGTA TTCAGCAAGTCCTTCTTTGGGACCATCTTCCTCTG | 3161 |
| | GAAGAAGAAGGCTGAGA | 3162 |
| | TCTCAGCCTTCTTCTTC | 3163 |
| Non-polyposis colorectal cancer Arg659Leu CGA-CTA | TACCCCTTCTGATTGACAACTATGTGCCCCCTTTGGAGGGAC TGCTATCTTCATTCTTCGACTAGCCACTGAGGTCAGTGATCA AGCAGATACTAAGCATTTCCGTACATGCATGTGTGC | 3164 |
| | GCACACATGCATGTACCGAAATGCTTAGTATCTGCTTGATCAC TGACCTCAGTGGCTAGTGAAGAATGAAGATAGGCAGTCCCT CCAAAGGGGGCACATAGTTGTCAATCAGAAGGGGTA | 3165 |
| | CATTCTTCGACTAGCCA | 3166 |
| | TGGCTAGTGAAGAATG | 3167 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Non-polyposis colorectal cancer Arg659Pro CGA-CCA | TACCCCTTCTGATTGACAACTATGTGCCCCCTTTGGAGGGAC TGCCATATCTTCATTCTTCGACTAGCCACTGAGGTCAGTGATCA AGCAGATACTAAGCATTTCGGTACATGCATGTGTGC | 3168 |
| | GCACACATGCATGTACCGAAATGCTTAGTATCTGCTTGATCAC TGACCTCAGTGGCTAGTCGAAGAATGAAGATAGGCAGTCCCT CCAAAGGGGGGCACATAGTTGTCAATCAGAAGGGGTA | 3169 |
| | CATTCTTCGACTAGCCA | 3170 |
| | TGGCTAGTCGAAGAATG | 3171 |
| Non-polyposis colorectal cancer Arg659Term CGA-TGA | TTACCCCTTCTGATTGACAACTATGTGCCCCCTTTGGAGGGA CTGCCTATCTTCATTCTTCGACTAGCCACTGAGGTCAGTGATC AAGCAGATACTAAGCATTTCGGTACATGCATGTGTG | 3172 |
| | CACACATGCATGTACCGAAATGCTTAGTATCTGCTTGATCACT GACCTCAGTGGCTAGTCCGAAGAATGAAGATAGGCAGTCCCTC CAAAGGGGGGCACATAGTTGTCAATCAGAAGGGGTAA | 3173 |
| | TCATTCTTCGACTAGCC | 3174 |
| | GGCTAGTCGAAGAATGA | 3175 |
| Non-polyposis colorectal cancer Ala681Thr GCT-ACT | TTGGACCAGGTGAATTGGGACGAAGAAAAGGAATGTTTTGAA AGCCTCAGTAAAGAATGCCGCTATGTTCTATTCCATCCGGAAG CAGTACATATCTGAGGAGTCGACCCTCTCAGGCCAGC | 3176 |
| | GCTGGCCTGAGAGGGTGCAGCTCCTCAGATATGTACTGCTTCC GGATGGAATAGAACATAGCGCATTCTTTACTGAGGCTTTCAA ACATTCTTTTCTTCGTCCCAATTCACCTGGTCCAA | 3177 |
| | AAGAATGCCGCTATGTTC | 3178 |
| | GAACATAGCGCATTCTT | 3179 |
| Non-polyposis colorectal cancer Trp712Term TGG-TAG | AGGCTTATGACATCTAATGTGTTTTCCAGAGTGAAGTGCCTG GCTCCATTCCAACTCCTGGAAGTGGACTGTGGAACACATTG TCTATAAAGCCTTGCGCTCACACATTCTGCCTCCTAA | 3180 |
| | TTAGGAGGCAGAATGTGTGAGCGCAAGGCTTTATAGACAATG TGTTCCACAGTCCACTTCCAGGAGTTTGAATGGAGCCAGGC ACTTCACTCTGGAACACATTAGATGTCATAAGCCT | 3181 |
| | AAACTCCTGGAAGTGGA | 3182 |
| | TCCACTTCCAGGAGTTT | 3183 |
| Non-polyposis colorectal cancer Trp714Term TGG-TAG | ATGACATCTAATGTGTTTTCCAGAGTGAAGTGCCTGGCTCCAT TCCAAACTCCTGGAAGTGGAAGTGTGGAACACATTGTCTATAAA GCCTTGCGCTCACACATTCTGCCTCCTAAACATTT | 3184 |
| | AAATGTTTAGGAGGCAGAATGTGTGAGCGCAAGGCTTTATAG ACAATGTGTTCCACAGTCCACTTCCAGGAGTTTGAATGGAG CCAGGCACTTCACTCTGGAAAACACATTAGATGTCAT | 3185 |
| | CTGGAAGTGGAAGTGTGG | 3186 |
| | CCACAGTCCACTTCCAG | 3187 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Non-polyposis colorectal cancer Trp714Term TGG-TGA | TGACATCTAATGTGTTTTCCAGAGTGAAGTGCCTGGCTCCATT CCAACTCCTGGAAGTG <u>G</u> ACTGTGGAACACATTGTCTATAAA GCCTTGCGCTCACACATTCTGCCTCCTAAACATTTTC | 3188 |
| | GAAATGTTTAGGAGGCAGAATGTGTGAGCGCAAGGCTTTATA GACAATGTGTTCCACAGT <u>C</u> CACTTCCAGGAGTTTGGAATGGA GCCAGGCACTTCACTCTGGAAAACACATTAGATGTCA | 3189 |
| | TGGAAGTG <u>G</u> ACTGTGGA | 3190 |
| | TCCACAGT <u>C</u> CACTTCCA | 3191 |
| Non-polyposis colorectal cancer Val716Met GTG-ATG | ATCTAATGTGTTTTCCAGAGTGAAGTGCCTGGCTCCATTCCAA ACTCCTGGAAGTGGACT <u>G</u> TGGAACACATTGTCTATAAAGCCT TGCGCTCACACATTCTGCCTCCTAAACATTTTCACAG | 3192 |
| | CTGTGAAATGTTTAGGAGGCAGAATGTGTGAGCGCAAGGCTT TATAGACAATGTGTTCCACAGTCCACTTCCAGGAGTTTGGAAT GGAGCCAGGCACTTCACTCTGGAAAACACATTAGAT | 3193 |
| | AGTGGACT <u>G</u> TGGAACAC | 3194 |
| | GTGTTCCACAGTCCACT | 3195 |
| Non-polyposis colorectal cancer Tyr721Term TAT-TAA | GAGTGAAGTGCCTGGCTCCATTCCAACTCCTGGAAGTGGAC TGTGGAACACATTGTCTATAAAGCCTTGCGCTCACACATTCTG CCTCCTAAACATTTACAGAAGATGGAAATATCCTG | 3196 |
| | CAGGATATTTCCATCTTCTGTGAAATGTTTAGGAGGCAGAATG TGTGAGCGCAAGGCTTT <u>A</u> TAGACAATGTGTTCCACAGTCCAC TTCCAGGAGTTTGGAATGGAGCCAGGCACTTCACTC | 3197 |
| | ATTGTCTATAAAGCCTT | 3198 |
| | AAGGCTTTATAGACAAT | 3199 |
| Non-polyposis colorectal cancer Lys751Arg AAA-AGA | CTAAACATTTACAGAAGATGGAAATATCCTGCAGCTTGCTAA CCTGCCTGATCTATACA <u>A</u> AGTCTTTGAGAGGTGTTAAATATGG TTATTTATGCACTGTGGGATGTGTTCTTCTTTCTC | 3200 |
| | GAGAAAGAAGAACACATCCACAGTGCATAAATAACCATATTT AACACCTCTCAAAGACTTTGTATAGATCAGGCAGGTTAGCAA GCTGCAGGATATTTCCATCTTCTGTGAAATGTTTAG | 3201 |
| | TCTATACA <u>A</u> AGTCTTTG | 3202 |
| | CAAAGACTTTGTATAGA | 3203 |
| Non-polyposis colorectal cancer Arg755Trp AGG-TGG | ACAGAAGATGGAAATATCCTGCAGCTTGCTAACCTGCCTGAT CTATACAAAGTCTTTGAGAGGTGTTAAATATGGTTATTTATGC ACTGTGGGATGTGTTCTTCTTTCTCTGTATTCCGAT | 3204 |
| | ATCGGAATACAGAGAAAGAAGAACACATCCACAGTGCATAA ATAACCATATTTAACACCTCTCAAAGACTTTGTATAGATCAGG CAGGTTAGCAAGCTGCAGGATATTTCCATCTTCTGT | 3205 |
| | TCTTTGAGAGGTGTTAA | 3206 |
| | TTAACACCTCTCAAAGA | 3207 |

EXAMPLE 19

Human mismatch repair - MSH2

[0231] The human MSH2 gene is homologous to the bacterial *mutS* gene, which is involved in mismatch repair. Mutations in the MSH2 gene have been identified in a variety of cancers, including, for example, ovarian tumors, colorectal cancer, endometrial cancer, uterine cancer. The attached table discloses the correcting oligonucleotide base sequences for the MSH2 oligonucleotides of the invention.

Table 21

MSH2 Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Non polyposis colorectal cancer Gln252Term CAG-TAG | TTTTCCACAAAAGACATTTATCAGGACCTCAACCGGTTGTTGA AAGGCAAAAAGGGAGAGCAGATGAATAGTGCTGTATTGCCAG AAATGGAGAATCAGGTACATGGATTATAAATGTGAA | 3208 |
| | TTCACATTTATAATCCATGTACCTGATTCTCCATTTCTGGCAAT ACAGCACTATTCATCTGCTCTCCCTTTTTGCCTTTCAACAACC GGTTGAGGTCCTGATAAATGTCTTTTGTGGAAAA | 3209 |
| | AGGGAGAGCAGATGAAT | 3210 |
| | ATTCATCTGCTCTCCCT | 3211 |
| Non polyposis colorectal cancer Gln288Term CAG-TAG | TCATCACTGTCTGCGGTAATCAAGTTTTTAGAACTCTTATCAG ATGATTCCAACCTTTGGACAGTTTGAAGTACTACTTTTGACTT CAGCCAGTATATGAAATTGGATATTGCAGCAGTCA | 3212 |
| | TGACTGCTGCAATATCCAATTTTCACTACTGGCTGAAGTCAAA AGTAGTCAGTTCAAAGTGTCCAAAGTTGGAATCATCTGATAAG AGTTCTAAAACTTGATTACCGCAGACAGTGATGA | 3213 |
| | ACTTTGGACAGTTTGAA | 3214 |
| | TTCAAAGTGTCCAAAGT | 3215 |
| Non polyposis colorectal cancer Ala305Thr GCA-ACA | AACCTTTGGACAGTTTGAAGTACTACTTTTGACTTCAGCCAGT ATATGAAATTGGATATTGCAGCAGTCAGAGCCCTTAACCTTTT TCAGGTAAAAAAAAAAAAAAAAAAAAAAAAAAGG | 3216 |
| | CCTTTTTTTTTTTTTTTTTTTTTTTTTTTTACCTGAAAAAGGTTAA GGGCTCTGACTGCTGCAATATCCAATTTTCACTACTGGCTGAA GTCAAAGTAGTCAGTTCAAAGTGTCCAAAGTT | 3217 |
| | TGGATATTGCAGCAGTC | 3218 |
| | GACTGCTGCAATATCCA | 3219 |
| Non polyposis colorectal cancer Gly322Asp GGC-GAC | AGCTTGCCATTCTTTCTATTTTATTTTTGTTTACTAGGGTTCT GTTGAAGATACCACTGGCTCTCAGTCTCTGGCTGCCTTGCTG AATAAGTGTAACCCCTCAAGGACAAAGACTTGT | 3220 |
| | ACAAGTCTTTGTCCTTGAGGGGTTTTACTTATTTCAGCAAGG CAGCCAGAGACTGAGAGCCAGTGGTATCTTCAACAGAACCCCT AGTAAACAAAAATAAATAGAAAGAATGGCAAGCT | 3221 |
| | TACCACTGGCTCTCAGT | 3222 |
| | ACTGAGAGCCAGTGGTA | 3223 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Non polyposis colorectal cancer Ser323Cys TCT-TGT | TTGCCATTCTTTCTATTTTATTTTTGTTTACTAGGGTTCTGTT GAAGATACCACTGGCTCTCAGTCTCTGGCTGCCTTGCTGAAT AAGTGTAACCCCTCAAGGACAAAGACTTGTTAA | 3224 |
| | TTAACAAGTCTTTGTCCTTGAGGGGTTTTACACTTATTCAGCA AGGCAGCCAGAGACTGAGAGCCAGTGGTATCTTCAACAGAAC CCTAGTAAACAAAAAATAAAATAGAAAGAATGGCAA | 3225 |
| | CACTGGCTCTCAGTCTC | 3226 |
| | GAGACTGAGAGCCAGTG | 3227 |
| Non polyposis colorectal cancer Arg383Term CGA-TGA | GTGGAAGCTTTTGTAGAAGATGCAGAATTGAGGCAGACTTTA CAAGAAGATTTACTTCGTCTGATTCCCAGATCTTAACCGACTTG CCAAGAAGTTTCAAAGACAAGCAGCAAACCTTACAAG | 3228 |
| | CTTGTAAGTTTGCTGCTTGTCTTTGAACTTCTTGGAAGTCG GTTAAGATCTGGGAATCGACGAAGTAAATCTTCTGTAAAGTC TGCCTCAATTCTGCATCTTCTACAAAAGCTTCCAC | 3229 |
| | TACTTCGTCTGATTCCCA | 3230 |
| | TGGGAATCGACGAAGTA | 3231 |
| Non polyposis colorectal cancer Gln397Term CAA-TAA | CAAGAAGATTTACTTCGTCTGATTCCCAGATCTTAACCGACTTG CCAAGAAGTTTCAAAGACAAGCAGCAAACCTTACAAGATTGTTA CCGACTCTATCAGGGTATAAATCAACTACCTAATG | 3232 |
| | CATTAGGTAGTTGATTTATACCCTGATAGAGTCGGTAACAATC TTGTAAGTTTGCTGCTTGCTTTGAACTTCTTGGAAGTCGG TTAAGATCTGGGAATCGACGAAGTAAATCTTCTTG | 3233 |
| | TTCAAAGACAAGCAGCA | 3234 |
| | TGCTGCTTGCTTTGAA | 3235 |
| Non polyposis colorectal cancer Arg406Term CGA-TGA | GATCTTAACCGACTTGCCAAGAAGTTTCAAAGACAAGCAGCA AACTTACAAGATTGTTACCGACTCTATCAGGGTATAAATCAAC TACCTAATGTTATACAGGCTCTGGAAAAACATGAAG | 3236 |
| | CTTCATGTTTTTCCAGAGCCTGTATAACATTAGGTAGTTGATTT ATACCCTGATAGAGTCGGTAACAATCTTGTAAAGTTTGCTGCTT GTCTTTGAACTTCTTGGAAGTCGGTTAAGATC | 3237 |
| | ATTGTTACCGACTCTAT | 3238 |
| | ATAGAGTCGGTAACAAT | 3239 |
| Non polyposis colorectal cancer Gln419Term CAG-TAG | GCAAACCTACAAGATTGTTACCGACTCTATCAGGGTATAAATC AACTACCTAATGTTATACAGGCTCTGGAAAAACATGAAGGTAA CAAGTGATTTTGTGTTTTGTTTTCTTCAACTCA | 3240 |
| | TGAGTTGAAGGAAAACAAAAAACAATCACTTGTTACCTTC ATGTTTTTCCAGAGCCTGTATAACATTAGGTAGTTGATTTATAC CCTGATAGAGTCGGTAACAATCTTGTAAAGTTTGC | 3241 |
| | ATGTTATACAGGCTCTG | 3242 |
| | CAGAGCCTGTATAACAT | 3243 |
| Non polyposis colorectal cancer Gln429Term | TATTCTGTAAATGAGATCTTTTTATTTGTTTGTGTTTACTACTTT CTTTTAGGAAAACACCAGAAATTATTGTTGGCAGTTTTTGTGA CTCCTCTTACTGATCTTCGTTCTGACTTCTCCA | 3244 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| CAG-TAG | TGGAGAAGTCAGAACGAAGATCAGTAAGAGGAGTCACAAAAA CTGCCAACAAATAATTTCTGGTGTTCCTAAAAAGAAAGTAGTA AAACAAACAAATAAAAAGATCTCATTCTTACAGAATA | 3245 |
| | GAAAACACCAGAAATTA | 3246 |
| | TAATTTCTGGTGTTC | 3247 |
| Non polyposis colorectal cancer Leu458Term TTA-TGA | CTCCTCTTACTGATCTTCGTTCTGACTTCTCCAAGTTTCAGGA AATGATAGAAACAACCTTAGATATGGATCAGGTATGCAATATA CTTTTAAATTAAGCAGTAGTTATTTTAAAAAGC | 3248 |
| | GCTTTTAAAAATAACTACTGCTTAAATTAAGTATATTGCA TACCTGATCCATATCTAAAGTTGTTTCTATCATTTCTGAACT TGGAGAAGTCAGAACGAAGATCAGTAAGAGGAG | 3249 |
| | AACAACCTTAGATATGG | 3250 |
| | CCATATCTAAAGTTGTT | 3251 |
| Non polyposis colorectal cancer Gln518Term CAG-TAG | TTTCTTCTTGATTATCAAGGCTTGGACCCTGGCAAACAGATTA AACTGGATTCCAGTGCAAGTTTGGATATTACTTTCTGTAAAC CTGTAAGGAAGAAAAAGTCCTTCGTAACAATAAAA | 3252 |
| | TTTTATTGTTACGAAGGACTTTTCTTCTTACAGGTTACACGA AAGTAATATCCAACTGTGCACTGGAATCCAGTTAATCTGTT TGCCAGGGTCCAAGCCTTGATAATCAAGAAGAAA | 3253 |
| | CCAGTGCAAGTTTGA | 3254 |
| | TCCAACTGTGCACTGG | 3255 |
| Non polyposis colorectal cancer Arg524Pro CGT-CCT | GCTTGGACCCTGGCAAACAGATTAACTGGATTCCAGTGCAAC AGTTTGGATATTACTTTCTGTGAACCTGTAAGGAAGAAAAAGT CCTTCGTAACAATAAAAACTTTAGTACTGTAGATAT | 3256 |
| | ATATCTACAGTACTAAAGTTTTTATTGTTACGAAGGACTTTTTC TTCCTTACAGGTTACAGGAAAGTAATATCCAACTGTGCACTG GAATCCAGTTAATCTGTTTGCCAGGGTCCAAGC | 3257 |
| | TTACTTTCTGTAACT | 3258 |
| | AGGTTACAGGAAAGTAA | 3259 |
| Non polyposis colorectal cancer Glu562Val GAG-GTG | TTAATATTTTTAATAAACTGTTATTTGATTTGCAGCAAATTG ACTTCTTTAAATGAAGAGTATACCAAAAATAAAACAGAATATG AAGAAGCCCAGGATGCCATTGTTAAAGAAATTGT | 3260 |
| | ACAATTTCTTTAACAATGGCATCCTGGGCTTCTTCATATTCTGT TTTATTTTGGTATACCTTCATTAAAGAAGTCAATTTGCTGC AAATCGAAATAACAGTTTATTAATAAATATTAA | 3261 |
| | AAATGAAGAGTATACCA | 3262 |
| | TGGTATACCTTCATT | 3263 |
| Glioma Glu580Term GAA-TAA | AATGAAGAGTATACCAAAAATAAAACAGAATATGAAGAAGCCC AGGATGCCATTGTTAAAGAAATTGTCAATATTTCTTCAGGTAA ACTTAATAGAACTAATAATGTTCTGAATGTCACCT | 3264 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | AGGTGACATTCAGAACATTATTAGTTCTATTAAGTTTACCTGAA GAAATATTGACAATTTCTTTAACAATGGCATCCTGGGCTTCTT CATATTCTGTTTTATTTTTGGTATACTCTTCATT | 3265 |
| | TTGTTAAAGAAATTGTC | 3266 |
| | GACAATTTCTTTAACAA | 3267 |
| Non polyposis colorectal cancer Gln601Term CAG-TAG | TGTTTTATTTTTATACAGGCTATGTAGAACCAATGCAGACACT CAATGATGTGTTAGCTCAGCTAGATGCTGTTGTCAGCTTTGCT CACGTGTCAAATGGAGCACCTGTTCCATATGTAC | 3268 |
| | GTACATATGGAACAGGTGCTCCATTTGACACGTGAGCAAAGC TGACAACAGCATCTAGCTGAGCTAACACATCATTGAGTGTCT GCATTGGTTCTACATAGCCTGTATAAAAAATAAAACA | 3269 |
| | TGTTAGCTCAGCTAGAT | 3270 |
| | ATCTAGCTGAGCTAACA | 3271 |
| Non polyposis colorectal cancer Tyr619Term TAT-TAG | AGCTCAGCTAGATGCTGTTGTCAGCTTTGCTCACGTGTCAAAT GGAGCACCTGTTCCATATGTACGACCAGCCATTTTGGAGAAA GGACAAGGAAGAATTATATTAAGCATCCAGGCAT | 3272 |
| | ATGCCTGGATGCTTTTAATATAATTCTTCCTTGTCCTTTCTCCA AAATGGCTGGTCGTACATATGGAACAGGTGCTCCATTTGACA CGTGAGCAAAGCTGACAACAGCATCTAGCTGAGCT | 3273 |
| | GTTCCATATGTACGACC | 3274 |
| | GGTCGTACATATGGAAC | 3275 |
| Non polyposis colorectal cancer Arg621Term CGA-TGA | CAGCTAGATGCTGTTGTCAGCTTTGCTCACGTGTCAAATGGA GCACCTGTTCCATATGTACGACCAGCCATTTTGGAGAAAGGA CAAGGAAGAATTATATTAAGCATCCAGGCATGCTT | 3276 |
| | AAGCATGCCTGGATGCTTTTAATATAATTCTTCCTTGTCCTTTC TCCAAAATGGCTGGTCGTACATATGGAACAGGTGCTCCATTT GACACGTGAGCAAAGCTGACAACAGCATCTAGCTG | 3277 |
| | CATATGTACGACCAGCC | 3278 |
| | GGCTGGTCGTACATATG | 3279 |
| Non polyposis colorectal cancer Pro622Leu CCA-CTA | TAGATGCTGTTGTCAGCTTTGCTCACGTGTCAAATGGAGCAC CTGTTCCATATGTACGACCAGCCATTTTGGAGAAAGGACAAG GAAGAATTATATTAAGCATCCAGGCATGCTTGTGT | 3280 |
| | ACACAAGCATGCCTGGATGCTTTTAATATAATTCTTCCTTGTC CTTTCTCCAAAATGGCTGGTCGTACATATGGAACAGGTGCTC CATTTGACACGTGAGCAAAGCTGACAACAGCATCTA | 3281 |
| | TGTACGACCAGCCATTT | 3282 |
| | AAATGGCTGGTCGTACA | 3283 |
| Non polyposis colorectal cancer Ala636Pro | CCTGTTCCATATGTACGACCAGCCATTTTGGAGAAAGGACAA GGAAGAATTATATTAAGCATCCAGGCATGCTTGTGTTGAAG TTCAAGATGAAATTGCATTTATTCCTAATGACGTAT | 3284 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| GCA-CCA | ATACGTCATTAGGAATAAATGCAATTTTCATCTTGAACCTTCAACA CAAGCATGCCTGGATGCTTTTAATATAATTCTTCCTTGTCCCTT CTCCAAAATGGCTGGTCGTACATATGGAACAGG | 3285 |
| | TATTTAAAGCATCCAGG | 3286 |
| | CCTGGATGCTTTTAATA | 3287 |
| Non polyposis colorectal cancer His639Arg CAT-CGT | ATGTACGACCAGCCATTTTGGAGAAAGGACAAGGAAGAATTA TATTTAAAGCATCCAGGCATGCTTGTGTTGAAGTTCAAGATGA AATTGCATTTATTCCTAATGACGTATACTTTGAAAA | 3288 |
| | TTTTCAAAGTATACGTCATTAGGAATAAATGCAATTTTCATCTTG AACTTCAACACAAGCATGCCTGGATGCTTTTAATATAATTCTT CCTTGTCTTTCTCCAAAATGGCTGGTCGTACAT | 3289 |
| | ATCCAGGCATGCTTGTG | 3290 |
| | CACAAGCATGCCTGGAT | 3291 |
| Non polyposis colorectal cancer His639Tyr CAT-TAT | TATGTACGACCAGCCATTTTGGAGAAAGGACAAGGAAGAATT ATATTTAAAGCATCCAGGCATGCTTGTGTTGAAGTTCAAGATG AAATTGCATTTATTCCTAATGACGTATACTTTGAAA | 3292 |
| | TTTCAAAGTATACGTCATTAGGAATAAATGCAATTTTCATCTTGA ACTTCAACACAAGCATGCCTGGATGCTTTTAATATAATTCTTC CTTGTCTTTCTCCAAAATGGCTGGTCGTACATA | 3293 |
| | CATCCAGGCATGCTTGT | 3294 |
| | ACAAGCATGCCTGGATG | 3295 |
| Non polyposis colorectal cancer Glu647Lys GAA-AAA | AAAGGACAAGGAAGAATTATATTTAAAGCATCCAGGCATGCTT GTGTTGAAGTTCAAGATGAAATTGCATTTATTCCTAATGACGT ATACTTTGAAAAAGATAAACAGATGTTCCACATCA | 3296 |
| | TGATGTGGAACATCTGTTTATCTTTTCAAAGTATACGTCATTA GGAATAAATGCAATTTTCATCTTGAACCTTCAACACAAGCATGCC TGGATGCTTTTAATATAATTCTTCCTTGTCCCTT | 3297 |
| | TTCAAGATGAAATTGCA | 3298 |
| | TGCAATTTTCATCTTGAA | 3299 |
| Non polyposis colorectal cancer Tyr656Term TAC-TAG | ATCCAGGCATGCTTGTGTTGAAGTTCAAGATGAAATTGCATTT ATTCCTAATGACGTATACCTTTGAAAAAGATAAACAGATGTTCC ACATCATTACTGGTAAAAAACCTGGTTTTTGGGCT | 3300 |
| | AGCCCCAAAACCAGGTTTTTTACCAGTAATGATGTGGAACATC TGTTTATCTTTTTCAAAGTATACGTCATTAGGAATAAATGCAAT TTCATCTTGAACCTTCAACACAAGCATGCCTGGAT | 3301 |
| | GACGTATACCTTTGAAAA | 3302 |
| | TTTTCAAAGTATACGTC | 3303 |
| Non polyposis colorectal cancer Gly674Asp GGT-GAT | GAAAGAAGTTTAAATCTTGCTTTCTGATATAATTTGTTTTGTA GGCCCCAATATGGGAGGTAAATCAACATATATTCGACAACT GGGGTGATAGTACTCATGGCCCAAATTGGGTGTTT | 3304 |
| | AAACACCCAATTTGGGCCATGAGTACTATCACCCCAAGTTTGTC GAATATATGTTGATTTACCTCCCATATTGGGGCCTACAAAACA AATTATATCAGAAAGCAAGATTTTAACTTCTTTC | 3305 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | TATGGGAGGTAAATCAA | 3306 |
| | TTGATTTACCTCCATA | 3307 |
| Non polyposis colorectal cancer Arg680Term CGA-TGA | TTGCTTTCTGATATAATTTGTTTTGTAGGCCCAATATGGGAG GTAAATCAACATATATTGACAAACTGGGGTGATAGTACTCAT GGCCCAAATTGGGTGTTTTGTGCCATGTGAGTCAG | 3308 |
| | CTGACTCACATGGCACAAAACACCCAATTTGGGCCATGAGTA CTATCACCCCAGTTTGTCCGAATATATGTTGATTTACCTCCCAT ATTGGGGCCTACAAAACAAATTATATCAGAAAGCAA | 3309 |
| | CATATATTGACAAACT | 3310 |
| | AGTTTGTCCGAATATATG | 3311 |
| Non polyposis colorectal cancer Gly692Arg GGG-CGG | ATGGGAGGTAAATCAACATATATTGACAAACTGGGGTGATA GACTCATGGCCCAAATTGGGTGTTTTGTGCCATGTGAGTCA GCAGAAGTGTCATTGTGGACTGCATCTTAGCCCGAG | 3312 |
| | CTCGGGCTAAGATGCAGTCCACAATGGACACTTCTGCTGACT CACATGGCACAAAACACCCCAATTTGGGCCATGAGTACTATCA CCCAGTTTGTCTGAATATATGTTGATTTACCTCCCAT | 3313 |
| | CCCAAATTGGGTGTTTT | 3314 |
| | AAAACACCCCAATTTGGG | 3315 |
| Non polyposis colorectal cancer Cys697Arg TGT-CGT | ACATATATTGACAAACTGGGGTGATAGTACTCATGGCCCAA ATTGGGTGTTTTGTGCCATGTGAGTCAGCAGAAGTGTCCATT GTGGACTGCATCTTAGCCCGAGTAGGGGCTGGTGACA | 3316 |
| | TGTCACCAGCCCCTACTCGGGCTAAGATGCAGTCCACAATGG ACACTTCTGCTGACTCACATGGCACAAAACACCCAATTTGGG CCATGAGTACTATCACCCAGTTTGTCTGAATATATGT | 3317 |
| | TTGTGCCATGTGAGTCA | 3318 |
| | TGACTCACATGGCACAA | 3319 |
| Non polyposis colorectal cancer Cys697Phe TGT-TTT | CATATATTGACAAACTGGGGTGATAGTACTCATGGCCCAAAT TGGGTGTTTTGTGCCATGTGAGTCAGCAGAAGTGTCCATTGT GGACTGCATCTTAGCCCGAGTAGGGGCTGGTGACAG | 3320 |
| | CTGTACCAGCCCCTACTCGGGCTAAGATGCAGTCCACAATG GACACTTCTGCTGACTCACATGGCACAAAACACCCAATTTGG GCCATGAGTACTATCACCCAGTTTGTCTGAATATATG | 3321 |
| | TGTGCCATGTGAGTCAG | 3322 |
| | CTGACTCACATGGCACA | 3323 |
| Non polyposis colorectal cancer Gln718Term CAA-TAA | GAGTCAGCAGAAGTGTCCATTGTGGACTGCATCTTAGCCCGA GTAGGGGCTGGTGACAGTCAATTGAAAGGAGTCTCCACGTTT ATGGCTGAAATGTTGGAACTGCTTCTATCCTCAGGT | 3324 |
| | ACCTGAGGATAGAAGCAGTTTCCAACATTTAGCCATGAACG TGGAGACTCCTTTCAATTGACTGTCACCAGCCCCTACTCGGG CTAAGATGCAGTCCACAATGGACACTTCTGCTGACTC | 3325 |
| | GTGACAGTCAATTGAAA | 3326 |
| | TTTCAATTGACTGTCAC | 3327 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Non polyposis colorectal cancer Leu811Term TTA-TGA | CCAATCAGATACCAACTGTTAATAATCTACATGTCACAGCACT CACCAGTGAAGAGACCTTAACTATGCTTTATCAGGTGAAGAAA GGTATGTACTATTGGAGTACTCTAAATTCAGAACT | 3328 |
| | AGTTCTGAATTTAGAGTACTCCAATAGTACATACCTTTCTTCAC CTGATAAAGCATAGTTAAGGTCTCTTCAGTGGTGAGTGCTGT GACATGTAGATTATTAACAGTTGGTATCTGATTGG | 3329 |
| | AGAGACCTTAACTATGC | 3330 |
| | GCATAGTTAAGGTCTCT | 3331 |
| Non polyposis colorectal cancer Ala834Thr GCT-ACT | TTCCCCAAATTTCTTATAGGTGTCTGTGATCAAAGTTTTGGGA TTCATGTTGCAGAGCTTGCTAATTTCCCTAAGCATGTAATAGA GTGTGCTAAACAGAAAGCCCTGGAAGTTGAGGAGT | 3332 |
| | ACTCCTCAAGTTCCAGGGCTTTCTGTTTAGCACACTCTATTAC ATGCTTAGGGAAATTAGCAAGCTCTGCAACATGAATCCCCAAA CTTTGATCACAGACACCTATAAGAAATTTGGGGAA | 3333 |
| | CAGAGCTTGCTAATTC | 3334 |
| | GAAATTAGCAAGCTCTG | 3335 |
| Non polyposis colorectal cancer Gln861Term CAA-TAA | ATAGAGTGTGCTAAACAGAAAGCCCTGGAAGTTGAGGAGTTT CAGTATATTGGAGAATCGCAAGGATATGATATCATGGAACCA GCAGCAAAGAAGTGCTATCTGGAAAGAGAGGTTTGTC | 3336 |
| | GACAAACCTCTCTTTCCAGATAGCACTTCTTTGCTGCTGGTTC CATGATATCATATCCTTGCGATTCTCCAATATACTGAACTCC TCAAGTTCCAGGGCTTTCTGTTTAGCACACTCTAT | 3337 |
| | GAGAATCGCAAGGATAT | 3338 |
| | ATATCCTTGCGATTCTC | 3339 |
| Non polyposis colorectal cancer Thr905Arg ACA-AGA | AGGAGTTCCTGTCCAAGGTGAAACAAATGCCCTTTACTGAAAT GTCAGAAGAAAACATCACAATAAAGTTAAACAGCTAAAAGCT GAAGTAATAGCAAAGAATAATAGCTTTGTAAATGA | 3340 |
| | TCATTTACAAAGCTATTATTCTTTGCTATTACTTCAGCTTTTAG CTGTTTTAACTTTATTGTGATGTTTTCTTCTGACATTCAGTAA AGGGCATTGTGTTTACCTTGGACAGGAACCTCT | 3341 |
| | AAACATCACAATAAAGT | 3342 |
| | ACTTTATTGTGATGTTT | 3343 |

EXAMPLE 20

Human mismatch repair - MSH6

[0232] The human MSH6 gene is homologous to the bacterial *mutS* gene, which is involved in mismatch repair. Mutations in the MSH6 gene have been identified in a variety of cancers, including particularly hereditary nonpolyposis colorectal cancer. The attached table discloses the correcting oligonucleotide base sequences for the MSH6 oligonucleotides of the invention.

Table 22

MSH6 Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Non-polypoid colorectal cancer Ser144Ile AGC-ATC | GGAAATCAGTCCGTGTTTCATGTACAGTTTTTTGATGACAGCCC AACAAAGGGGCTGGGTTAGCAAAGGCTTTTAAAGCCATATAC AGGTAAGAGTCACTACTGCCATGTGTGTGTGTTGT | 3344 |
| | ACAAACACACACACATGGCAGTAGTACTCTTACCTGTATATG GCTTTAAAGCCTTTTGCTAACCAGCCCCCTTGTGGGCTGT CATCAAAAACTGTACATGAACACGGACTGATTTCC | 3345 |
| | CTGGGTTAGCAAAGGC | 3346 |
| | GCCTTTTGCTAACCAG | 3347 |
| Endometrial cancer Ser156Term TCA-TGA | CGTGAGCCTCTGCACCCGGCCCTTATTGTTTATAAATACATTT CTTTCTAGGTTCAAATCAAAGGAAGCCCAGAAGGGAGGTCA TTTTTACAGTGCAAAGCCTGAAATACTGAGAGCAAT | 3348 |
| | ATTGCTCTCAGTATTTAGGCTTTGCACTGTAAAAATGACCTC CCTTCTGGGCTTCCTTTGATTTGAACCTAGAAAGAAATGTAT TTATAACAATAAGGGCCGGGTGCAGAGGCTCACG | 3349 |
| | TTCAAATCAAAGGAAG | 3350 |
| | CTTCCTTTGATTTTGAA | 3351 |
| Early onset colorectal cancer Tyr214Term TAC-TAG | TTCCAAATTTGATTTGTTTTAAATACTCTTTCCTTGCCTGGC AGGTAGGCACAACCTACGTAACAGATAAGAGTGAAGAAGATA ATGAAATTGAGAGTGAAGAGGAAGTACAGCCTAAG | 3352 |
| | CTTAGGCTGTACTTCCTCTTCACTCTCAATTTCAATTATCTTCTT CACTCTTATCTGTTACGTAAGTTGTGCCTACCTGCCAGGCAA GGAAAGAGTATTTAAAAACAAATCAAATTTTGAA | 3353 |
| | ACAACCTACGTAACAGA | 3354 |
| | TCTGTTACGTAAGTTGT | 3355 |
| Endometrial cancer Arg248Term CGA-TGA | GAAGAGGAAGTACAGCCTAAGACACAAGGATCTAGGCGAAGT AGCCGCCAAATAAAAAACGAAGGGTCATATCAGATTCTGAG AGTGACATTGGTGGCTCTGATGTGGAATTTAAGCCAG | 3356 |
| | CTGGCTTAAATTCCACATCAGAGCCACCAATGTCACCTCTCAGA ATCTGATATGACCCTTCGTTTTTTTATTTGGCGGCTACTTCGC CTAGATCCTTGTGTCTTAGGCTGTACTTCCTCTTC | 3357 |
| | TAAAAAACGAAGGGTC | 3358 |
| | GACCCTTCGTTTTTTTA | 3359 |
| Colorectal cancer Ser285Ile AGT-ATT | TTAAGCCAGACACTAAGGAGGAAGGAAGCAGTGATGAAATAA GCAGTGGAGTGGGGGATAGTGAGAGTGAAGGCCTGAACAGC CCTGTCAAAGTTGCTCGAAAGCGGAAGAGAATGGTGAC | 3360 |
| | GTCACCATTCTCTCCGCTTTCGAGCAACTTTGACAGGGCTG TTCAGGCCCTTCACTCTCACTATCCCCCACTCCACTGCTTATTT CATCACTGCTTCCTTCCTCCTTAGTGTCTGGCTTAA | 3361 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | GGGGGATAGTGAGAGTG | 3362 |
| | CACTCTCACTATCCCCC | 3363 |
| Colorectal cancer Gly566Arg GGA-AGA | GAGGAAGATTCTTCTGGCCATACTCGTG CATATGGTGTGTGC TTTGTTGATACTTCACTGGGAAAGTTTTTCATAGGTCAGTTTTC AGATGATCGCCATTGTTTCGAGATTTAGGACTCTAG | 3364 |
| | CTAGAGTCCTAAATCTCGAACAATGGCGATCATCTGAAAAGT ACCTATGAAAAACTTTCCAGTGAAGTATCAACAAAGCACACA CCATATGCACGAGTATGGCCAGAAGAATCTTCCTC | 3365 |
| | CTTCACTGGGAAAGTTT | 3366 |
| | AAACTTTCCAGTGAAG | 3367 |
| Non-polypoid colorectal cancer Gln698Glu CAG-GAG | GAATTGGCCCTCTCTGCTCTAGGTGGTGTGTCTTCTACCTCA AAAAATGCCTTATTGATCAGGAGCTTTTATCAATGGCTAATTTT GAAGAATATATTCCCTTGGATTCTGACACAGTCA | 3368 |
| | TGACTGTGTGAGAATCCAAGGGAATATATTCTTCAAATAGC CATTGATAAAAGCTCCTGATCAATAAGGCATTTTTTGAGGTAG AAGACACAACCACCTAGAGCAGAGAGGGCCAATTC | 3369 |
| | TTATTGATCAGGAGCTT | 3370 |
| | AAGCTCCTGATCAATAA | 3371 |
| Endometrial cancer Gln731Term CAA-TAA | CCCTTGGATTCTGACACAGTCAGCACTACAAGATCTGGTGCT ATCTTCACCAAAGCCTATCAACGAATGGTGCTAGATGCAGTG ACATTAAACAACCTGGAGATTTTTCTGAATGGAACAA | 3372 |
| | TTGTTCCATTGAGAAAAATCTCCAAGTTGTTAATGTCACTGC ATCTAGCACCATTGCTTGATAGGCTTTGGTGAAGATAGCACC AGATCTTGTAGTGCTGACTGTGTGAGAATCCAAGGG | 3373 |
| | AAGCCTATCAACGAATG | 3374 |
| | CATTCGTTGATAGGCTT | 3375 |
| Colorectal cancer Val800Leu GTT-CTT | GCCCCACTCTGTAACCATTATGCTATTAATGATCGTCTAGATG CCATAGAAGACCTCATGGTTGTGCCTGACAAAATCTCCGAAG TTGTAGAGCTTCTAAAGAAGCTTCCAGATCTTGAGA | 3376 |
| | TCTCAAGATCTGGAAGCTTCTTTAGAAGCTCTACAACCTCGGA GATTTTGTGAGGCACAAACCATGAGGTCTTCTATGGCATCTAGA CGATCATTAAATAGCATAATGGTTACAGAGTGGGGC | 3377 |
| | ACCTCATGGTTGTGCCT | 3378 |
| | AGGCACAACCATGAGGT | 3379 |
| Colorectal cancer Asp803Gly GAC-GGC | GTAACCATTATGCTATTAATGATCGTCTAGATGCCATAGAAGA CCTCATGGTTGTGCCTGACAAAATCTCCGAAGTTGTAGAGCT TCTAAAGAAGCTTCCAGATCTTGAGAGGCTACTCAG | 3380 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | CTGAGTAGCCTCTCAAGATCTGGAAGCTTCTTTAGAAGCTCTA CAACTTCGGAGATTTTGTCAGGCACAACCATGAGGTCTTCTAT GGCATCTAGACGATCATTAAATAGCATAATGGTTAC | 3381 |
| | TGTGCCTGACAAAATCT | 3382 |
| | AGATTTTGTCAGGCACA | 3383 |
| Non-polyposis colorectal cancer Tyr850Cys TAC-TGC | CTCCCCTGAAGAGTCAGAACCACCCAGACAGCAGGGCTATAA TGTATGAAGAACTACATACAGCAAGAAGAAGATTATTGATTT TCTTTCTGCTCTGGAAGGATTCAAAGTAATGTGTAA | 3384 |
| | TTACACATTACTTTGAATCCTTCCAGAGCAGAAAGAAAATCAA TAATCTTCTTCTTGCTGTATGTAGTTTCTTCATACATTATAGCC CTGCTGTCTGGGTGGTTCTGACTCTTCAGGGGAG | 3385 |
| | AACTACATACAGCAAGA | 3386 |
| | TCTTGCTGTATGTAGTT | 3387 |
| Colorectal cancer Pro1087Thr CCC-ACC | TATAGTCGAGGGGGTGATGGTCCTATGTGTCGCCAGTAATT CTGTTGCCGGAAGATACCCCCCCCTTCTTAGAGCTTAAAGGA TCACGCCATCCTTGCATTACGAAGACTTTTTTTGGAG | 3388 |
| | CTCCAAAAAAGTCTTCGTAATGCAAGGATGGCGTGATCCTTT AAGCTCTAAGAAGGGGGGGGTATCTTCCGGCAACAGAATTAC TGGGCGACACATAGGACCATCACCCCTCGACTATA | 3389 |
| | AAGATACCCCCCCCTTC | 3390 |
| | GAAGGGGGGGGTATCTT | 3391 |
| Non-polyposis colorectal cancer Gln1258Term CAA-TAA | ACTATAAATGTCGTACATTATTTTCAACTCACTACCATTCATT AGTAGAAGATTATTCTCAAAATGTTGCTGTGCGCCTAGGACAT ATGGTATGTGCAAATTGTTTTTTCCACAAATTC | 3392 |
| | GAATTTGTGAAAAAACAATTTGCACATACCATATGTCCTAG GCGCACAGCAACATTTTGAGAATAATCTTCTACTAATGAATGG TAGTGAGTTGAAAATAATGTACGACATTTTATAGT | 3393 |
| | ATTATTCTCAAAATGTT | 3394 |
| | AACATTTTGAGAATAAT | 3395 |

EXAMPLE 21

Hyperlipidemia - APOE

[0233] Hyperlipidemia is the abnormal elevation of plasma cholesterol and/or triglyceride levels and it is one of the most common diseases. The human apolipoprotein E protein is involved in the transport of endogenous lipids and appears to be crucial for both the direct removal of cholesterol-rich LDL from plasma and conversion of IDL particles to LDL particles. Individuals who either lack apolipoprotein E or who are homozygous for particular alleles of apoE may have have a condition

known as dysbetalipoproteinemia, which is characterized by elevated plasma cholesterol and triglyceride levels and an increased risk for atherosclerosis.

[0234] In a comprehensive review of apoE variants, de Knijff et al., *Hum. Mutat.* 4:178-194 (1994) found that 30 variants had been characterized, including the most common variant, apoE3. To that time, 14 apoE variants had been found to be associated with familial dysbetalipoproteinemia. The attached table discloses the correcting oligonucleotide base sequences for the APOE oligonucleotides of the invention.

Table 23

ApoE Mutations And Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Apolipoprotein E Glu13Lys cGAG-AAG | TTGTTCCACACAGGATGCCAGGCCAAGGTGGAGCAAGCGGT GGAGACAGAGCCGGAGCCC <u>G</u> AGCTGCGCCAGCAGACCGAG TGGCAGAGCGGCCAGCGCTGGGAAGTGGCACTGGGTGCT | 3396 |
| | AGCGACCCAGTGCCAGTTCCAGCGCTGGCCGCTCTGCCAC TCGGTCTGCTGGCGCAGCTC <u>G</u> GGGCTCCGGCTCTGTCTCCAC CGCTTGCTCCACCTTGCCCTGGCATCCTGTGTGGAACAA | 3397 |
| | CGGAGCCC <u>G</u> AGCTGCGC | 3398 |
| | GCGCAGCTC <u>G</u> GGGCTCCG | 3399 |
| | | |
| Apolipoprotein E Trp20Term TGGc-TGA | CAAGGTGGAGCAAGCGGTGGAGACAGAGCCGGAGCCCGAG CTGCGCCAGCAGACCGAGTG <u>G</u> CAGAGCGGCCAGCGCTGGG AACTGGCACTGGGTGCTTTTGGGATTACCTGCGCTGGGTG | 3400 |
| | CACCCAGCGCAGGTAATCCCAAAGCGACCCAGTGCCAGTT CCCAGCGCTGGCCGCTCTG <u>C</u> CACTCGGTCTGCTGGCGCAGC TCGGGCTCCGGCTCTGTCTCCACCGCTTGCTCCACCTTG | 3401 |
| | ACCGAGTG <u>G</u> CAGAGCGG | 3402 |
| | CCGCTCTG <u>C</u> CACTCGGT | 3403 |
| | | |
| Apolipoprotein E Leu28Pro CTG-CCG | CAGAGCCGGAGCCCGAGCTGCGCCAGCAGACCGAGTGGA GAGCGGCCAGCGCTGGGAAC <u>T</u> GGCACTGGGTGCTTTTGGG ATTACCTGCGCTGGGTGCAGACACTGTCTGAGCAGGTGCA | 3404 |
| | TGCACCTGCTCAGACAGTGTCTGCACCCAGCGCAGGTAATCC CAAAAGCGACCCAGTGCC <u>A</u> GTTCCAGCGCTGGCCGCTCTG CCACTCGGTCTGCTGGCGCAGCTCGGGCTCCGGCTCTG | 3405 |
| | CTGGGAAC <u>T</u> GGCACTGG | 3406 |
| | CCAGTGCC <u>A</u> GTTCCAG | 3407 |
| | | |
| Apolipoprotein E Cys112Arg gTGC-CGC | CGGCTGTCCAAGGAGCTGCAGGCGGCGCAGGCCCGGCTGG GCGCGGACATGGAGGACGTG <u>T</u> GCGGCCGCCTGGTGCAGTA CCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGCACCGAG G | 3408 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | CCTCGGTGCTCTGGCCGAGCATGGCCTGCACCTCGCCGCGG TACTGCACCAGGCGGCCGCACACGTCCTCCATGTCCGCGCC CAGCCGGGCCTGCGCCGCCTGCAGCTCCTTGGACAGCCG | 3409 |
| | AGGACGTGTGCGGCCGC | 3410 |
| | GCGGCCGCACACGTCCT | 3411 |
| | | |
| Apolipoprotein E Gly127Asp GGC-GAC | ACATGGAGGACGTGTGCGGCCGCCTGGTGCAGTACCGCGGC GAGGTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGC GGGTGCGCCTCGCCTCCACCTGCGCAAGCTGCGTAAGCG | 3412 |
| | CGCTTACGCAGCTTGCAGGTGGGAGGCGAGGCGCACCC GCAGCTCCTCGGTGCTCTGGCCGAGCATGGCCTGCACCTCG CCGCGGTACTGCACCAGGCGGCCGCACACGTCCTCCATGT | 3413 |
| | CATGCTCGGCCAGAGCA | 3414 |
| | TGCTCTGGCCGAGCATG | 3415 |
| | | |
| Apolipoprotein E Arg136Cys gCGC-TGC | GTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGA GCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCACCTGCG CAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGC | 3416 |
| | GCAGGTCATCGGCATCGCGGAGGAGCCGCTTACGCAGCTTG CGCAGGTGGGAGGCGAGGCGCACCCGCAGCTCCTCGGTGC TCTGGCCGAGCATGGCCTGCACCTCGCCGCGGTACTGCAC | 3417 |
| | TGCGGGTGCGCCTCGCC | 3418 |
| | GGCGAGGCGCACCCGCA | 3419 |
| | | |
| Apolipoprotein E Arg136His CGC-CAC | TGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGAGC ACCGAGGAGCTGCGGGTGCGCCTCGCCTCCACCTGCGCAA GCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGCA | 3420 |
| | TGCAGGTCATCGGCATCGCGGAGGAGCCGCTTACGCAGCTT GCGCAGGTGGGAGGCGAGGCGCACCCGCAGCTCCTCGGTG CTCTGGCCGAGCATGGCCTGCACCTCGCCGCGGTACTGCA | 3421 |
| | GCGGGTGCGCCTCGCCT | 3422 |
| | AGGCGAGGCGCACCCGC | 3423 |
| | | |
| Apolipoprotein E Arg136Ser gCGC-AGC | GTGCAGTACCGCGGCGAGGTGCAGGCCATGCTCGGCCAGA GCACCGAGGAGCTGCGGGTGCGCCTCGCCTCCACCTGCG CAAGCTGCGTAAGCGGCTCCTCCGCGATGCCGATGACCTGC | 3424 |
| | GCAGGTCATCGGCATCGCGGAGGAGCCGCTTACGCAGCTTG CGCAGGTGGGAGGCGAGGCGCACCCGCAGCTCCTCGGTGC TCTGGCCGAGCATGGCCTGCACCTCGCCGCGGTACTGCAC | 3425 |
| | TGCGGGTGCGCCTCGCC | 3426 |
| | GGCGAGGCGCACCCGCA | 3427 |
| | | |
| Apolipoprotein E Arg142Cys gCGC-TGC | GTGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGG TGCGCCTCGCCTCCACCTGCGCAAGCTGCGTAAGCGGCTC CTCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCAGTGT | 3428 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | ACACTGCCAGGCGCTTCTGCAGGTCATCGGCATCGCGGAGG AGCCGCTTACGCAGCTTGCGCAGGTGGGAGGCGAGGCGCA CCCGCAGCTCCTCGGTGCTCTGGCCGAGCATGGCCTGCAC | 3429 |
| | CCCACCTGCGCAAGCTG | 3430 |
| | CAGCTTGCGCAGGTGGG | 3431 |
| Apolipoprotein E Arg142Leu CGC-CTC | TGCAGGCCATGCTCGGCCAGAGCACCGAGGAGCTGCGGGT GCGCCTCGCCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCC TCCGCGATGCCGATGACCTGCAGAAGCGCCTGGCAGTGT | 3432 |
| | TACACTGCCAGGCGCTTCTGCAGGTCATCGGCATCGCGGAG GAGCCGCTTACGCAGCTTGCGCAGGTGGGAGGCGAGGCGC ACCCGCAGCTCCTCGGTGCTCTGGCCGAGCATGGCCTGCA | 3433 |
| | CCACCTGCGCAAGCTGC | 3434 |
| | GCAGCTTGCGCAGGTGG | 3435 |
| Apolipoprotein E Arg145Cys gCGT-TGT | ATGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCG CCTCCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGAT GCCGATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCG | 3436 |
| | CGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCGGCA TCGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGAGG CGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAGCAT | 3437 |
| | GCAAGCTGCGTAAGCGG | 3438 |
| | CCGCTTACGCAGCTTG | 3439 |
| Apolipoprotein E Arg145Pro CGT-CCT | TGCTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGC CTCCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATG CCGATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGG | 3440 |
| | CCGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCGGC ATCGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGAGG CGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAGCA | 3441 |
| | CAAGCTGCGTAAGCGGC | 3442 |
| | GCCGCTTACGCAGCTTG | 3443 |
| Apolipoprotein E Lys146Gln tAAG-CAG | CTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCT CCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCC GATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGGGG | 3444 |
| | CCCCGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCG GCATCGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGA GGCGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAG | 3445 |
| | AGCTGCGTAAGCGGCTC | 3446 |
| | GAGCCGCTTACGCAGCT | 3447 |
| Apolipoprotein E Lys146Glu tAAG-GAG | CTCGGCCAGAGCACCGAGGAGCTGCGGGTGCGCCTCGCCT CCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGATGCC GATGACCTGCAGAAGCGCCTGGCAGTGTACCAGGCCGGGG | 3448 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | CCCCGGCCTGGTACACTGCCAGGCGCTTCTGCAGGTCATCG GCATCGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGA GGCGAGGCGCACCCGCAGCTCCTCGGTGCTCTGGCCGAG | 3449 |
| | AGCTGCGT <u>A</u> AGCGGCTC | 3450 |
| | GAGCCGCTTACGCAGCT | 3451 |
| Apolipoprotein E Arg158Cys gCGC-TGC | GCCTCCACCTGCGCAAGCTGCGTAAGCGGCTCCTCCGCGA TGCCGATGACCTGCAGAAGCGCCTGGCAGTGACCAGGCCG GGGCCCCGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCC | 3452 |
| | GGATGGCGCTGAGGCCGCGCTCGGCGCCCTCGCGGGCCCC GGCCTGGTACACTGCCAGGC <u>G</u> CTTCTGCAGGTCATCGGCAT CGCGGAGGAGCCGCTTACGCAGCTTGCGCAGGTGGGAGGC | 3453 |
| | TGCAGAAGCGCCTGGCA | 3454 |
| | TGCCAGGC <u>G</u> CTTCTGCA | 3455 |
| Apolipoprotein E Gln187Glu aCAG-GAG | CGCGAGGGCGCCGAGCGCGGCCTCAGCGCCATCCGCGAGC GCCTGGGGCCCCTGGTGGA <u>A</u> CAGGGCCGCGTGCGGGCCGC CACTGTGGGCTCCCTGGCCGGCCAGCCGCTACAGGAGCGG G | 3456 |
| | CCCGCTCCTGTAGCGGCTGGCCGGCCAGGGAGCCCACAGT GGCGGCCCGCACGCGGCCCT <u>G</u> TTCCACCAGGGGCCCCAGG CGCTCGCGGATGGCGCTGAGGCCGCGCTCGGCGCCCTCGC G | 3457 |
| | TGGTGGA <u>A</u> CAGGGCCGC | 3458 |
| | GCGGCCCT <u>G</u> TTCCACCA | 3459 |
| Apolipoprotein E Trp210Term TGG-TAG | TGCGGGCCGCCACTGTGGGCTCCCTGGCCGGCCAGCCGCT ACAGGAGCGGGCCCAGGCCT <u>G</u> GGGCGAGCGGCTGCGCGCG CGGATGGAGGAGATGGGCAGCCGACCCGCGACCGCCTGG A | 3460 |
| | TCCAGGCGGTGCGGGGTCCGGCTGCCATCTCCTCCATCCG CGCGCGCAGCCGCTCGCCCC <u>C</u> AGGCCTGGGCCCCGCTCCTGT AGCGGCTGGCCGGCCAGGGAGCCCACAGTGGCGGGCCGCA | 3461 |
| | CCAGGCCT <u>G</u> GGGCGAGC | 3462 |
| | GCTCGCCCC <u>C</u> AGGCCTGG | 3463 |
| Apolipoprotein E Arg228Cys cCGC-TGC | CAGGCCTGGGGCGAGCGGCTGCGCGCGCGGATGGAGGAGA TGGGCAGCCGACCCGCGAC <u>C</u> GCCTGGACGAGGTGAAGGA GCAGGTGGCGGAGGTGCGCGCCAAGCTGGAGGAGCAGGCC C | 3464 |
| | GGGCCTGCTCCTCCAGCTTGGCGCGCACCTCCGCCACCTGC TCCTTACCTCGTCCAGGC <u>G</u> TGCGGGGTCCGGCTGCCCAT CTCCTCCATCCGCGCGCGCAGCCGCTCGCCCCAGGCCTG | 3465 |
| | CCGCGAC <u>C</u> GCCTGGAC | 3466 |
| | GTCCAGGC <u>G</u> GTGCGGG | 3467 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Apolipoprotein E Glu244Lys gGAG-AAG | CGGACCCGCGACCGCCTGGACGAGGTGAAGGAGCAGGTGG CGGAGGTGCGCGCCAAGCTG <u>G</u> AGGAGCAGGCCCAGCAGAT ACGCCTGCAGGCCGAGGCCTTCCAGGCCCGCCTCAAGAGCT | 3468 |
| | AGCTCTTGAGGCGGGCCTGGAAGGCCTCGGCCTGCAGGCGT ATCTGCTGGGCCTGCTCCT <u>C</u> CAGCTTGGCGCGCACCTCCGC CACCTGCTCCTTACCTCGTCCAGGCGGTGCGGGGTCCG | 3469 |
| | CCAAGCTG <u>G</u> AGGAGCAG | 3470 |
| | CTGCTCCT <u>C</u> CAGCTTGG | 3471 |

EXAMPLE 22

Familial hypercholesterolemia - LDLR

[0235] Familial hypercholesterolemia is characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL) and is, hence, one of the conditions producing a hyperlipoproteinemia phenotype. Familial hypercholesterolemia is an autosomal dominant disorder characterized by elevation of serum cholesterol bound to low density lipoprotein (LDL). Mutations in the LDL receptor (LDLR) gene cause this disorder. The attached table discloses the correcting oligonucleotide base sequences for the LDLR oligonucleotides of the invention.

Table 24

LDLR Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Hypercholesterolaemia Glu10Term CGAG-TAG | GCGTTGAGAGACCCTTTCTCCTTTTCTCTCTCTCAGTGGGC GACAGATGCGAAAGAAAC <u>G</u> AGTTCCAGTGCCAAGACGGGAA ATGCATCTCCTACAAGTGGGTCTGCGATGGCAGCGCTG | 3472 |
| | CAGCGCTGCCATCGCAGACCCACTTGTAGGAGATGCATTTCC CGTCTTGGCACTGGAAC <u>T</u> CGTTTCTTTTCGCATCTGTGCCCCA CTGAGAGAGAGGAAAAGGAGAAAGGGTCTCTCAACGC | 3473 |
| | AAAGAAAC <u>G</u> AGTTCCAG | 3474 |
| | CTGGAAC <u>T</u> CGTTTCTTT | 3475 |
| Hypercholesterolaemia Gln12Term cCAG-TAG | AGAGACCCTTTCTCCTTTTCTCTCTCTCAGTGGGCGACAGAT GCGAAAGAAACGAGTT <u>C</u> CAGTGCCAAGACGGGAAATGCATCT CCTACAAGTGGGTCTGCGATGGCAGCGCTGAGTGCC | 3476 |
| | GGCACTCAGCGCTGCCATCGCAGACCCACTTGTAGGAGATG CATTTCCCGTCTTGGCACT <u>G</u> GAACTCGTTTCTTTTCGCATCTGT CGCCCACTGAGAGAGAGGAAAAGGAGAAAGGGTCTCT | 3477 |
| | ACGAGTT <u>C</u> CAGTGCCAA | 3478 |
| | TTGGCACT <u>G</u> GAACTCGT | 3479 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Hypercholesterolaemia Gln14Term cCAA-TAA | CCTTTCTCCTTTTCCTCTCTCTCAGTGGGCGACAGATGCGAAA GAAACGAGTTCCAGTGCC <u>A</u> AGACGGGAAATGCATCTCCTACA AGTGGGTCTGCGATGGCAGCGCTGAGTGCCAGGATG | 3480 |
| | CATCCTGGCACTCAGCGCTGCCATCGCAGACCCACTTGTAGG AGATGCATTTCCCGTCTTGGCACTGGAACGTTTCTTTTCGCA TCTGTCGCCCCACTGAGAGAGAGGAAAAGGAGAAAGG | 3481 |
| | TCCAGTGCC <u>A</u> AGACGGG | 3482 |
| | CCCGTCTTGGCACTGGA | 3483 |
| Hypercholesterolaemia Trp23Term TGG-TAG | GCGACAGATGCGAAAGAAACGAGTTCCAGTGCCAAGACGGG AAATGCATCTCCTACAAGTGGGTCTGCGATGGCAGCGCTGAG TGCCAGGATGGCTCTGATGAGTCCCAGGAGACGTGCTG | 3484 |
| | CAGCACGTCTCCTGGGACTCATCAGAGCCATCCTGGCACTCA GCGCTGCCATCGCAGACCC <u>A</u> CTTGTAGGAGATGCATTTCCCG TCTTGGCACTGGAACGTTTCTTTTCGCATCTGTCTGC | 3485 |
| | CTACAAGTGGGTCTGCG | 3486 |
| | CGCAGACCCACTTGTAG | 3487 |
| Hypercholesterolaemia Ala29Ser cGCT-TCT | AACGAGTTCCAGTGCCAAGACGGGAAATGCATCTCCTACAAG TGGGTCTGCGATGGCAGCGCTGAGTGCCAGGATGGCTCTGA TGAGTCCCAGGAGACGTGCTGTGAGTCCCCTTTGGGCA | 3488 |
| | TGCCCCAAAGGGGACTCACAGCACGTCTCCTGGGACTCATCA GAGCCATCCTGGCACTCAGCGCTGCCATCGCAGACCCACTT GTAGGAGATGCATTTCCCGTCTTGGCACTGGAACGCTT | 3489 |
| | ATGGCAGCGCTGAGTGC | 3490 |
| | GCACTCAGCGCTGCCAT | 3491 |
| Hypercholesterolaemia Cys31Tyr TGC-TAC | TCCAGTGCCAAGACGGGAAATGCATCTCCTACAAGTGGGTCT GCGATGGCAGCGCTGAGTGCCAGGATGGCTCTGATGAGTCC CAGGAGACGTGCTGTGAGTCCCCTTTGGGCATGATATG | 3492 |
| | CATATCATGCCCAAAGGGGACTCACAGCACGTCTCCTGGGAC TCATCAGAGCCATCCTGGCACTCAGCGCTGCCATCGCAGACC CACTTGTAGGAGATGCATTTCCCGTCTTGGCACTGGA | 3493 |
| | CGCTGAGTGCCAGGATG | 3494 |
| | CATCCTGGCACTCAGCG | 3495 |
| Hypercholesterolaemia Arg57Cys cCGT-TGT | AATCCTGTCTCTTCTGTAGTGTCTGTACCTGCAAATCCGGG GACTTCAGCTGTGGGGGCGCGTGTCAACCGCTGCATTCTCA GTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACAACG | 3496 |
| | CGTTGTCGCAGTCCACTTGCCATCGCACCTCCAGAACTGAG GAATGCAGCGGTTGACACGGCCCCCACAGCTGAAGTCCCCG GATTTGCAGGTGACAGACACTACAGAAGAGACAGGATT | 3497 |
| | GTGGGGGCGCGTGTCAAC | 3498 |
| | GTTGACACGGCCCCCAC | 3499 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Hypercholesterolaemia Gln64Term tCAG-TAG | TCTGTCACCTGCAAATCCGGGGACTTCAGCTGTGGGGGCCG TGTC AACCGCTGCATTCTCAGTTCTGGAGGTGCGATGGCCA AGTGGACTGCGACAACGGCTCAGACGAGCAAGGCTGTC | 3500 |
| | GACAGCCTTGCTCGTCTGAGCCGTTGTGCGAGTCCACTTGGC CATCGCACCTCCAGAACTGAGGAATGCAGCGGTTGACACGG CCCCACAGCTGAAGTCCCCGGATTTGCAGGTGACAGA | 3501 |
| | GCATTCTCAGTTCTGG | 3502 |
| | CCAGAACTGAGGAATGC | 3503 |
| Hypercholesterolaemia Trp66Gly cTGG-GGG | ACCTGCAAATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAA CCGCTGCATTCTCAGTTCTGGAGGTGCGATGGCCAAGTGG ACTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGT | 3504 |
| | ACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTGCGAGTCCA CTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCGGTTG ACACGGCCCCCACAGCTGAAGTCCCCGGATTTGCAGGT | 3505 |
| | CTCAGTTCTGGAGGTGC | 3506 |
| | GCACCTCCAGAACTGAG | 3507 |
| Hypercholesterolaemia Trp66Term TGG-TAG | CCTGCAAATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAAC CGCTGCATTCTCAGTTCTGGAGGTGCGATGGCCAAGTGGGA CTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGTG | 3508 |
| | CACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTGCGAGTCC ACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCGGTTG ACACGGCCCCCACAGCTGAAGTCCCCGGATTTGCAGG | 3509 |
| | TCAGTTCTGGAGGTGCG | 3510 |
| | CGCACCTCCAGAACTGA | 3511 |
| Hypercholesterolaemia Cys68Arg gTGC-CGC | AAATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAACCGCTG CATTCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGA CAACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCC | 3512 |
| | GGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTGCG AGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGC GGTTGACACGGCCCCCACAGCTGAAGTCCCCGGATTT | 3513 |
| | TCTGGAGGTGCGATGGC | 3514 |
| | GCCATCGCACCTCCAGA | 3515 |
| Hypercholesterolaemia Cys68Trp TGCg-TGG | ATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAACCGCTGCA TTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACA ACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCT | 3516 |
| | AGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTC GCAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGCA GCGGTTGACACGGCCCCCACAGCTGAAGTCCCCGGAT | 3517 |
| | TGGAGGTGCGATGGCCA | 3518 |
| | TGGCCATCGCACCTCCA | 3519 |
| Hypercholesterolaemia Cys68Tyr TGC-TAC | AATCCGGGGACTTCAGCTGTGGGGGCCGTGTCAACCGCTGC ATTCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGAC AACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCC | 3520 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | GGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCTG CAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAG CGGTTGACACGGCCCCACAGCTGAAGTCCCCGGATT | 3521 |
| | CTGGAGGTGCGATGGCC | 3522 |
| | GGCCATCGCACCTCCAG | 3523 |
| Hypercholesterolaemia Asp69Asn cGAT-AAT | TCCGGGGACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCAT TCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACA ACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTG | 3524 |
| | CAGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGT CGCAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGC AGCGGTTGACACGGCCCCACAGCTGAAGTCCCCGGA | 3525 |
| | GGAGGTGCGATGGCCAA | 3526 |
| | TTGGCCATCGCACCTCC | 3527 |
| Hypercholesterolaemia Asp69Gly GAT-GGT | CCGGGGACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCATT CCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACAA CGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTGC | 3528 |
| | GCAGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTT GTCGCAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAAT GCAGCGGTTGACACGGCCCCACAGCTGAAGTCCCCGG | 3529 |
| | GAGGTGCGATGGCCAAAG | 3530 |
| | CTTGGCCATCGCACCTC | 3531 |
| Hypercholesterolaemia Asp69Tyr cGAT-TAT | TCCGGGGACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCAT TCCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACA ACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTG | 3532 |
| | CAGGGCCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGT CGCAGTCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGC AGCGGTTGACACGGCCCCACAGCTGAAGTCCCCGGA | 3533 |
| | GGAGGTGCGATGGCCAA | 3534 |
| | TTGGCCATCGCACCTCC | 3535 |
| Hypercholesterolaemia Gln71Glu cCAA-GAA | GACTTCAGCTGTGGGGGCGGTGTCAACCGCTGCATTCTCA GTTCTGGAGGTGCGATGGCCAAGTGGACTGCGACAACGGCT CAGACGAGCAAGGCTGTCGTAAGTGTGGCCCTGCCTTTG | 3536 |
| | CAAAGGCAGGGCCACACTTACGACAGCCTTGCTCGTCTGAG CCGTTGTCGCAGTCCACTTGGCCATCGCACCTCCAGAACTGA GGAATGCAGCGGTTGACACGGCCCCACAGCTGAAGTC | 3537 |
| | GCGATGGCCAAGTGGAC | 3538 |
| | GTCCACTTGGCCATCGC | 3539 |
| Hypercholesterolaemia Cys74Gly cTGC-GGC | TGTGGGGGCGGTGTCAACCGCTGCATTCTCAGTTCTGGAG GTGCGATGGCCAAGTGGACTGCGACAACGGCTCAGACGAGC AAGGCTGTCGTAAGTGTGGCCCTGCCTTTGCTATTGAGC | 3540 |
| | GCTCAATAGCAAAGGCAGGGCCACACTTACGACAGCCTTGCT CGTCTGAGCCGTTGTGCGAGTCCACTTGGCCATCGCACCTCC AGAACTGAGGAATGCAGCGGTTGACACGGCCCCCACA | 3541 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | AAGTGGACTGCGACAAC | 3542 |
| | GTTGTCGCAGTCCACTT | 3543 |
| Hypercholesterolaemia Ser78Term TCA-TGA | TCAACCGCTGCATTCTCAGTTCTGGAGGTGCGATGGCCAAG TGGACTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAG TGTGGCCCTGCCTTTGCTATTGAGCCTATCTGAGTCCT | 3544 |
| | AGGACTCAGATAGGCTCAATAGCAAAGGCAGGGCCACACTTA CGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCCACTTGG CCATCGCACCTCCAGAACTGAGGAATGCAGCGGTTGA | 3545 |
| | CAACGGCTCAGACGAGC | 3546 |
| | GCTCGTCTGAGCCGTTG | 3547 |
| Hypercholesterolaemia Glu80Lys cGAG-AAG | CGCTGCATTCTCAGTTCTGGAGGTGCGATGGCCAAGTGA CTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTG GCCCTGCCTTTGCTATTGAGCCTATCTGAGTCCTGGGGA | 3548 |
| | TCCCCAGGACTCAGATAGGCTCAATAGCAAAGGCAGGGCCA CACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCC ACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCG | 3549 |
| | GCTCAGACGAGCAAGGC | 3550 |
| | GCCTTGCTCGTCTGAGC | 3551 |
| Hypercholesterolaemia Glu80Term cGAG-TAG | CGCTGCATTCTCAGTTCTGGAGGTGCGATGGCCAAGTGA CTGCGACAACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTG GCCCTGCCTTTGCTATTGAGCCTATCTGAGTCCTGGGGA | 3552 |
| | TCCCCAGGACTCAGATAGGCTCAATAGCAAAGGCAGGGCCA CACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAGTCC ACTTGGCCATCGCACCTCCAGAACTGAGGAATGCAGCG | 3553 |
| | GCTCAGACGAGCAAGGC | 3554 |
| | GCCTTGCTCGTCTGAGC | 3555 |
| Hypercholesterolaemia Gln81Term gCAA-TAA | TGCATTCTCAGTTCTGGAGGTGCGATGGCCAAGTGGACTGC GACAACGGCTCAGACGAGCAAGGCTGTCGTAAGTGTGGCCC TGCCTTTGCTATTGAGCCTATCTGAGTCCTGGGGAGTG | 3556 |
| | CACTCCCCAGGACTCAGATAGGCTCAATAGCAAAGGCAGGG CCACACTTACGACAGCCTTGCTCGTCTGAGCCGTTGTCGCAG TCCACTTGGCCATCGCACCTCCAGAACTGAGGAATGCA | 3557 |
| | CAGACGAGCAAGGCTGT | 3558 |
| | ACAGCCTTGCTCGTCTG | 3559 |
| Hypercholesterolaemia Cys88Arg gTGC-CGC | TGGGAGACTTCACACGGTGATGGTGGTCTCGGCCCATCCATC CCTGCAGCCCCAAGACGTGCTCCCAGGACGAGTTTCGCTG CCACGATGGGAAGTGCATCTCTCGGCAGTTCGTCTGTG | 3560 |
| | CACAGACGAACTGCCGAGAGATGCACTTCCCATCGTGGCAG CGAAACTCGTCCTGGGAGCACGTCTTGGGGGCTGCAGGGAT GGATGGGCCGAGACCACCATCACCGTGTGAAGTCTCCCA | 3561 |
| | CCAAGACGTGCTCCAG | 3562 |
| | CTGGGAGCACGTCTTG | 3563 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| Hypercholesterolaemia Glu92Term cGAG-TAG | CACGGTGATGGTGGTCTCGGCCCATCCATCCCTGCAGCCCC CAAGACGTGCTCCCAGGAC <u>G</u> AGTTTCGCTGCCACGATGGGA AGTGCATCTCTCGGCAGTTCGTCTGTGACTCAGACCGGG | 3564 |
| | CCCGGTCTGAGTCACAGACGAACTGCCGAGAGATGCACTTC CCATCGTGGCAGCGAAACT <u>C</u> GTCTCTGGGAGCACGTCTTGGG GGCTGCAGGGATGGATGGGCCGAGACCACCATCACCGTG | 3565 |
| | CCCAGGAC <u>G</u> AGTTTCGC | 3566 |
| | GCGAAACT <u>C</u> GTCTCTGGG | 3567 |
| Hypercholesterolaemia Cys95Arg cTGC-CGC | GGTGGTCTCGGCCCATCCATCCCTGCAGCCCCCAAGACGTG CTCCCAGGACGAGTTTCGCT <u>T</u> GCCACGATGGGAAGTGCATCTC TCGGCAGTTCGTCTGTGACTCAGACCGGGACTGCTTGG | 3568 |
| | CCAAGCAGTCCCGGTCTGAGTCACAGACGAACTGCCGAGAG ATGCACTTCCCATCGTGGC <u>A</u> GCGAAACTCGTCCTGGGAGCA CGTCTTGGGGGCTGCAGGGATGGATGGGCCGAGACCACC | 3569 |
| | AGTTTCGCT <u>T</u> GCCACGAT | 3570 |
| | ATCGTGGC <u>A</u> GCGAAACT | 3571 |
| Hypercholesterolaemia Asp97Tyr cGAT-TAT | CTCGGCCCATCCATCCCTGCAGCCCCCAAGACGTGCTCCCA GGACGAGTTTCGCTGCCAC <u>G</u> ATGGGAAGTGCATCTCTCGGC AGTTCGTCTGTGACTCAGACCGGGACTGCTTGGACGGCT | 3572 |
| | AGCCGTCCAAGCAGTCCCGGTCTGAGTCACAGACGAACTGC CGAGAGATGCACTTCCCAT <u>C</u> GTGGCAGCGAAACTCGTCCTG GGAGCACGTCTTGGGGGCTGCAGGGATGGATGGGCCGAG | 3573 |
| | GCTGCCAC <u>G</u> ATGGGAAG | 3574 |
| | CTTCCCAT <u>C</u> GTGGCAGC | 3575 |
| Hypercholesterolaemia Trp(-12)Arg cTGG-AGG | GGGTCGGGACACTGCCTGGCAGAGGCTGCGAGCATGGGGC CCTGGGGGCTGGAAATTGCGCTGGACCGTGCCTTGCTCCTC GCCGCGGCGGGGACTGCAGGTAAGGCTTGCTCCAGGCGCC | 3576 |
| | GGCGCCTGGAGCAAGCCTTACCTGCAGTCCCCGCCGCGGCG AGGAGCAAGGCGACGGTCC <u>A</u> GCGCAATTTCCAGCCCCAGGG CCCCATGCTCGCAGCCTCTGCCAGGCAGTGTCCCGACCC | 3577 |
| | AATTGCGCTGGACCGTC | 3578 |
| | GACGGTCC <u>A</u> GCGCAATT | 3579 |
| Hypercholesterolaemia Trp(-18)Term TGGg-TGA | CAGCAGGTCGTGATCCGGGTCGGGACACTGCCTGGCAGAGG CTGCGAGCATGGGGCCCTG <u>G</u> GGCTGGAAATTGCGCTGGACC GTCGCCTTGCTCCTCGCCGCGGCGGGGACTGCAGGTAAG | 3580 |
| | CTTACCTGCAGTCCCCGCCGCGGCGAGGAGCAAGGCGACG GTCCAGCGCAATTTCCAGCC <u>C</u> CAGGGCCCCATGCTCGCAGC CTCTGCCAGGCAGTGTCCCGACCCGGATCACGACCTGCTG | 3581 |
| | GGGCCCTG <u>G</u> GGGCTGGAA | 3582 |
| | TTCCAGCC <u>C</u> CAGGGCCC | 3583 |
| Hypercholesterolaemia Met(-21)Leu cATG-TTG | CAGCTAGGACACAGCAGGTCTGTGATCCGGGTCGGGACACTG CCTGGCAGAGGCTGCGAGC <u>A</u> TGGGGGCCCTGGGGCTGGAAA TTGCGCTGGACCGTCGCCTTGCTCCTCGCCGCGGCGGGGA | 3584 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | TCCCCGCCGCGGGCAGGAGCAAGGCGACGGTCCAGCGCAA TTTCCAGCCCCAGGGCCCCATGCTCGCAGCCTCTGCCAGGC AGTGTCCCGACCCGGATCACGACCTGCTGTGTCCTAGCTG | 3585 |
| | CTGCGAGCATGGGGCCC | 3586 |
| | GGGCCCCATGCTCGCAG | 3587 |
| | | |
| Hypercholesterolaemia Met(-21)Val cATG-GTG | CAGCTAGGACACAGCAGGTCGTGATCCGGGTCGGGACACTG CCTGGCAGAGGCTGCGAGCATGGGGCCCTGGGGCTGGAAA TTGCGCTGGACCGTCGCCTTGCTCCTCGCCGCGGCGGGGA | 3588 |
| | TCCCCGCCGCGGGCAGGAGCAAGGCGACGGTCCAGCGCAA TTTCCAGCCCCAGGGCCCCATGCTCGCAGCCTCTGCCAGGC AGTGTCCCGACCCGGATCACGACCTGCTGTGTCCTAGCTG | 3589 |
| | CTGCGAGCATGGGGCCC | 3590 |
| | GGGCCCCATGCTCGCAG | 3591 |
| Hypercholesterolaemia Ile101Phe cATC-TTC | ATCCCTGCAGCCCCCAAGACGTGCTCCCAGGACGAGTTTCG CTGCCACGATGGGAAGTGCATCTCTCGGCAGTTCGTCTGTGA CTCAGACCGGGACTGCTTGACGGCTCAGACGAGGCCT | 3592 |
| | AGGCCTCGTCTGAGCCGTCCAAGCAGTCCCGGTCTGAGTCA CAGACGAACTGCCGAGAGATGCACTTCCCATCGTGGCAGCG AAACTCGTCCTGGGAGCACGTCTTGGGGGCTGCAGGGAT | 3593 |
| | GGAAGTGCATCTCTCGG | 3594 |
| | CCGAGAGATGCACTTCC | 3595 |
| Hypercholesterolaemia Gln104Term gCAG-TAG | GCCCCAAGACGTGCTCCCAGGACGAGTTTCGCTGCCACGA TGGAAGTGCATCTCTCGGCAGTTCGTCTGTGACTCAGACCG GGAAGTCTTGACGGCTCAGACGAGGCCTCCTGCCCGG | 3596 |
| | CCGGGACAGGAGGCCTCGTCTGAGCCGTCCAAGCAGTCCCGG TCTGAGTCACAGACGAACTGCCGAGAGATGCACTTCCCATCG TGGCAGCGAAACTCGTCCTGGGAGCACGTCTTGGGGGC | 3597 |
| | TCTCTCGGCAGTTCGTC | 3598 |
| | GACGAACTGCCGAGAGA | 3599 |
| Hypercholesterolaemia Cys113Arg cTGC-CGC | TTTCGCTGCCACGATGGGAAGTGCATCTCTCGGCAGTTCGTC TGTGACTCAGACCGGGACTGCTTGACGGCTCAGACGAGGC CTCCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTTCC | 3600 |
| | GGAAGCTGGCGGGACCACAGGTGAGCACCGGGCAGGAGGC CTCGTCTGAGCCGTCCAAGCAGTCCCGGTCTGAGTCACAGA CGAACTGCCGAGAGATGCACTTCCCATCGTGGCAGCGAAA | 3601 |
| | ACCGGGACTGCTTGAC | 3602 |
| | GTCCAAGCAGTCCCGGT | 3603 |
| Hypercholesterolaemia Glu119Lys cGAG-AAG | AAGTGCATCTCTCGGCAGTTCGTCTGTGACTCAGACCGGGAC TGCTTGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCAC CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCT | 3604 |
| | AGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACAGGTG AGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAAGCAGTC CCGGTCTGAGTCACAGACGAACTGCCGAGAGATGCACTT | 3605 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | GCTCAGAC <u>G</u> AGGCCTCC | 3606 |
| | GGAGGCCT <u>C</u> GTCTGAGC | 3607 |
| Hypercholesterolaemia Glu119Term cGAG-TAG | AAGTGCATCTCTCGGCAGTTCGTCTGTGACTCAGACCGGGAC TGCTTGGACGGCTCAGAC <u>G</u> AGGCCTCCTGCCCGGTGCTCAC CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCT | 3608 |
| | AGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACAGGTG AGCACCGGGCAGGAGGCCT <u>C</u> GTCTGAGCCGTCCAAGCAGTC CCGGTCTGAGTCACAGACGAACTGCCGAGAGATGCACTT | 3609 |
| | GCTCAGAC <u>G</u> AGGCCTCC | 3610 |
| | GGAGGCCT <u>C</u> GTCTGAGC | 3611 |
| | | |
| Hypercholesterolaemia Cys122Term TGCC-TGA | TCGGCAGTTCTGTCTGTGACTCAGACCGGGACTGCTTGGACG GCTCAGACGAGGCCTCCTG <u>C</u> CCGGTGCTCACCTGTGGTCCC GCCAGCTTCCAGTGCAACAGCTCCACCTGCATCCCCAG | 3612 |
| | CTGGGGGATGCAGGTGGAGCTGTTGCACTGGAAGCTGGCGG GACCACAGGTGAGCACCGGG <u>G</u> CAGGAGGCCTCGTCTGAGCC GTCCAAGCAGTCCCGGTCTGAGTCACAGACGAACTGCCGA | 3613 |
| | GCCTCCTG <u>C</u> CCCGGTGCT | 3614 |
| | AGCACCGGG <u>G</u> CAGGAGGC | 3615 |
| | | |
| Hypercholesterolaemia Cys127Trp TGTg-TGG | TGACTCAGACCGGGACTGCTTGGACGGCTCAGACGAGGCCT CCTGCCCGGTGCTCACCTGT <u>T</u> GGTCCCGCCAGCTTCCAGTGC AACAGCTCCACCTGCATCCCCAGCTGTGGGCCTGCGAC | 3616 |
| | GTCGCAGGCCCACAGCTGGGGGATGCAGGTGGAGCTGTTGC ACTGGAAGCTGGCGGGACC <u>A</u> CAGGTGAGCACCGGGCAGGA GGCCTCGTCTGAGCCGTCCAAGCAGTCCCGGTCTGAGTCA | 3617 |
| | CTCACCTGT <u>T</u> GGTCCCGC | 3618 |
| | GCGGGACC <u>A</u> CAGGTGAG | 3619 |
| | | |
| Hypercholesterolaemia Gln133Term cCAG-TAG | TGCTTGGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCAC CTGTGGTCCCGCCAGCTTCC <u>A</u> GTGCAACAGCTCCACCTGCAT CCCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCG | 3620 |
| | CGCAGTCGGGGTCGTTGTGCGAGGCCACAGCTGGGGGATG CAGGTGGAGCTGTTGCACT <u>G</u> GAAGCTGGCGGGACCACAGGT GAGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAAGCA | 3621 |
| | CCAGCTTCC <u>C</u> AGTGCAAC | 3622 |
| | GTTGCACT <u>G</u> GAAGCTGG | 3623 |
| | | |
| Hypercholesterolaemia Cys134Gly gTGC-GGC | TTGGACGGCTCAGACGAGGCCTCCTGCCCGGTGCTCACCTG TGGTCCCGCCAGCTTCCAGT <u>G</u> GCAACAGCTCCACCTGCATCCC CCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAG | 3624 |
| | CTTCGCAGTCGGGGTCGTTGTGCGAGGCCACAGCTGGGGG ATGCAGGTGGAGCTGTTGC <u>A</u> CTGGAAGCTGGCGGGACCACA GGTGAGCACCGGGCAGGAGGCCTCGTCTGAGCCGTCCAA | 3625 |
| | GCTTCCAGT <u>G</u> GCAACAGC | 3626 |
| | GCTGTTGC <u>A</u> CTGGAAGC | 3627 |
| | | |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| Hypercholesterolaemia Cys139Gly cTGC-GGC | GAGGCCTCCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTT CCAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCCT GCGACAACGACCCCGACTGCGAAGATGGCTCGGATGAGT | 3628 |
| | ACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTGTCGCAG GCCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGAA GCTGGCGGGACCACAGGTGAGCACCGGGCAGGAGGCCTC | 3629 |
| | GCTCCACCTGCATCCCC | 3630 |
| | GGGGATGCAGGTGGAGC | 3631 |
| Hypercholesterolaemia Cys139Tyr TGC-TAC | AGGCCTCCTGCCCGGTGCTCACCTGTGGTCCCGCCAGCTTC CAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCCTG CGACAACGACCCCGACTGCGAAGATGGCTCGGATGAGTG | 3632 |
| | CACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTGTCGCAG GCCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGAA GCTGGCGGGACCACAGGTGAGCACCGGGCAGGAGGCCT | 3633 |
| | CTCCACCTGCATCCCC | 3634 |
| | GGGGGATGCAGGTGGAG | 3635 |
| Hypercholesterolaemia Cys146Term TGCg-TGA | CTGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCAT CCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAG ATGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTT | 3636 |
| | AAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTTC GCAGTCGGGGTCGTTGTGCGAGGCCACAGCTGGGGGATGC AGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACAG | 3637 |
| | TGGGCCTGCGACAACGA | 3638 |
| | TCGTTGTGCGAGGCCCA | 3639 |
| Hypercholesterolaemia Asp147Asn cGAC-AAC | TGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCATC CCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAGA TGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTT | 3640 |
| | AAAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTT CGCAGTCGGGGTCGTTGTGCGAGGCCACAGCTGGGGGATG CAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACA | 3641 |
| | GGGCCTGCGACAACGAC | 3642 |
| | GTCGTTGTGCGAGGCCCA | 3643 |
| Hypercholesterolaemia Asp147His cGAC-CAC | TGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCATC CCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAGA TGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTT | 3644 |
| | AAAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTT CGCAGTCGGGGTCGTTGTGCGAGGCCACAGCTGGGGGATG CAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACA | 3645 |
| | GGGCCTGCGACAACGAC | 3646 |
| | GTCGTTGTGCGAGGCCCA | 3647 |
| Hypercholesterolaemia Asp147Tyr cGAC-TAC | TGTGGTCCCGCCAGCTTCCAGTGCAACAGCTCCACCTGCATC CCCCAGCTGTGGGCCTGCGACAACGACCCCGACTGCGAAGA TGGCTCGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTT | 3648 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | AAAGACCCCTACAGCGCTGCGGCCACTCATCCGAGCCATCTT CGCAGTCGGGGTCGTTGT <u>C</u> GCAGGCCACAGCTGGGGGATG CAGGTGGAGCTGTTGCACTGGAAGCTGGCGGGACCACA | 3649 |
| | GGGCCTGC <u>G</u> ACAACGAC | 3650 |
| | GTCGTTGT <u>C</u> GCAGGCC | 3651 |
| Hypercholesterolaemia Cys152Arg cTGC-CGC | TTCCAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCC TGCGACAACGACCCCGACT <u>T</u> GCGAAGATGGCTCGGATGAGTG GCCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGG | 3652 |
| | CCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCGGCCAC TCATCCGAGCCATCTTCGC <u>A</u> GTCGGGGTCGTTGTCGCAGGC CCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGAA | 3653 |
| | ACCCCGACT <u>T</u> GCGAAGAT | 3654 |
| | ATCTTCGC <u>A</u> GTCGGGGT | 3655 |
| Hypercholesterolaemia Cys152Gly cTGC-GGC | TTCCAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCC TGCGACAACGACCCCGACT <u>T</u> GCGAAGATGGCTCGGATGAGTG GCCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGG | 3656 |
| | CCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCGGCCAC TCATCCGAGCCATCTTCGC <u>A</u> GTCGGGGTCGTTGTCGCAGGC CCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGGAA | 3657 |
| | ACCCCGACT <u>T</u> GCGAAGAT | 3658 |
| | ATCTTCGC <u>A</u> GTCGGGGT | 3659 |
| Hypercholesterolaemia Cys152Trp TGCg-TGG | CCAGTGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCCT GCGACAACGACCCCGACT <u>G</u> CGAAGATGGCTCGGATGAGTGG CCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGGAC | 3660 |
| | GTCCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCGGCC ACTCATCCGAGCCATCTTC <u>G</u> CAGTCGGGGTCGTTGTCGCAG GCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCACTGG | 3661 |
| | CCCGACT <u>G</u> CGAAGATGG | 3662 |
| | CCATCTTC <u>G</u> CAGTCGGG | 3663 |
| Hypercholesterolaemia Asp154Asn aGAT-AAT | TGCAACAGCTCCACCTGCATCCCCAGCTGTGGGCCTGCGA CAACGACCCCGACTGCGA <u>A</u> GATGGCTCGGATGAGTGCCGC AGCGCTGTAGGGGTCTTTACGTGTTCCAAGGGGACAGTA | 3664 |
| | TACTGTCCCCTTGGAACACGTAAAGACCCCTACAGCGCTGCG GCCACTCATCCGAGCCAT <u>C</u> TTGCGAGTCGGGGTCGTTGTCG CAGGCCACAGCTGGGGGATGCAGGTGGAGCTGTTGCA | 3665 |
| | ACTGCGA <u>A</u> GATGGCTCG | 3666 |
| | CGAGCCAT <u>C</u> TTGCGAGT | 3667 |
| Hypercholesterolaemia Ser156Leu TCG-TTG | GCTCCACCTGCATCCCCAGCTGTGGGCCTGCGACAACGAC CCCGACTGCGAAGATGGCT <u>C</u> GGATGAGTGCCGCAGCGCTG TAGGGGTCTTTACGTGTTCCAAGGGGACAGTAGCCCTG | 3668 |
| | CAGGGGCTACTGTCCCCTTGGAACACGTAAAGACCCCTACAG CGCTGCGGCCACTCATCC <u>G</u> AGCCATCTTCGCAGTCGGGGTC GTTGTCGCAGGCCACAGCTGGGGGATGCAGGTGGAGC | 3669 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | AGATGGCT <u>C</u> GGATGAGT | 3670 |
| | ACTCATCC <u>G</u> AGCCATCT | 3671 |
| Hypercholesterolaemia Cys163Tyr TGT-TAT | TGTGGGCCTGCGACAACGACCCCGACTGCGAAGATGGCTCG GATGAGTGGCCGACGCT <u>G</u> TAGGGGTCTTTACGTGTTCCAA GGGGACAGTAGCCCCTGCTCGGCCTTCGAGTTCCACTG | 3672 |
| | CAGTGGAACTCGAAGGCCGAGCAGGGGCTACTGTCCCCTTG GAACACGTAAAGACCCCTA <u>C</u> AGCGCTGCGGCCACTCATCCG AGCCATCTTCGCAGTCGGGGTCGTTGTCGCAGGCCCA | 3673 |
| | GCAGCGCT <u>G</u> TAGGGGTC | 3674 |
| | GACCCCTA <u>C</u> AGCGCTGC | 3675 |
| | | |
| Hypercholesterolaemia Tyr167Term TACg-TAG | CAACGACCCCGACTGCGAAGATGGCTCGGATGAGTGGCCGC AGCGCTGTAGGGGTCTTTA <u>C</u> GTGTTCCAAGGGGACAGTAGC CCCTGCTCGGCCTTCGAGTTCCACTGCCTAAGTGGCGAG | 3676 |
| | CTCGCCACTTAGGCAGTGGAAGTGAAGGCCGAGCAGGGG TACTGTCCCCTTGGAACAC <u>G</u> TAAAGACCCCTACAGCGCTGCG GCCACTCATCCGAGCCATCTTCGCAGTCGGGGTCGTTG | 3677 |
| | GGTCTTTA <u>C</u> GTGTTCCA | 3678 |
| | TGGAACAC <u>G</u> TAAAGACC | 3679 |
| Hypercholesterolaemia Gln170Term cCAA-TAA | CCCGACTGCGAAGATGGCTCGGATGAGTGGCCGCAGCGCTG TAGGGGTCTTTACGTGTT <u>C</u> AAGGGGACAGTAGCCCCTGCTC GGCCTTCGAGTTCCACTGCCTAAGTGGCGAGTGCATCC | 3680 |
| | GGATGCACTCGCCACTTAGGCAGTGGAAGTGAAGGCCGAG CAGGGGCTACTGTCCCCTT <u>G</u> GAACACGTAAAGACCCCTACAG CGCTGCGGCCACTCATCCGAGCCATCTTCGCAGTCGGG | 3681 |
| | ACGTGTT <u>C</u> AAGGGGAC | 3682 |
| | GTCCCCTT <u>G</u> GAACACGT | 3683 |
| Hypercholesterolaemia Cys176Phe TGC-TTC | CGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTTACGTGTTT CAAGGGGACAGTAGCCCCT <u>G</u> CTCGGCCTTCGAGTTCCACTG CCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGA | 3684 |
| | TCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCA GTGGAAGTGAAGGCCGAG <u>C</u> AGGGGCTACTGTCCCCTTGGA ACACGTAAAGACCCCTACAGCGCTGCGGCCACTCATCCG | 3685 |
| | TAGCCCCT <u>G</u> CTCGGCCT | 3686 |
| | AGGCCGAG <u>C</u> AGGGGCTA | 3687 |
| Hypercholesterolaemia Cys176Tyr TGC-TAC | CGGATGAGTGGCCGCAGCGCTGTAGGGGTCTTTACGTGTTT CAAGGGGACAGTAGCCCCT <u>G</u> CTCGGCCTTCGAGTTCCACTG CCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGA | 3688 |
| | TCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCA GTGGAAGTGAAGGCCGAG <u>C</u> AGGGGCTACTGTCCCCTTGGA ACACGTAAAGACCCCTACAGCGCTGCGGCCACTCATCCG | 3689 |
| | TAGCCCCT <u>G</u> CTCGGCCT | 3690 |
| | AGGCCGAG <u>C</u> AGGGGCTA | 3691 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Hypercholesterolaemia Ser177Leu TCG-TTG | ATGAGTGGCCGCAGCGCTGTAGGGGTCTTTACGTGTTCCAAG GGGACAGTAGCCCCTGCTCGGCCTTCGAGTTCCACTGCCTAA GTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGATGG | 3692 |
| | CCATCACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAG GCAGTGGAACTCGAAGGCCGAGCAGGGGCTACTGTCCCCTT GGAACACGTAAAGACCCCTACAGCGCTGCGGCCACTCAT | 3693 |
| | CCCCTGCTCGGCCTTCG | 3694 |
| | CGAAGGCCGAGCAGGGG | 3695 |
| Hypercholesterolaemia Glu187Lys cGAG-AAG | TACGTGTTCCAAGGGGACAGTAGCCCCTGCTCGGCCTTCGA GTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGC GCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACG | 3696 |
| | CGTCAGATTTGTCCTTGCAGTCGGGGCCACCATCACAGCGCC AGCTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAACTCG AAGGCCGAGCAGGGGCTACTGTCCCCTTGGAACACGTA | 3697 |
| | TAAGTGGCGAGTGCATC | 3698 |
| | GATGCACTCGCCACTTA | 3699 |
| Hypercholesterolaemia His190Tyr cCAC-TAC | CAAGGGGACAGTAGCCCCTGCTCGGCCTTCGAGTTCCACTG CCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGATG GTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAACT | 3700 |
| | AGTTTTCTCGTCAGATTTGTCCTTGCAGTCGGGGCCACCAT CACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCAG TGGAAGTCTGAAGGCCGAGCAGGGGCTACTGTCCCCTTG | 3701 |
| | AGTGCATCCACTCCAGC | 3702 |
| | GCTGGAGTGGATGCACT | 3703 |
| Hypercholesterolaemia Gly198Asp GGC-GAC | CCTTCGAGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCA GCTGGCGCTGTGATGGTGGCCCCGACTGCAAGGACAAATCT GACGAGGAAACTGCGGTATGGGCGGGGCCAGGGTGGG | 3704 |
| | CCCACCCTGGCCCCGCCCATACCGCAGTTTTCTCGTCAGAT TTGTCCTTGCAGTCGGGGCCACCATCACAGCGCCAGCTGGA GTGGATGCACTCGCCACTTAGGCAGTGGAACTCGAAGG | 3705 |
| | TGATGGTGGCCCCGACT | 3706 |
| | AGTCGGGGCCACCATCA | 3707 |
| Hypercholesterolaemia Asp200Asn cGAC-AAC | GAGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGG CGCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGA GGAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGG | 3708 |
| | CCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCTCG TCAGATTTGTCCTTGCAGTGGGGGCCACCATCACAGCGCCAG CTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAACTC | 3709 |
| | GTGGCCCCGACTGCAAG | 3710 |
| | CTTGCACTCGGGGCCAC | 3711 |
| Hypercholesterolaemia Asp200Gly GAC-GGC | AGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGC GCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAG GAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGG | 3712 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | CCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCCTC GTCAGATTTGTCCTTGCAGTCGGGGCCACCATCACAGCGCCA GCTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAAGT | 3713 |
| | TGGCCCCGACTGCAAGG | 3714 |
| | CCTTGCAGTCGGGGCCA | 3715 |
| Hypercholesterolaemia Asp200Tyr cGAC-TAC | GAGTTCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGG CGCTGTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGA GGAAACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGG | 3716 |
| | CCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTCCTCGT CAGATTTGTCCTTGCAGTCGGGGCCACCATCACAGCGCCAG CTGGAGTGGATGCACTCGCCACTTAGGCAGTGGAAGT | 3717 |
| | GTGGCCCCGACTGCAAG | 3718 |
| | CTTGCAGTCGGGGCCAC | 3719 |
| Hypercholesterolaemia Cys201Term TGCa-TGA | CCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCT GTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAA AACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGT | 3720 |
| | ACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTT CCTCGTCAGATTTGTCCTTGCAAGTCGGGGCCACCATCACAGC GCCAGCTGGAGTGGATGCACTCGCCACTTAGGCAGTGG | 3721 |
| | CCCGACTGCAAGGACAA | 3722 |
| | TTGTCCTTGCAAGTCGGG | 3723 |
| Hypercholesterolaemia Cys201Tyr TGC-TAC | TCCACTGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCT GTGATGGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAA AACTGCGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCG | 3724 |
| | CGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAGTTTTC CTCGTCAGATTTGTCCTTGCAAGTCGGGGCCACCATCACAGCG CCAGCTGGAGTGGATGCACTCGCCACTTAGGCAGTGGA | 3725 |
| | CCCGACTGCAAGGACA | 3726 |
| | TGTCCTTGCAAGTCGGG | 3727 |
| Hypercholesterolaemia Asp203Asn gGAC-AAC | TGCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGAT GGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAAAGT CGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTA | 3728 |
| | TAGGACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCAG TTTTCTCGTCAGATTTGTCCTTGCAAGTCGGGGCCACCATCA CAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGCA | 3729 |
| | ACTGCAAGGACAAATCT | 3730 |
| | AGATTTGTCCTTGCAAGT | 3731 |
| Hypercholesterolaemia Asp203Gly GAC-GGC | GCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGAT GGTGGCCCCGACTGCAAGGACAAATCTGACGAGGAAAAGT CGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTAT | 3732 |
| | ATAGGACGCCCCGCCCCCACCCTGGCCCCGCCCATACCGCA GTTTTCTCGTCAGATTTGTCCTTGCAAGTCGGGGCCACCATC ACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGC | 3733 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | CTGCAAGG <u>A</u> CAAATCTG | 3734 |
| | CAGATTTG <u>T</u> CCTTGCAG | 3735 |
| Hypercholesterolaemia Asp203Val GAC-GTC | GCCTAAGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGAT GGTGGCCCCGACTGCAAGG <u>A</u> CAAATCTGACGAGGAAAACCTG CGGTATGGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTAT | 3736 |
| | ATAGGACGCCCCGCCCCACCCTGGCCCCGCCCATACCGCA GTTTTCTCTCGTCAGATTTG <u>T</u> CCTTGCAGTCGGGGCCACCATC ACAGCGCCAGCTGGAGTGGATGCACTCGCCACTTAGGC | 3737 |
| | CTGCAAGG <u>A</u> CAAATCTG | 3738 |
| | CAGATTTG <u>T</u> CCTTGCAG | 3739 |
| Hypercholesterolaemia Ser205Pro aTCT-CCT | AGTGGCGAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGG CCCCGACTGCAAGGACAAAT <u>T</u> CTGACGAGGAAAACCTGCGGTAT GGGCGGGGCCAGGGTGGGGGCGGGGCGTCCTATCACCT | 3740 |
| | AGGTGATAGGACGCCCCGCCCCACCCTGGCCCCGCCCATAC CCGCAGTTTTCTCTCGTCAG <u>A</u> TTTGTCTTGCAGTCGGGGCCA CCATCACAGCGCCAGCTGGAGTGGATGCACTCGCCACT | 3741 |
| | AGGACAAAT <u>T</u> CTGACGAG | 3742 |
| | CTCGTCAG <u>A</u> TTTGTCTT | 3743 |
| Hypercholesterolaemia Asp206Glu GACg-GAG | CGAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCG ACTGCAAGGACAAATCTGAC <u>G</u> AGGAAAACCTGCGGTATGGGC GGGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCC | 3744 |
| | GGGACAGGTGATAGGACGCCCCGCCCCACCCTGGCCCCG CCCATACCGCAGTTTTCTC <u>G</u> TCAGATTTGTCTTGCAGTCG GGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTCG | 3745 |
| | AAATCTGAC <u>G</u> AGGAAAA | 3746 |
| | TTTTCTC <u>G</u> TCAGATT | 3747 |
| Hypercholesterolaemia Glu207Gln cGAG-CAG | GAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGA CTGCAAGGACAAATCTGAC <u>G</u> AGGAAAACCTGCGGTATGGGCG GGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCCT | 3748 |
| | AGGGACAGGTGATAGGACGCCCCGCCCCACCCTGGCCCC GCCCATACCGCAGTTTTCTC <u>G</u> TCAGATTTGTCTTGCAGTC GGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTC | 3749 |
| | AATCTGAC <u>G</u> AGGAAAAC | 3750 |
| | GTTTTCTC <u>G</u> TCAGATT | 3751 |
| Hypercholesterolaemia Glu207Lys cGAG-AAG | GAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGA CTGCAAGGACAAATCTGAC <u>G</u> AGGAAAACCTGCGGTATGGGCG GGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCCT | 3752 |
| | AGGGACAGGTGATAGGACGCCCCGCCCCACCCTGGCCCC GCCCATACCGCAGTTTTCTC <u>G</u> TCAGATTTGTCTTGCAGTC GGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTC | 3753 |
| | AATCTGAC <u>G</u> AGGAAAAC | 3754 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | GTTTTCCT <u>C</u> GTCAGATT | 3755 |
| Hypercholesterolaemia Glu207Term cGAG-TAG | GAGTGCATCCACTCCAGCTGGCGCTGTGATGGTGGCCCCGA CTGCAAGGACAAATCTGAC <u>G</u> AGGAAAAGTGCAGTATGGGCG GGGCCAGGGTGGGGGCGGGGCGTCCTATCACCTGTCCCT | 3756 |
| | AGGGACAGGTGATAGGACGCCCCGCCCCCACCCTGGCCCC GCCCATACCGCAGTTTTCTC <u>C</u> GTCAGATTTGTCCTTGCACTC GGGGCCACCATCACAGCGCCAGCTGGAGTGGATGCACTC | 3757 |
| | AATCTGAC <u>G</u> AGGAAAAC | 3758 |
| | GTTTTCCT <u>C</u> GTCAGATT | 3759 |
| Hypercholesterolaemia Glu219Lys cGAA-AAA | TCTTGAGAAAATCAACACACTCTGTCCTGTTTTCCAGCTGTGG CCACCTGTGCGCCTGAC <u>G</u> AATTCCAGTGCTCTGATGGAAACT GCATCCATGGCAGCCGGCAGTGTGACCGGGAATATG | 3760 |
| | CATATTCCCGGTCACACTGCCGGCTGCCATGGATGCAGTTTC CATCAGAGCACTGGAATT <u>C</u> GTCAGGGCGACAGGTGGCCACA GCTGGAAAACAGGACAGAGTGTGTTGATTTTCTCAAGA | 3761 |
| | GCCCTGAC <u>G</u> AATTCCAG | 3762 |
| | CTGGAATT <u>C</u> GTCAGGGC | 3763 |
| Hypercholesterolaemia Gln221Term cCAG-TAG | GAAAATCAACACACTCTGTCCTGTTTTCCAGCTGTGGCCACCT GTCGCCCTGACGAATT <u>C</u> AGTGCTCTGATGGAAACTGCATCC ATGGCAGCCGGCAGTGTGACCGGGAATATGACTGCA | 3764 |
| | TGCAGTCATATTCCCGGTCACACTGCCGGCTGCCATGGATGC AGTTTCCATCAGAGCACT <u>G</u> GAAATTCGTCAGGGCGACAGGTGG CCACAGCTGGAAAACAGGACAGAGTGTGTTGATTTTC | 3765 |
| | ACGAATT <u>C</u> AGTGCTCT | 3766 |
| | AGAGCACT <u>G</u> GAAATTCGT | 3767 |
| Hypercholesterolaemia Cys227Phe TGC-TTC | CCTGTTTTCCAGCTGTGGCCACCTGTCGCCCTGACGAATTCC AGTGCTCTGATGGAAACT <u>G</u> CATCCATGGCAGCCGGCAGTGT GACCGGGAATATGACTGCAAGGACATGAGCGATGAAGT | 3768 |
| | ACTTCATCGCTCATGTCCTTGCACTCATATTCCCGGTCACACT GCCGGCTGCCATGGATG <u>C</u> AGTTTCCATCAGAGCACTGGAATT CGTCAGGGCGACAGGTGGCCACAGCTGGAAAACAGG | 3769 |
| | TGGAAACT <u>G</u> CATCCATG | 3770 |
| | CATGGATG <u>C</u> AGTTTCCA | 3771 |
| Hypercholesterolaemia Asp235Glu GACc-GAA | TCGCCCTGACGAATTCCAGTGCTCTGATGGAAACTGCATCCA TGGCAGCCGGCAGTGTGAC <u>C</u> GGGGAATATGACTGCAAGGACA TGAGCGATGAAGTTGGCTGCGTTAATGGTGAGCGCTGG | 3772 |
| | CCAGCGCTCACCATTAAACGCAGCCAACTTCATCGCTCATGTC CTTGCACTCATATTCCCG <u>G</u> TCACACTGCCGGCTGCCATGGAT GCAGTTTCCATCAGAGCACTGGAATTCGTCAGGGCGA | 3773 |
| | CAGTGTGAC <u>C</u> GGGGAATA | 3774 |
| | TATTCCTCG <u>G</u> TCACACTG | 3775 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Hypercholesterolaemia Asp235Gly GAC-GGC | GTCGCCCTGACGAATTCCAGTGCTCTGATGGAACTGCATCC ATGGCAGCCGGCAGTGTG <u>A</u> CCGGGAATATGACTGCAAGGAC ATGAGCGATGAAGTTGGCTGCGTTAATGGTGAGCGCTG | 3776 |
| | CAGCGCTCACCATTAACGCAGCCAACTTCATCGCTCATGTCC TTGCAGTCATATTCCCGGT <u>C</u> ACACTGCCGGCTGCCATGGATG CAGTTTCCATCAGAGCACTGGAATTCGTCAGGGCGAC | 3777 |
| | GCAGTGTG <u>A</u> CCGGGAAT | 3778 |
| | ATTCCCGGT <u>C</u> ACACTGC | 3779 |
| Hypercholesterolaemia Glu237Lys gGAA-AAA | CCTGACGAATTCCAGTGCTCTGATGGAACTGCATCCATGGC AGCCGGCAGTGTGACCGGG <u>G</u> AATATGACTGCAAGGACATGAG CGATGAAGTTGGCTGCGTTAATGGTGAGCGCTGGCCAT | 3780 |
| | ATGGCCAGCGCTCACCATTAACGCAGCCAACTTCATCGCTCA TGTCCTTGCAAGTCATATT <u>C</u> CCGGTCACACTGCCGGCTGCCAT GGATGCAGTTTCCATCAGAGCACTGGAATTCGTCAGG | 3781 |
| | GTGACCGGG <u>G</u> AATATGAC | 3782 |
| | GTCATATT <u>C</u> CCGGTCAC | 3783 |
| Hypercholesterolaemia Cys240Phe TGC-TTC | TCCAGTGCTCTGATGGAACTGCATCCATGGCAGCCGGCAGT GTGACCGGGGAATATGACT <u>G</u> CAAGGACATGAGCGATGAAGTT GGCTGCGTTAATGGTGAGCGCTGGCCATCTGGTTTTCC | 3784 |
| | GGAAAACCAGATGGCCAGCGCTCACCATTAACGCAGCCAACT TCATCGCTCATGTCTTG <u>C</u> AGTCATATTCCCGGTACACTGCC GGCTGCCATGGATGCAGTTTCCATCAGAGCACTGGA | 3785 |
| | ATATGACT <u>G</u> CAAGGACA | 3786 |
| | TGTCCTTG <u>C</u> AGTCATAT | 3787 |
| Hypercholesterolaemia Asp245Glu GATg-GAA | AAACTGCATCCATGGCAGCCGGCAGTGTGACCGGGGAATATG ACTGCAAGGACATGAGCGAT <u>G</u> AAGTTGGCTGCGTTAATGGTG AGCGCTGGCCATCTGGTTTTCCATCCCCATTCTCTGT | 3788 |
| | ACAGAGAATGGGGGATGGAAAACCAGATGGCCAGCGCTCAC CATTAAACGCAGCCAACTTC <u>A</u> TCGCTCATGTCTTGCAAGTCATA TTCCCGGTACACTGCCGGCTGCCATGGATGCAGTTT | 3789 |
| | ATGAGCGAT <u>G</u> AAGTTGG | 3790 |
| | CCAACTTC <u>A</u> TCGCTCAT | 3791 |
| Hypercholesterolaemia Cys249Tyr TGC-TAC | ATGGCAGCCGGCAGTGTGACCGGGGAATATGACTGCAAGGAC ATGAGCGATGAAGTTGGCT <u>G</u> CGTTAATGGTGAGCGCTGGCC ATCTGGTTTTCCATCCCCATTCTCTGTGCCTTGCTGCT | 3792 |
| | AGCAGCAAGGCACAGAGAATGGGGGATGGAAAACCAGATGG CCAGCGCTCACCATTAACG <u>C</u> AGCCAACTTCATCGCTCATGTC CTTGCAAGTCATATTCCCGGTACACTGCCGGCTGCCAT | 3793 |
| | AGTTGGCT <u>G</u> CGTTAATG | 3794 |
| | CATTAAACG <u>C</u> AGCCAACT | 3795 |
| Hypercholesterolaemia Glu256Lys cGAG-AAG | AGGCTCAGACACACCTGACCTTCCTCCTCCTCTCTGGCT CTCACAGTGACACTCTG <u>C</u> GAGGGACCCAACAAGTTCAAGTGT CACAGCGGCGAATGCATCACCTGGACAAAGTCTGCA | 3796 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|--|------------|
| | TGCAGACTTTGTCCAGGGTGATGCATTGCCGCTGTGACACT TGAAGTTGTTGGGTCCTCGCAGAGTGTCAGTGTGAGAGCCA GAGAGAGGAAGGAGGAAGGTCAGGTGTGTCTGAGCCT | 3797 |
| | CACTCTGCGAGGGACCC | 3798 |
| | GGGTCCCTCGCAGAGTG | 3799 |
| Hypercholesterolaemia Ser265Arg AGCg-AGA | CCTCTCTCTGGCTCTCACAGTGACACTCTGCGAGGGACCCAA CAAGTTCAAGTGTCACAGCGGCGAATGCATCACCTGGACAA AGTCTGCAACATGGCTAGAGACTGCCGGGACTGGTCA | 3800 |
| | TGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTGTC CAGGGTGATGCATTGCCGCTGTGACACTTGAAGTTGTTGGG TCCCTCGCAGAGTGTCAGTGTGAGAGCCAGAGAGAGG | 3801 |
| | TGTCACAGCGGCGAATG | 3802 |
| | CATTCGCCGCTGTGACA | 3803 |
| Hypercholesterolaemia Glu267Lys cGAA-AAA | TCTCTGGCTCTCACAGTGACACTCTGCGAGGGACCCAACAAG TTCAAGTGTCACAGCGGCGAATGCATCACCTGGACAAAGTC TGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATG | 3804 |
| | CATCTGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTT TGTCCAGGGTGATGCATTGCCGCTGTGACACTTGAAGTTGT TGGGTCCCTCGCAGAGTGTCAGTGTGAGAGCCAGAGA | 3805 |
| | ACAGCGGCGAATGCATC | 3806 |
| | GATGCATTGCCGCTGT | 3807 |
| Hypercholesterolaemia Glu267Term cGAA-TAA | TCTCTGGCTCTCACAGTGACACTCTGCGAGGGACCCAACAAG TTCAAGTGTCACAGCGGCGAATGCATCACCTGGACAAAGTC TGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATG | 3808 |
| | CATCTGACCAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTT TGTCCAGGGTGATGCATTGCCGCTGTGACACTTGAAGTTGT TGGGTCCCTCGCAGAGTGTCAGTGTGAGAGCCAGAGA | 3809 |
| | ACAGCGGCGAATGCATC | 3810 |
| | GATGCATTGCCGCTGT | 3811 |
| Hypercholesterolaemia Lys273Glu cAAA-GAA | CACTCTGCGAGGGACCCAACAAGTTCAAGTGTCACAGCGG CGAATGCATCACCTGGACAAGTCTGCAACATGGCTAGAGA CTGCCGGGACTGGTCAGATGAACCCATCAAAGAGTGCG | 3812 |
| | CGCACTCTTTGATGGGTTTCTGACCAAGTCCCGGCAGTCTC TAGCCATGTTGCAGACTTTGTCCAGGGTGATGCATTGCCCGC TGTGACACTTGAAGTTGTTGGGTCCCTCGCAGAGTGT | 3813 |
| | CCCTGGACAAGTCTGC | 3814 |
| | GCAGACTTTGTCCAGGG | 3815 |
| Hypercholesterolaemia Cys275Term TGCg-TGA | CGAGGGACCCAACAAGTTCAAGTGTCACAGCGGCGAATGCA TCACCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGG GACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCT | 3816 |
| | AGACTCACCGCACTCTTTGATGGGTTCTGACCAAGTCCCG GCAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGGTGATGCA TTCGCCGCTGTGACACTTGAAGTTGTTGGGTCCCTCG | 3817 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | AAAGTCTGCAACATGGC | 3818 |
| | GCCATGTTGCAGACTTT | 3819 |
| Hypercholesterolaemia Asp280Gly GAC-GGC | AGTTCAAGTGTACAGCGGCGAATGCATCACCTGGACAAAG TCTGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATGAA CCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCT | 3820 |
| | AGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTCA TCTGACCAAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTG TCCAGGGTGATGCATTCGCCGCTGTGACACTTGA | 3821 |
| | GGCTAGAGACTGCCGGG | 3822 |
| | CCCGGCAGTCTCTAGCC | 3823 |
| | | |
| Hypercholesterolaemia Cys281Tyr TGC-TAC | TCAAGTGTACAGCGGCGAATGCATCACCTGGACAAAGTCT GCAACATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCC ATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGC | 3824 |
| | GCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGG TTCATCTGACCAAGTCCCGGCAGTCTCTAGCCATGTTGCAGAC TTTGTCCAGGGTGATGCATTCGCCGCTGTGACACTTGA | 3825 |
| | TAGAGACTGCCGGGACT | 3826 |
| | AGTCCCGGCAGTCTCTA | 3827 |
| Hypercholesterolaemia Asp283Asn gGAC-AAC | TGTCACAGCGGCGAATGCATCACCTGGACAAAGTCTGCAAC ATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAA GAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGT | 3828 |
| | ACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGA TGGGTTTCATCTGACCAAGTCCCGGCAGTCTCTAGCCATGTTGC AGACTTTGTCCAGGGTGATGCATTCGCCGCTGTGACA | 3829 |
| | ACTGCCGGGACTGGTCA | 3830 |
| | TGACCAAGTCCCGGCAGT | 3831 |
| Hypercholesterolaemia Asp283Glu GACt-GAG | TCACAGCGGCGAATGCATCACCTGGACAAAGTCTGCAACAT GGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAAAG AGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTT | 3832 |
| | AAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTT GATGGGTTTCATCTGACCAAGTCCCGGCAGTCTCTAGCCATGTT GCAGACTTTGTCCAGGGTGATGCATTCGCCGCTGTGA | 3833 |
| | TGCCGGGACTGGTCAGA | 3834 |
| | TCTGACCAAGTCCCGGCA | 3835 |
| Hypercholesterolaemia Asp283Tyr gGAC-TAC | TGTCACAGCGGCGAATGCATCACCTGGACAAAGTCTGCAAC ATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAA GAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGT | 3836 |
| | ACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGA TGGGTTTCATCTGACCAAGTCCCGGCAGTCTCTAGCCATGTTGC AGACTTTGTCCAGGGTGATGCATTCGCCGCTGTGACA | 3837 |
| | ACTGCCGGGACTGGTCA | 3838 |
| | TGACCAAGTCCCGGCAGT | 3839 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| Hypercholesterolaemia Trp284Term TGGt-TGA | CAGCGGCGAATGCATCACCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTTGTG | 3840 |
| | CACAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTTCATCTGACAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGGTGATGCATTGCGCCGTG | 3841 |
| | CGGGACTGGTCAGATGA | 3842 |
| | TCATCTGACAGTCCCG | 3843 |
| Hypercholesterolaemia Ser285Leu TCA-TTA | GCGGCGAATGCATCACCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTTGTGGG | 3844 |
| | CCCACAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTTCATCTGACAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGGTGATGCATTGCGCCG | 3845 |
| | GGACTGGTCAGATGAAC | 3846 |
| | GTTTCATCTGACAGTCC | 3847 |
| Hypercholesterolaemia Lys290Arg AAA-AGA | CCCTGGACAAAGTCTGCAACATGGCTAGAGACTGCCGGGACTGGTCAGATGAACCCATCAAAGAGTGCGGTGAGTCTCGGTGCAGGCGGCTTGCAGAGTTTGTGGGGAGCCAGGAAAGGGA | 3848 |
| | TCCCTTTCTGGCTCCCCACAACTCTGCAAGCCGCCTGCACCGAGACTCACCGCACTCTTTGATGGGTTTCATCTGACAGTCCCGGCAGTCTCTAGCCATGTTGCAGACTTTGTCCAGGG | 3849 |
| | ACCCATCAAAGAGTGCG | 3850 |
| | CGCACTCTTTGATGGGT | 3851 |
| Hypercholesterolaemia Cys297Phe TGC-TTC | GGGTAGGGGCCCCGAGAGTGACCAGTCTGCATCCCCTGGCCCTGCGCAGGGACCAACGAATGCTTGGACAACAACGGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTG | 3852 |
| | CACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCATTTCGTTGGTCCCTGCGCAGGGCCAGGGGATGCAGACTGGTCACTCTCGGGCCCCCTACCC | 3853 |
| | CAACGAATGCTTGGACA | 3854 |
| | TGTCCAAGCATTTCGTTG | 3855 |
| Hypercholesterolaemia Cys297Tyr TGC-TAC | GGGTAGGGGCCCCGAGAGTGACCAGTCTGCATCCCCTGGCCCTGCGCAGGGACCAACGAATGCTTGGACAACAACGGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTG | 3856 |
| | CACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCATTTCGTTGGTCCCTGCGCAGGGCCAGGGGATGCAGACTGGTCACTCTCGGGCCCCCTACCC | 3857 |
| | CAACGAATGCTTGGACA | 3858 |
| | TGTCCAAGCATTTCGTTG | 3859 |
| Hypercholesterolaemia His306Tyr cCAC-TAC | TGCATCCCCTGGCCCTGCGCAGGGACCAACGAATGCTTGGACAACAACGGCGGCTGTTCCACAGTCTGCAATGACCTTAAGATCGGCTACGAGTGCTGTGCCCGACGGCTTCCAGCTGG | 3860 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | CCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTAGCCGATC TTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGTTGTCC AAGCATTTCGTTGGTCCCTGCGCAGGGCCAGGGGATGCA | 3861 |
| | GCTGTTCCACGTCTGC | 3862 |
| | GCAGACGTGGGAACAGC | 3863 |
| Hypercholesterolaemia Cys308Gly cTGC-GGC | CCCTGGCCCTGCGCAGGGACCAACGAATGCTTGGACAACAA CGGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTA CGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCC | 3864 |
| | GGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTA GCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGT TGTGTCCAAGCATTTCGTTGGTCCCTGCGCAGGGCCAGGG | 3865 |
| | CCCACGTCTGCAATGAC | 3866 |
| | GTCATTGCAGACGTGGG | 3867 |
| Hypercholesterolaemia Cys308Tyr TGC-TAC | CCTGGCCCTGCGCAGGGACCAACGAATGCTTGGACAACAAC GGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTAC GAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCA | 3868 |
| | TGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTA GCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGT GTTGTCCAAGCATTTCGTTGGTCCCTGCGCAGGGCCAGG | 3869 |
| | CCACGTCTGCAATGACC | 3870 |
| | GGTCATTGCAGACGTGG | 3871 |
| Hypercholesterolaemia Gly314Ser cGGC-AGC | ACCAACGAATGCTTGGACAACAACGGCGGCTGTTCCACGTCT TGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGAC GGCTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTG | 3872 |
| | CACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCTG GGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGAC GTGGGAACAGCCGCCGTTGTTGTCCAAGCATTTCGTTGGT | 3873 |
| | TTAAGATCGGCTACGAG | 3874 |
| | CTCGTAGCCGATCTTA | 3875 |
| Hypercholesterolaemia Gly314Val GGC-GTC | CCAACGAATGCTTGGACAACAACGGCGGCTGTTCCACGTCT GCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGAC GGCTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGA | 3876 |
| | TCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCTG GGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGACG TGGGAACAGCCGCCGTTGTTGTCCAAGCATTTCGTTGG | 3877 |
| | TAAGATCGGCTACGAGT | 3878 |
| | ACTCGTAGCCGATCTTA | 3879 |
| Hypercholesterolaemia Tyr315Term TACg-TAA | CGAATGCTTGGACAACAACGGCGGCTGTTCCACGTCTGCAA TGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTT CCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTT | 3880 |
| | GAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCC GTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCA GACGTGGGAACAGCCGCCGTTGTTGTCCAAGCATTTCG | 3881 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | ATCGGCTAC <u>G</u> AGTGCCT | 3882 |
| | AGGCACTC <u>G</u> TAGCCGAT | 3883 |
| Hypercholesterolaemia Cys317Gly gTGC-GGC | TGCTTGGACAACAACGGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTCCGGG | 3884 |
| | CCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGC <u>A</u> CTCGTAGCCGATCTTAAGGTCA TTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCA | 3885 |
| | GCTACGAGTGCCTGTGC | 3886 |
| | GCACAGGC <u>A</u> CTCGTAGC | 3887 |
| Hypercholesterolaemia Cys317Ser gTGC-AGC | TGCTTGGACAACAACGGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTCCGGG | 3888 |
| | CCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGC <u>A</u> CTCGTAGCCGATCTTAAGGTCA TTGCAGACGTGGGAACAGCCGCCGTTGTTGTCCAAGCA | 3889 |
| | GCTACGAGTGCCTGTGC | 3890 |
| | GCACAGGC <u>A</u> CTCGTAGC | 3891 |
| Hypercholesterolaemia Pro320Arg CCC-CGC | ACAACGGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCC <u>C</u> GACGGCTTCCAGCTGGTGGCC CAGCGAAGATGCGAAGGTGATTTCCGGGTGGGACTGAG | 3892 |
| | CTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCG <u>G</u> GGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTTGT | 3893 |
| | CCTGTGCC <u>C</u> GACGGCT | 3894 |
| | AGCCGTCG <u>G</u> GGGCACAGG | 3895 |
| Hypercholesterolaemia Asp321Asn cGAC-AAC | AACGGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCC <u>G</u> ACGGCTTCCAGCTGGTGGCCCA GCGAAGATGCGAAGGTGATTTCCGGGTGGGACTGAGCC | 3896 |
| | GGCTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCCGTCG <u>G</u> GGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCGTT | 3897 |
| | TGTGCCCC <u>G</u> ACGGCTTC | 3898 |
| | GAAGCCGTCG <u>G</u> GGGCACA | 3899 |
| Hypercholesterolaemia Asp321Glu GACg-GAG | CGGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGAC <u>G</u> GGCTTCCAGCTGGTGGCCAGC GAAGATGCGAAGGTGATTTCCGGGTGGGACTGAGCCCT | 3900 |
| | AGGGCTCAGTCCCACCCGGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCC <u>G</u> TCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCCG | 3901 |
| | TGCCCCGACGGCTTCCA | 3902 |
| | TGGAAGCC <u>G</u> TCGGGGCA | 3903 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| Hypercholesterolaemia Gly322Ser cGGC-AGC | GGCGGCTGTTCCACGTCTGCAATGACCTTAAGATCGGCTAC GAGTGCCTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGCG AAGATGCGAAGGTGATTTCCGGGTGGGACTGAGCCCTG | 3904 |
| | CAGGGCTCAGTCCCACCCGAAATCACCTTCGCATCTTCGCT GGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCACTCGTA GCCGATCTTAAGGTCATTGCAGACGTGGGAACAGCCGCC | 3905 |
| | GCCCCGACGGCTTCCAG | 3906 |
| | CTGGAAGCCGTCGGGGC | 3907 |
| Hypercholesterolaemia Gln324Term cCAG-TAG | TGTTCCACGTCTGCAATGACCTTAAGATCGGCTACGAGTGC CTGTGCCCCGACGGCTTCCAGCTGGTGGCCCAGCGAAGATG CGAAGGTGATTTCCGGGTGGGACTGAGCCCTGGGCCCC | 3908 |
| | GGGGCCCAGGGCTCAGTCCCACCCGAAATCACCTTCGCAT CTTCGCTGGGCCACCAGCTGGAAGCCGTCGGGGCACAGGCA CTCGTAGCCGATCTTAAGGTCATTGCAGACGTGGGAACA | 3909 |
| | ACGGCTTCCAGCTGGTG | 3910 |
| | CACCAGCTGGAAGCCGT | 3911 |
| Hypercholesterolaemia Arg329Pro CGA-CCA | ATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGGCT TCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTCCGG GTGGGACTGAGCCCTGGGCCCCCTCTGCGCTTCCTGAC | 3912 |
| | GTCAGGAAGCGCAGAGGGGGGCCAGGGCTCAGTCCCACCC GGAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGC CGTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCAT | 3913 |
| | GGCCCAGCGAAGATGCG | 3914 |
| | CGCATCTTCGCTGGGCC | 3915 |
| Hypercholesterolaemia Arg329Term gCGA-TGA | AATGACCTTAAGATCGGCTACGAGTGCCTGTGCCCCGACGG CTTCCAGCTGGTGGCCCAGCGAAGATGCGAAGGTGATTTCC GGGTGGGACTGAGCCCTGGGCCCCCTCTGCGCTTCCTGA | 3916 |
| | TCAGGAAGCGCAGAGGGGGGCCAGGGCTCAGTCCCACCCG GAAATCACCTTCGCATCTTCGCTGGGCCACCAGCTGGAAGCC GTCGGGGCACAGGCACTCGTAGCCGATCTTAAGGTCATT | 3917 |
| | TGGCCCAGCGAAGATGC | 3918 |
| | GCATCTTCGCTGGGCCA | 3919 |
| Hypercholesterolaemia Glu336Lys tGAG-AAG | TCTAGCCATTGGGGAAGAGCCTCCCCACCAAGCCTCTTTCTC TCTCTTCCAGATATCGATGAGTGTGAGGATCCCGACACCTGC AGCCAGCTCTGCGTGAACCTGGAGGGTGGCTACAAGT | 3920 |
| | ACTTGTAGCCACCCTCCAGGTTACGCAGAGCTGGCTGCAG GTGTCGGGATCCTGACACTCATCGATATCTGGAAGAGAGAGA AAGAGGCTTGGTGGGGAGGCTCTTCCCCAATGGCTAGA | 3921 |
| | ATATCGATGAGTGTCAG | 3922 |
| | CTGACACTCATCGATAT | 3923 |
| Hypercholesterolaemia Gln338Term tCAG-TAG | CATTGGGGAAGAGCCTCCCCACCAAGCCTCTTTCTCTCTT CCAGATATCGATGAGTGTGAGGATCCCGACACCTGCAGCCAG CTCTGCGTGAACCTGGAGGGTGGCTACAAGTGCCAGT | 3924 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | ACTGGCACTTGTAGCCACCCTCCAGGTTACGCAGAGCTGG CTGCAGGTGTCGGGATCCTGACACTCATCGATATCTGGAAGA GAGAGAAAGAGGCTTGGTGGGGAGGCTCTTCCCCAATG | 3925 |
| | ATGAGTGTGAGGATCCC | 3926 |
| | GGGATCCTGACACTCAT | 3927 |
| Hypercholesterolaemia Cys343Arg cTGC-CGC | TCCCCACCAAGCCTCTTTCTCTCTTCCAGATATCGATGAGT GTCAGGATCCCGACACCTGCAGCCAGCTCTGCGTGAACCTG GAGGGTGGCTACAAGTGCCAGTGTGAGGAAGGCTTCC | 3928 |
| | GGAAGCCTTCCTCACACTGGCACTTGTAGCCACCCTCCAGGT TCACGCAGAGCTGGCTGCAGGTGTCGGGATCCTGACACTCA TCGATATCTGGAAGAGAGAGAAAGAGGCTTGGTGGGGA | 3929 |
| | CCGACACCTGCAGCCAG | 3930 |
| | CTGGCTGCAGGTGTCGG | 3931 |
| Hypercholesterolaemia Gln345Arg CAG-CGG | CAAGCCTCTTTCTCTCTTCCAGATATCGATGAGTGTGAGGA TCCCGACACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTG GCTACAAGTGCCAGTGTGAGGAAGGCTTCCAGCTGGA | 3932 |
| | TCCAGCTGGAAGCCTTCCTCACACTGGCACTTGTAGCCACCC TCCAGGTTACGCAGAGCTGGCTGCAGGTGTCGGGATCCTG ACACTCATCGATATCTGGAAGAGAGAGAAAGAGGCTTG | 3933 |
| | CTGCAGCCAGCTCTGCG | 3934 |
| | CGCAGAGCTGGCTGCAG | 3935 |
| Hypercholesterolaemia Cys347Tyr TGC-TAC | TCTTTCTCTCTTCCAGATATCGATGAGTGTGAGGATCCCGA CACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTACA AGTGCCAGTGTGAGGAAGGCTTCCAGCTGGACCCCCA | 3936 |
| | TGGGGTCCAGCTGGAAGCCTTCCTCACACTGGCACTTGTAG CCACCCTCCAGGTTACGCAGAGCTGGCTGCAGGTGTCGGG ATCCTGACACTCATCGATATCTGGAAGAGAGAGAAAGA | 3937 |
| | CCAGCTCTGCGTGAACC | 3938 |
| | GGTTCACGCAGAGCTGG | 3939 |
| Hypercholesterolaemia Cys347Arg cTGC-CGC | CTTTTCTCTCTTCCAGATATCGATGAGTGTGAGGATCCCG ACACCTGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTAC AAGTGCCAGTGTGAGGAAGGCTTCCAGCTGGACCCCC | 3940 |
| | GGGGGTCCAGCTGGAAGCCTTCCTCACACTGGCACTTGTAG CCACCCTCCAGGTTACGCAGAGCTGGCTGCAGGTGTCGGG ATCCTGACACTCATCGATATCTGGAAGAGAGAGAAAGAG | 3941 |
| | GCCAGCTCTGCGTGAAC | 3942 |
| | GTTACGCAGAGCTGGC | 3943 |
| Hypercholesterolaemia Gly352Asp GGT-GAT | CAGATATCGATGAGTGTGAGGATCCCGACACCTGCAGCCAGC TCTGCGTGAACCTGGAGGGTGGCTACAAGTGCCAGTGTGAG GAAGGCTTCCAGCTGGACCCCCACACGAAGGCCTGCAA | 3944 |
| | TTGCAGGCCTTCGTGTGGGGTCCAGCTGGAAGCCTTCCTC ACACTGGCACTTGTAGCCACCTCCAGGTTACGCAGAGCTG GCTGCAGGTGTCGGGATCCTGACACTCATCGATATCTG | 3945 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | CCTGGAGGGTGGCTACA | 3946 |
| | TGTAGCCACCCTCCAGG | 3947 |
| Hypercholesterolaemia Tyr354Cys TAC-TGC | TCGATGAGTGTGAGGATCCCGACACCTGCAGCCAGCTCTGC GTGAACCTGGAGGGTGGCTACAAGTGCCAGTGTGAGGAAGG CTTCCAGCTGGACCCCCACACGAAGGCCTGCAAGGCTGT | 3948 |
| | ACAGCCTTGCAGGCCTTCGTGTGGGGGTCCAGCTGGAAGCC TTCCTCACACTGGCACTTGTAGCCACCCTCCAGGTTACGCA GAGCTGGCTGCAGGTGTCGGGATCCTGACACTCATCGA | 3949 |
| | GGGTGGCTACAAGTGCC | 3950 |
| | GGCACTTGTAGCCACCC | 3951 |
| Hypercholesterolaemia Cys358Arg gTGT-CGT | CAGGATCCCGACACCTGCAGCCAGCTCTGCGTGAACCTGGA GGGTGGCTACAAGTGCCAGTGTGAGGAAGGCTTCCAGCTGG ACCCCCACACGAAGGCCTGCAAGGCTGTGGGTGAGCACG | 3952 |
| | CGTGCTACCCACAGCCTTGCAGGCCTTCGTGTGGGGGTCC AGCTGGAAGCCTTCCTCACACTGGCACTTGTAGCCACCCTCC AGGTTACGCAGAGCTGGCTGCAGGTGTCGGGATCCTG | 3953 |
| | AGTGCCAGTGTGAGGAA | 3954 |
| | TTCCTCACACTGGCACT | 3955 |
| Hypercholesterolaemia Gln363Term cCAG-TAG | TGCAGCCAGCTCTGCGTGAACCTGGAGGGTGGCTACAAGTG CCAGTGTGAGGAAGGCTTCCAGCTGGACCCCCACACGAAGG CCTGCAAGGCTGTGGGTGAGCACGGGAAGGCGGCGGGTG | 3956 |
| | CACCCGCCGCTTCCCGTGCTACCCACAGCCTTGCAGGCC TTCGTGTGGGGGTCCAGCTGGAAGCCTTCCTCACACTGGCA CTTGTAGCCACCCTCCAGGTTACGCAGAGCTGGCTGCA | 3957 |
| | AAGGCTTCCAGCTGGAC | 3958 |
| | GTCCAGCTGGAAGCCTT | 3959 |

EXAMPLE 23

UDP-glucuronosyltransferase - UGT1

[0236] Mutations in the human UGT1 gene result in a range of disease syndromes, ranging from relatively common diseases such as Gilbert's syndrome, which effects up to 7% of the population, to rare disorders such as Crigler-Najjar syndrome. Symptoms of these diseases are the result of diminished bilirubin conjugation and typically present with jaundice or, when mild, as an incidental finding during routing laboratory analysis. Severe cases of Crigler-Najjar syndrome are caused by an absence of UGT1 activity and the majority of these patients die in the neonatal period. The only known treatment is liver transplant. The attached table discloses the correcting oligonucleotide base sequences for the UGT1 oligonucleotides of the invention.

Table 25

UGT1 Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Crigler-Najjar syndrome 2 Leu15Arg CTG-CGG | GCAGGAGCAAAGGCGCCATGGCTGTGGAGTCCCAGGGCGG ACGCCCACCTTGTCTGGGCC <u>T</u> GCTGCTGTGTGTGCTGGGCC CAGTGGTGTCCCATGCTGGGAAGATACTGTTGATCCCAGT | 3960 |
| | ACTGGGATCAACAGTATCTTCCCAGCATGGGACACCACTGGG CCCAGCACACACAGCAGC <u>A</u> GGCCCAGGACAAGTGGGCGTCC GCCCTGGGACTCCACAGCCATGGCGCCTTTGCTCCTGC | 3961 |
| | CCTGGGCC <u>T</u> GCTGCTGT | 3962 |
| | ACAGCAGC <u>A</u> GGCCCAGG | 3963 |
| Crigler-Najjar syndrome 1 Gln49Term CAG-TAG | GGAAGATACTGTTGATCCCAGTGGATGGCAGCCACTGGCT GAGCATGCTTGGGGCCATC <u>C</u> AGCAGCTGCAGCAGAGGGGAC ATGAAATAGTTGTCTAGCACCTGACGCCTCGTTGTACA | 3964 |
| | TGTACAACGAGGCGTCAGGTGCTAGGACAACATTTTCATGTC CCCTCTGCTGCAGCTGCT <u>G</u> GATGGCCCCAAGCATGCTCAGC CAGTGGCTGCCATCCACTGGGATCAACAGTATCTTCCC | 3965 |
| | GGGCCATC <u>C</u> AGCAGCTG | 3966 |
| | CAGCTGCT <u>G</u> GATGGCCC | 3967 |
| Crigler-Najjar syndrome 1 Gly71Arg GGA-AGA | CAGCAGAGGGGACATGAAATAGTTGTCTAGCACCTGACGCC TCGTTGTACATCAGAGAC <u>G</u> GAGCATTTTACACCTTGAAGACG TACCCTGTGCCATTCCAAAGGGAGGATGTGAAAGAGT | 3968 |
| | ACTCTTTCACATCCTCCCTTTGGAATGGCACAGGGTACGTCTT CAAGGTGTAAAATGCTC <u>C</u> GTCTCTGATGTACAACGAGGCGTC AGGTGCTAGGACAACATTTTCATGTCCCCTCTGCTG | 3969 |
| | TCAGAGAC <u>G</u> GAGCATTT | 3970 |
| | AAATGCTC <u>C</u> GTCTCTGA | 3971 |
| Gilbert syndrome Pro229Gln CCG-CAG | GGGTGAAGAACATGCTCATTGCCTTTTACAGAACTTTCTGTG CGACGTGGTTTATTCCC <u>C</u> GTATGCAACCCTTGCCTCAGAATTC CTTCAGAGAGAGGTGACTGTCCAGGACCTATTGAG | 3972 |
| | CTCAATAGGTCCTGGACAGTCACCTCTCTCTGAAGGAATTCT GAGGCAAGGGTTGCATAC <u>G</u> GGGAATAAACCACGTGCGACAG AAAGTTCTGTGAAAAGGCAATGAGCATGTTCTTCACCC | 3973 |
| | TTATTCCC <u>C</u> GTATGCAA | 3974 |
| | TTGCATAC <u>G</u> GGGAATAA | 3975 |
| Crigler-Najjar syndrome 1 Cys280Term TGC-TGA | TGTGAAGGATTACCCTAGGCCCATCATGCCCAATATGGTTTTT GTTGGTGGAAATCAACTG <u>C</u> CTTCACCAAAAATCCACTATCCCAG GTGTGTATTGGAGTGGGACTTTTACATGCGTATATT | 3976 |
| | AATATACGCATGTAAAAGTCCCACTCCAATACACACCTGGGAT AGTGGATTTTGGTGAAG <u>G</u> CAGTTGATTCCACCAACAAAAACC ATATTGGGCATGATGGGCCTAGGGTAATCCTTCACA | 3977 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | ATCAACTG <u>C</u> CTTCACCA | 3978 |
| | TGGTGAAG <u>G</u> CAGTTGAT | 3979 |
| Crigler-Najjar syndrome 1 Ala292Val GCC-GTC | ATCAAAGAATATGAGAAAAAATTAAGTAAAATTTTTCTTCTGGCTCTAGGAATTTGAAG <u>C</u> CTACATTAATGCTTCTGGAGAACATGGAATTGTGGTTTTCTCTTTGGGATCAATGGTCTC | 3980 |
| | GAGACCATTGATCCCAAAGAGAAAACCACAATTCCATGTTCTCAGAAAGCATTAAATGTAG <u>G</u> CTTCAAATTCCTAGAGCCAGAAGAAAATTTTCAGTTAATTTTTTCTCATATTCTTTGAT | 3981 |
| | ATTTGAAG <u>C</u> CTACATTA | 3982 |
| | TAATGTAG <u>G</u> CTTCAAAT | 3983 |
| Crigler-Najjar syndrome 1 Gly308Glu GGA-GAA | AGGAATTTGAAGCCTACATTAATGCTTCTGGAGAACATGGAATGTGGTTTTCTCTTTGG <u>G</u> ATCAATGGTCTCAGAAATTCAGAGAAGAAAGCTATGGCAATTGCTGATGCTTTGGGCAA | 3984 |
| | TTGCCCAAAGCATCAGCAATTGCCATAGCTTTCTTCTCTGGAA TTTCTGAGACCATTGAT <u>C</u> CCCAAAGAGAAAACCACAATTCCATGTTCTCCAGAAGCATTAAATGTAGGCTTCAAATTCCT | 3985 |
| | CTCTTTGG <u>G</u> ATCAATGG | 3986 |
| | CCATTGAT <u>C</u> CCCAAAGAG | 3987 |
| Crigler-Najjar syndrome 1 Gln331Term CAG-TAG | GTCTCAGAAATTCAGAGAAGAAAGCTATGGCAATTGCTGATGCTTTGGGCAAAATCCCT <u>C</u> AGACAGTAAGAAGATTCTATACCATGGCCTCATATCTATTTTCACAGGAGCGCTAATCCC | 3988 |
| | GGGATTAGCGCTCCTGTGAAAATAGATATGAGGCCATGGTATAGAATCTTCTTACTGTCT <u>G</u> AGGGATTTTGCCCAAAGCATCAGCAATTGCCATAGCTTTCTTCTCTGGAATTTCTGAGAC | 3989 |
| | AAATCCCT <u>C</u> AGACAGTA | 3990 |
| | TACTGTCT <u>G</u> AGGGATTT | 3991 |
| Crigler-Najjar syndrome 1 Trp335Term TGG-TGA | TCTAATCATATTATGTTCTTTCTTTACGTTCTGCTCTTTTTGCCCTCCCAGGTCCTGTG <u>G</u> CGGTACACTGGAACCCGACCATCGAATCTTGCGAACAACACGATACTTGTTAAGTGGCTA | 3992 |
| | TAGCCACTTAACAAGTATCGTGTTGTTGCAAGATTTCGATGGTCGGGTTCCAGTGTACCG <u>C</u> CACAGGACCTGGGAGGGGGCAAAAAGAGCAGAACGTAAAGAAAGAACATAATATGATTAGA | 3993 |
| | GTCCTGTG <u>G</u> CGGTACAC | 3994 |
| | GTGTACCG <u>C</u> CACAGGAC | 3995 |
| Crigler-Najjar syndrome 1 Gln357Arg | ACACTGGAACCCGACCATCGAATCTTGCGAACAACACGATAC TTGTTAAGTGGCTACCCC <u>A</u> AAACGATCTGCTTGGTATGTTGGCGGATTGGATGTATAGGTCAAACCAGGGTCAAATTA | 3996 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| CAA-CGA | TAATTTGACCCTGGTTTGACCTATACATCCAATCCGCCCAACA TACCAAGCAGATCGTTTTGGGGTAGCCACTTAACAAGTATCG TGTTGTTTCGCAAGATTCGATGGTCGGGTTCCAGTGT | 3997 |
| | GCTACCCC <u>A</u> AAACGATC | 3998 |
| | GATCGTTTT <u>T</u> GGGGTAGC | 3999 |
| Crigler-Najjar syndrome 1 Gln357Term CAA-TAA | TACACTGGAACCCGACCATCGAATCTTGCGAACAACACGATA CTTGTTAAGTGGCTACCCC <u>C</u> AAAACGATCTGCTTGGTATGTTG GGCGGATTGGATGTATAGGTCAAACCAGGGTCAAATT | 4000 |
| | AATTTGACCCTGGTTTGACCTATACATCCAATCCGCCCAACAT ACCAAGCAGATCGTTTT <u>G</u> GGGTAGCCACTTAACAAGTATCGT GTTGTTTCGCAAGATTCGATGGTCGGGTTCCAGTGT | 4001 |
| | GGCTACCCC <u>C</u> AAAACGAT | 4002 |
| | ATCGTTTT <u>G</u> GGGTAGCC | 4003 |
| Gilbert syndrome Arg367Gly CGT-GGT | AACTCAGAGATGTAAGTCTGACATCCTCCCTATTTTGCATCT CAGGTCACCCGATGACCC <u>G</u> TGCCTTTATCACCCATGCTGGTT CCCATGGTGTATGAAAGCATATGCAATGGCGTTC | 4004 |
| | GAACGCCATTGCATATGCTTTCATAAACACCATGGGAACCAG CATGGGTGATAAAGGCAC <u>G</u> GGTCATCGGGTGACCTGAGATG CAAAATAGGGAGGATGTCAGCAGTTACATCTCTGAGTT | 4005 |
| | CGATGACCC <u>G</u> TGCCTTT | 4006 |
| | AAAGGCAC <u>G</u> GGTCATCG | 4007 |
| Crigler-Najjar syndrome 1 Ala368Thr GCC-ACC | TCAGAGATGTAAGTCTGACATCCTCCCTATTTTGCATCTCAG GTCACCCGATGACCC <u>G</u> TGCCTTTATCACCCATGCTGGTTCCC ATGGTGTATGAAAGCATATGCAATGGCGTTCCCA | 4008 |
| | TGGGAACGCCATTGCATATGCTTTCATAAACACCATGGGAAC CAGCATGGGTGATAAAGGCAC <u>G</u> GGTCATCGGGTGACCTGAG ATGCAAAATAGGGAGGATGTCAGCAGTTACATCTCTGA | 4009 |
| | TGACCCGT <u>G</u> CCTTTATC | 4010 |
| | GATAAAGGC <u>C</u> ACGGGTCA | 4011 |
| Crigler-Najjar syndrome 1 Ser375Phe TCC-TTC | CCTCCCTATTTTGCATCTCAGGTCACCCGATGACCCGTGCCT TTATCACCCATGCTGGTT <u>C</u> CCATGGTGTTTATGAAAGCATATG CAATGGCGTTCCCATGGTGATGATGCCCTTGTTTGG | 4012 |
| | CCAAACAAGGGCATCATCACCATGGGAACGCCATTGCATATG CTTTCATAAACACCATGGG <u>G</u> AACCAGCATGGGTGATAAAGGCA CGGGTCATCGGGTGACCTGAGATGCAAAATAGGGAGG | 4013 |
| | TGCTGGTT <u>C</u> CCATGGTG | 4014 |
| | CACCATGGG <u>G</u> AACCAGCA | 4015 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| Crigler-Najjar syndrome 1 Ser381Arg AGC-AGG | AGGTCACCCGATGACCCGTGCCTTTATCACCCATGCTGGTTC CCATGGTGTGTTTATGAAAGCATATGCAATGGCGTTCCCATGGT GATGATGCCCTTGTTTGGTGATCAGATGGACAATGCA | 4016 |
| | TGCATTGTCCATCTGATCACCAAACAAGGGCATCATCACCAT GGGAACGCCATTGCATATGCTTTTCATAAACACCATGGGAACC AGCATGGGTGATAAAGGCACGGGTCATCGGGTGACCT | 4017 |
| | TATGAAAGCATATGCAA | 4018 |
| | TTGCATATGCTTTTCATA | 4019 |
| Crigler-Najjar syndrome 1 Ala401Pro GCA-CCA | AGCATATGCAATGGCGTTCCCATGGTGATGATGCCCTTGTTT GGTGATCAGATGGACAATGCAAAGCGCATGGAGACTAAGGG AGCTGGAGTGACCCTGAATGTTCTGGAAATGACTTCTG | 4020 |
| | CAGAAGTCATTTCCAGAACATTCAGGGTCACTCCAGCTCCCT TAGTCTCCATGCGCTTTGCATTGTCCATCTGATCACCAAACAA GGGCATCATCACCATGGGAACGCCATTGCATATGCT | 4021 |
| | TGGACAATGCAAAGCGC | 4022 |
| | GCGCTTTGCATTGTCCA | 4023 |
| Crigler-Najjar syndrome 1 Lys428Glu AAA-GAA | GGAGCTGGAGTGACCCTGAATGTTCTGGAAATGACTTCTGAA GATTTAGAAAATGCTCTAAAGCAGTCATCAATGACAAAAGGT AAGAAAGAAGATACAGAAGAATACTTTGGTCATGGC | 4024 |
| | GCCATGACCAAAGTATTCTTCTGTATCTTCTTTCTTACCTTTTG TCATTGATGACTGCTTTAGAGCATTCTTCTAAATCTTCAGAAGT CATTTCCAGAACATTCAGGGTCACTCCAGCTCC | 4025 |
| | ATGCTCTAAAGCAGTC | 4026 |
| | GACTGCTTTAGAGCAT | 4027 |
| Crigler-Najjar syndrome 1 Tyr486Asp TAC-GAC | ATGAGGCACAAGGGCGCGCCACACCTGCGCCCCGCAGCCCA CGACCTCACCTGGTACCAGTACCATTCTTGACGTGATTGG TTTCCTCTTGCGCGTCGTGCTGACAGTGGCCTTCATCA | 4028 |
| | TGATGAAGGCCACTGTCAGCACGACGGCCAAGAGGAAACCA ATCACGTCCAAGGAATGGTACTGGTACCAGGTGAGGTCGTG GGCTGCGGGGCGCAGGTGTGGCGCGCCCTTGTCCTCAT | 4029 |
| | GGTACCAGTACCATTCC | 4030 |
| | GGAATGGTACTGGTACC | 4031 |
| Crigler-Najjar syndrome 1 Ser488Phe TCC-TTC | ACAAGGGCGCGCCACACCTGCGCCCCGCAGCCACGACCTC ACCTGGTACCAGTACCATTCTTGACGTGATTGGTTTCTCT TGGCCGTCTGTGCTGACAGTGGCCTTCATCACCTTTAA | 4032 |
| | TTAAAGGTGATGAAGGCCACTGTCAGCACGACGGCCAAGAG GAAACCAATCACGTCCAAGGAATGGTACTGGTACCAGGTGAG GTCGTGGGCTGCGGGGCGCAGGTGTGGCGCGCCCTTG | 4033 |
| | GTACCATTCTTGACG | 4034 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|-------------------------------|-------------------|------------|
| | CGTCCAAGGAATGGTAC | 4035 |

EXAMPLE 24

Alzheimer's Disease - Amyloid precursor protein (APP)

[0237] Over the past few decades Alzheimer's disease (AD), once considered a rare disorder, has become recognized as a major public health problem. Although there is no agreement on the exact prevalence of Alzheimer's disease, in part due to difficulties of diagnosis, studies consistently point to an exponential rise in prevalence of this disease with age. After age 65, the percentage of affected people approximately doubles with every decade of life, regardless of definition. Among people age 85 or older, studies suggest that 25 to 35 percent have dementia, including Alzheimer's disease; one study reports that 47.2 percent of people over age 85 have Alzheimer's disease, exclusive of other dementias.

[0238] Alzheimer's disease progressively destroys memory, reason, judgment, language, and, eventually, the ability to carry out even the simplest tasks. Anatomic changes associated with Alzheimer's disease begin in the entorhinal cortex, proceed to the hippocampus, and then gradually spread to other regions, particularly the cerebral cortex. Chief among such anatomic changes are the presence of characteristic extracellular plaques and internal neurofibrillary tangles.

[0239] At least four genes have been identified to date that contribute to development of Alzheimer's disease: AD1 is caused by mutations in the amyloid precursor gene (APP); AD2 is associated with a particular allele of APOE (see Example 20); AD3 is caused by mutation in a gene encoding a 7-transmembrane domain protein, presenilin-1 (PSEN1), and AD4 is caused by mutation in a gene that encodes a similar 7-transmembrane domain protein, presenilin-2 (PSEN2). The attached table discloses the correcting oligonucleotide base sequences for the APP oligonucleotides of the invention.

Table 26

APP Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| Alzheimer disease Glu665Asp GAG-GAC | CTGCATACTTTAATTATGATGTAATACAGGTTCTGGGTTGACA AATATCAAGACGGAGGAGATCTCTGAAGTGAAGATGGATGCA GAATTCCGACATGACTCAGGATATGAAGTTCATCAT | 4036 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | ATGATGAACTTCATATCCTGAGTCATGTCGGAATTCTGCATCC ATCTTCACTTCAGAGATCTCCTCCGTCTTGATATTTGTCAACC CAGAACCTGTATTACATCATAATTAAAGTATGCAG | 4037 |
| | ACGGAGGAGATCTCTGA | 4038 |
| | TCAGAGATCTCCTCCGT | 4039 |
| Alzheimer disease Ala692Gly GCA-GGA | ATTATATTGCATTTAGAAATTAATAATTCTTTTTCTTAATTTGTTT TCAAGGTGTTCTTTGCAGAGATGTGGGTTCAAACAAAGGTG CAATCATTGGACTCATGGTGGGCGGTGTTGTCAT | 4040 |
| | ATGACAACACCGCCACCATGAGTCCAATGATTGCACCTTTG TTTGAACCCACATCTTCTGCAAAGAACACCTTGAAAACAAATT AAGAAAAAGAATTTTAATTTCTAAATGCAATATAAT | 4041 |
| | GTTCTTTGCAGAAGATG | 4042 |
| | CATCTTCTGCAAAGAAC | 4043 |
| Alzheimer disease Glu693Gln GAA-CAA | TATATTGCATTTAGAAATTAATAATTCTTTTTCTTAATTTGTTTT AAGGTGTTCTTTGCAGAGATGTGGGTTCAAACAAAGGTGCA ATCATTGGACTCATGGTGGGCGGTGTTGTCATAG | 4044 |
| | CTATGACAACACCGCCACCATGAGTCCAATGATTGCACCTT TGTTTGAACCCACATCTTCTGCAAAGAACACCTTGAAAACAAA TTAAGAAAAAGAATTTTAATTTCTAAATGCAATATA | 4045 |
| | TCTTTGCAGAGATGTG | 4046 |
| | CACATCTTCTGCAAAGA | 4047 |
| Alzheimer disease Glu693Gly GAA-GGA | ATATTGCATTTAGAAATTAATAATTCTTTTTCTTAATTTGTTTTCA AGGTGTTCTTTGCAGAGATGTGGGTTCAAACAAAGGTGCAA TCATTGGACTCATGGTGGGCGGTGTTGTCATAGC | 4048 |
| | GCTATGACAACACCGCCACCATGAGTCCAATGATTGCACCT TTGTTTGAACCCACATCTTCTGCAAAGAACACCTTGAAAACAA ATTAAGAAAAAGAATTTTAATTTCTAAATGCAATAT | 4049 |
| | CTTTGCAGAGATGTGG | 4050 |
| | CCACATCTTCTGCAAAG | 4051 |
| Alzheimer disease Ala713Thr GCG-ACG | GAAGATGTGGGTTCAAACAAAGGTGCAATCATTGGACTCATG GTGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTG GTGATGCTGAAGAAGAAACAGTACACATCCATTCATC | 4052 |
| | GATGAATGGATGTGTACTGTTTCTTCTTCAGCATCACCAAGGT GATGACGATCACTGTGCTATGACAACACCGCCACCATGAG TCCAATGATTGCACCTTTGTTTGAACCCACATCTTC | 4053 |
| | TTGTCATAGCGACAGTG | 4054 |
| | CACTGTCGCTATGACAA | 4055 |
| Schizophrenia Ala713Val GCG-GTG | AAGATGTGGGTTCAAACAAAGGTGCAATCATTGGACTCATGG TGGGCGGTGTTGTCATAGCGACAGTGATCGTCATCACCTTGG TGATGCTGAAGAAGAAACAGTACACATCCATTCATCA | 4056 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | TGATGAATGGATGTGTACTGTTTCTTCTTCAGCATCACCAAGG TGATGACGATCACTGT <u>C</u> GCTATGACAACACCGCCCACCATGA GTCCAATGATTGCACCTTTGTTTGAACCCACATCTT | 4057 |
| | TGTCATAG <u>C</u> GACAGTGA | 4058 |
| | TCACTGT <u>C</u> GCTATGACA | 4059 |
| Alzheimer disease Val715Met GTG-ATG | GTGGGTTCAAACAAAGGTGCAATCATTGGACTCATGGTGGGC GGTGTGTGCATAGCGACAGT <u>G</u> TGATCGTCATCACCTTGGTGATG CTGAAGAAGAAACAGTACACATCCATTTCATCATGGTG | 4060 |
| | CACCATGATGAATGGATGTGTACTGTTTCTTCTTCAGCATCAC CAAGGTGATGACGATCA <u>C</u> TGTCGCTATGACAACACCGCCCAC CATGAGTCCAATGATTGCACCTTTGTTTGAACCCAC | 4061 |
| | TAGCGACAGT <u>G</u> TGATCGTC | 4062 |
| | GACGATCA <u>C</u> TGTCGCTA | 4063 |
| Alzheimer disease Ile716Val ATC-GTC | GGTTCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGT GTTGTGCATAGCGACAGTG <u>A</u> TGTCATCACCTTGGTGATGCTG AAGAAGAAACAGTACACATCCATTTCATCATGGTGTGG | 4064 |
| | CCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAGCAT CACCAAGGTGATGACGAT <u>C</u> ACTGTCGCTATGACAACACCGCC CACCATGAGTCCAATGATTGCACCTTTGTTTGAACC | 4065 |
| | CGACAGTG <u>A</u> TGTCATC | 4066 |
| | GATGACGAT <u>C</u> ACTGTGCG | 4067 |
| Alzheimer disease Val717Gly GTC-GGC | CAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTTG TCATAGCGACAGTGATCGT <u>I</u> CATCACCTTGGTGATGCTGAAGA AGAAACAGTACACATCCATTTCATCATGGTGTGGTGG | 4068 |
| | TCCACCACCATGATGAATGGATGTGTACTGTTTCTTCTTCA GCATCACCAGGTGATG <u>A</u> CGATCACTGTCGCTATGACAACAC CGCCACCATGAGTCCAATGATTGCACCTTTGTTTG | 4069 |
| | AGTGATCGT <u>I</u> CATCACCT | 4070 |
| | AGGTGATG <u>A</u> CGATCACT | 4071 |
| Alzheimer disease Val717Ile GTC-ATC | TCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTT GTCATAGCGACAGTGATC <u>G</u> TGTCATCACCTTGGTGATGCTGAAG AAGAAACAGTACACATCCATTTCATCATGGTGTGGTGG | 4072 |
| | CCACCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAG CATCACCAGGTGATG <u>A</u> CGATCACTGTCGCTATGACAACACC GCCCACCATGAGTCCAATGATTGCACCTTTGTTTGA | 4073 |
| | CAGTGATC <u>G</u> TGTCATCACC | 4074 |
| | GGTGATG <u>A</u> CGATCACTG | 4075 |
| Alzheimer disease Val717Phe GTC-TTC | TCAAACAAAGGTGCAATCATTGGACTCATGGTGGGCGGTGTT GTCATAGCGACAGTGATC <u>G</u> TGTCATCACCTTGGTGATGCTGAAG AAGAAACAGTACACATCCATTTCATCATGGTGTGGTGG | 4076 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | CCACCACACCATGATGAATGGATGTGTACTGTTTCTTCTTCAG CATCACCAAGGTGATGACGATCACTGTCGCTATGACAACACC GCCCACCATGAGTCCAATGATTGCACCTTTGTTTGA | 4077 |
| | CAGTGATCGTCATCACC | 4078 |
| | GGTGATGACGATCACTG | 4079 |
| Alzheimer disease Leu723Pro CTG-CCG | TTGGACTCATGGTGGGCGGTGTTGTCATAGCGACAGTGATCG TCATCACCTTGGTGATGCTGAAGAAGAAACAGTACACATCCAT TCATCATGGTGTGGTGGAGGTAGGTAAACTTGACTG | 4080 |
| | CAGTCAAGTTTACCTACCTCCACCACACCATGATGAATGGAT GTGTACTGTTTCTTCTTCAGCATCACCAAGGTGATGACGATCA CTGTCGCTATGACAACACCGCCCACCATGAGTCCAA | 4081 |
| | GGTGATGCTGAAGAAGA | 4082 |
| | TCTTCTTCAGCATCACC | 4083 |

EXAMPLE 25

Alzheimer's Disease - presenilin-1 (PSEN1)

[0240] The attached table discloses the correcting oligonucleotide base sequences for the PSEN1 oligonucleotides of the invention.

5

Table 27

PSEN1 Mutations and Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| Alzheimer disease Ala79Val GCC-GTC | CCCGGCAGGTGGTGGAGCAAGATGAGGAAGAAGATGAGGAG CTGACATTGAAATATGGCGCCAAGCATGTGATCATGCTCTTTG TCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTAC | 4084 |
| | GTAGCCACGACCACCACCATGCAGAGAGTCACAGGGACAAA GAGCATGATCACATGCTTGCGCCATATTTCAATGTCAGCTC CTCATCTTCTTCCTCATCTTGCTCCACCACCTGCCGGG | 4085 |
| | ATATGGCGCCAAGCATG | 4086 |
| | CATGCTTGCGCCATAT | 4087 |
| Alzheimer disease Val82Leu tGTG-CTG | GTGGTGGAGCAAGATGAGGAAGAAGATGAGGAGCTGACATT GAAATATGGCGCCAAGCATGTGATCATGCTCTTTGTCCCTGT GACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGT | 4088 |
| | ACTTAATGGTAGCCACGACCACCACCATGCAGAGAGTCACAG GGACAAAGAGCATGATCATGCTTGCGCCATATTTCAATG TCAGCTCCTCATCTTCTTCCTCATCTTGCTCCACCAC | 4089 |
| | CCAAGCATGTGATCATG | 4090 |
| | CATGATCATGCTTG | 4091 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Alzheimer disease Val96Phe gGTC-TTC | AAATATGGCGCCAAGCATGTGATCATGCTCTTTGTCCCTGTG ACTCTCTGCATGGTGGTGGTCGTGGCTACCATTAAGTCAGTC AGCTTTTATACCCGGAAGGATGGGCAGCTGTACGTAT | 4092 |
| | ATACGTACAGCTGCCCATCCTTCGGGTATAAAAGCTGACTG ACTTAATGGTAGCCACGACCACCACCATGCAGAGAGTCACAG GGACAAAGAGCATGATCACATGCTTGGCGCCATATTT | 4093 |
| | TGGTGGTGGTCGTGGCT | 4094 |
| | AGCCACGACCACCACCA | 4095 |
| Alzheimer disease Phe105Leu TTTt-TTG | CTTTGTCCCTGTGACTCTCTGCATGGTGGTGGTCGTGGCTAC CATTAAAGTCAGTCAGCTTTTATACCCGGAAGGATGGGCAGCT GTACGTATGAGTTTTGTTTTATTATTCTCAAAGCCAG | 4096 |
| | CTGGCTTTGAGAATAATAAAACAAACTCATACGTACAGCTGC CCATCCTTCGGGTATAAAGCTGACTGACTTAATGGTAGCC ACGACCACCACCATGCAGAGAGTCACAGGGACAAAG | 4097 |
| | GTCAGCTTTTATACCCG | 4098 |
| | CGGGTATAAAGCTGAC | 4099 |
| Alzheimer disease Thr116Asn ACC-AAC | TGGTGATCTCCATTAACACTGACCTAGGGCTTTTGTGTTTGT TTATTGTAGAATCTATACCCATTCACAGAAGATACCGAGACT GTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGC | 4100 |
| | GCATTACAGAATTGAGTGCAGGGCTCTCTGGCCACAGTCTCG GTATCTTCTGTGAATGGGGTATAGATTCTACAATAAAACAAAC ACAAAAGCCCTAGGTCAGTGTTAATGGAGATCACCA | 4101 |
| | AATCTATACCCATTCA | 4102 |
| | TGAATGGGGTATAGATT | 4103 |
| Alzheimer disease Pro117Leu CCA-CTA | TGATCTCCATTAACACTGACCTAGGGCTTTTGTGTTTGT TGTAAGATCTATACCCATTACACAGAAGATACCGAGACTGTG GGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGC | 4104 |
| | GCAGCATTACAGAATTGAGTGCAGGGCTCTCTGGCCACAGTC TCGGTATCTTCTGTGAATGGGGTATAGATTCTACAATAAAACA AACACAAAAGCCCTAGGTCAGTGTTAATGGAGATCA | 4105 |
| | CTATACCCATTACAG | 4106 |
| | CTGTGAATGGGGTATAG | 4107 |
| Alzheimer disease Glu120Asp GAAg-GAT | TAACACTGACCTAGGGCTTTTGTGTTTGT ATACCCATTACAGAAAGATACCGAGACTGTGGGCCAGAGAG CCCTGCACTCAATTCTGAATGCTGCCATCATGATC | 4108 |
| | GATCATGATGGCAGCATTACAGAATTGAGTGCAGGGCTCTCTG GCCACAGTCTCGGTATCTTCTGTGAATGGGGTATAGATTCT ACAATAAAACAAACACAAAAGCCCTAGGTCAGTGTTA | 4109 |
| | TTCACAGAAAGATACCGA | 4110 |
| | TCGGTATCTTCTGTGAA | 4111 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Alzheimer disease Glu120Asp GAAg-GAC | TAACACTGACCTAGGGCTTTTGTGTTTGTGTTTATTGTAGAATCT ATACCCCATTCACAGAAGATACCGAGACTGTGGGCCAGAGAG CCCTGCACTCAATTCTGAATGCTGCCATCATGATC | 4112 |
| | GATCATGATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTG GCCCACAGTCTCGGTATCTTCTGTGAATGGGGTATAGATTCT ACAATAAAACAAACACAAAAGCCCTAGGTCAGTGTTA | 4113 |
| | TTCACAGAAGATACCGA | 4114 |
| | TCGGTATCTTCTGTGAA | 4115 |
| Alzheimer disease Glu120Lys aGAA-AAA | ATTAACACTGACCTAGGGCTTTTGTGTTTGTGTTTATTGTAGAAT CTATACCCCATTCACAGAAGATACCGAGACTGTGGGCCAGAG AGCCCTGCACTCAATTCTGAATGCTGCCATCATGA | 4116 |
| | TCATGATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGGC CCACAGTCTCGGTATCTTCTGTGAATGGGGTATAGATTCTACA ATAAAACAAACACAAAAGCCCTAGGTCAGTGTTAAT | 4117 |
| | CATTCACAGAAGATACC | 4118 |
| | GGTATCTTCTGTGAATG | 4119 |
| Alzheimer disease Glu123Lys cGAG-AAG | GACCTAGGGCTTTTGTGTTTGTGTTTATTGTAGAATCTATACCC CATTACAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTG CACTCAATTCTGAATGCTGCCATCATGATCAGTGTC | 4120 |
| | TGACACTGATCATGATGGCAGCATTGAGAATTGAGTGCAGGG CTCTCTGGCCCACAGTCTCGGTATCTTCTGTGAATGGGGTAT AGATTCTACAATAAAACAAACACAAAAGCCCTAGGTC | 4121 |
| | AAGATACCGAGACTGTG | 4122 |
| | CACAGTCTCGGTATCTT | 4123 |
| Alzheimer disease Asn135Asp gAAT-GAT | TATACCCCATTCACAGAAGATACCGAGACTGTGGGCCAGAGA GCCCTGCACTCAATTCTGAATGCTGCCATCATGATCAGTGTC ATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTATA | 4124 |
| | TATACAGAACCACCAGGAGGATAGTCATGACAACAATGACAC TGATCATGATGGCAGCATTCAGAATTGAGTGCAGGGCTCTCT GGCCCACAGTCTCGGTATCTTCTGTGAATGGGGTATA | 4125 |
| | CAATTCTGAATGCTGCC | 4126 |
| | GGCAGCATTCAGAATTG | 4127 |
| Alzheimer disease Met139Ile ATGa-ATA | AGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCAA TTCTGAATGCTGCCATCATGATCAGTGTCATTGTTGTCATGAC TATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTAT | 4128 |
| | ATAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCAT GACAACAATGACACTGATCATGATGGCAGCATTGAGAATTGA GTGCAGGGCTCTCTGGCCCACAGTCTCGGTATCTTCT | 4129 |
| | GCCATCATGATCAGTGT | 4130 |
| | AACTGATCATGATGGC | 4131 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Alzheimer disease Met139Lys ATG-AAG | CAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCA ATTCTGAATGCTGCCATCATGATCAGTGTCAATTGTTGTCATGA CTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTA | 4132 |
| | TAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATG ACAACAATGACACTGATCATGATGGCAGCATTGAGAATTGAG TGCAGGGCTCTCTGGCCACAGTCTCGGTATCTTCTG | 4133 |
| | TGCCATCATGATCAGTG | 4134 |
| | CACTGATCATGATGGCA | 4135 |
| Alzheimer disease Met139Thr ATG-ACG | CAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTCA ATTCTGAATGCTGCCATCATGATCAGTGTCAATTGTTGTCATGA CTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCTA | 4136 |
| | TAGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATG ACAACAATGACACTGATCATGATGGCAGCATTGAGAATTGAG TGCAGGGCTCTCTGGCCACAGTCTCGGTATCTTCTG | 4137 |
| | TGCCATCATGATCAGTG | 4138 |
| | CACTGATCATGATGGCA | 4139 |
| Alzheimer disease Met139Val cATG-GTG | ACAGAAGATACCGAGACTGTGGGCCAGAGAGCCCTGCACTC AATTCTGAATGCTGCCATCATGATCAGTGTCAATTGTTGTCATG ACTATCCTCCTGGTGGTTCTGTATAAATACAGGTGCT | 4140 |
| | AGCACCTGTATTTATACAGAACCACCAGGAGGATAGTCATGA CAACAATGACACTGATCATGATGGCAGCATTGAGAATTGAGT GCAGGGCTCTCTGGCCACAGTCTCGGTATCTTCTGT | 4141 |
| | CTGCCATCATGATCAGT | 4142 |
| | ACTGATCATGATGGCAG | 4143 |
| Alzheimer disease Ile143Phe cATT-TTT | GAGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCT GCCATCATGATCAGTGTCAATTGTTGTCATGACTATCCTCCTGG TGGTTCTGTATAAATACAGGTGCTATAAGGTGAGCA | 4144 |
| | TGCTCACCTTATAGCACCTGTATTTATACAGAACCACCAGGAG GATAGTCATGACAACAATGACACTGATCATGATGGCAGCATT CAGAATTGAGTGCAGGGCTCTCTGGCCACAGTCTC | 4145 |
| | TCAGTGTCATTGTTGTC | 4146 |
| | GACAACAATGACACTGA | 4147 |
| Alzheimer disease Ile143Thr ATT-ACT | AGACTGTGGGCCAGAGAGCCCTGCACTCAATTCTGAATGCTG CCATCATGATCAGTGTCAATTGTTGTCATGACTATCCTCCTGGT GGTTCTGTATAAATACAGGTGCTATAAGGTGAGCAT | 4148 |
| | ATGCTCACCTTATAGCACCTGTATTTATACAGAACCACCAGGA GGATAGTCATGACAACAATGACACTGATCATGATGGCAGCAT TCAGAATTGAGTGCAGGGCTCTCTGGCCACAGTCT | 4149 |
| | CAGTGTCATTGTTGTCA | 4150 |
| | TGACAACAATGACACTG | 4151 |
| Alzheimer disease Met146Ile ATGa-ATA | CCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGAT CAGTGTCATTGTTGTCATGACTATCCTCCTGGTGGTTCTGTAT AAATACAGGTGCTATAAGGTGAGCATGAGACACAGA | 4152 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | TCTGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGA ACCACCAGGAGGATAGT <u>C</u> ATGACAACAATGACACTGATCATG ATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGG | 4153 |
| | GTTGT <u>C</u> ATGACTATCCT | 4154 |
| | AGGATAGT <u>C</u> ATGACAAC | 4155 |
| Alzheimer disease Met146Ile ATGa-ATC | CCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGAT CAGTGTCAATTGTTGTCAT <u>G</u> ACTATCCTCCTGGTGGTTCTGTAT AAATACAGGTGCTATAAGGTGAGCATGAGACACAGA | 4156 |
| | TCTGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGA ACCACCAGGAGGATAGT <u>C</u> ATGACAACAATGACACTGATCATG ATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGG | 4157 |
| | GTTGT <u>C</u> ATGACTATCCT | 4158 |
| | AGGATAGT <u>C</u> ATGACAAC | 4159 |
| Alzheimer disease Met146Leu cATG-TTG | GGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATG ATCAGTGTCAATTGTTGTC <u>A</u> TGACTATCCTCCTGGTGGTTCTGT ATAAATACAGGTGCTATAAGGTGAGCATGAGACACA | 4160 |
| | TGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGAAC CACCAGGAGGATAGTCA <u>T</u> GACAACAATGACACTGATCATGAT GGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGGCC | 4161 |
| | TTGTTGTC <u>A</u> TGACTATC | 4162 |
| | GATAGTCA <u>T</u> GACAACAA | 4163 |
| Alzheimer disease Met146Val cATG-GTG | GGCCAGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATG ATCAGTGTCAATTGTTGTC <u>A</u> TGACTATCCTCCTGGTGGTTCTGT ATAAATACAGGTGCTATAAGGTGAGCATGAGACACA | 4164 |
| | TGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACAGAAC CACCAGGAGGATAGTCA <u>T</u> GACAACAATGACACTGATCATGAT GGCAGCATTGAGAATTGAGTGCAGGGCTCTCTGGCC | 4165 |
| | TTGTTGTC <u>A</u> TGACTATC | 4166 |
| | GATAGTCA <u>T</u> GACAACAA | 4167 |
| Alzheimer disease Thr147Ile ACT-ATT | AGAGAGCCCTGCACTCAATTCTGAATGCTGCCATCATGATCA GTGTCATTGTTGTCATG <u>A</u> CTATCCTCCTGGTGGTTCTGTATAA ATACAGGTGCTATAAGGTGAGCATGAGACACAGATC | 4168 |
| | GATCTGTGTCTCATGCTCACCTTATAGCACCTGTATTTATACA GAACCACCAGGAGGATAGTCA <u>T</u> GACAACAATGACACTGATCA TGATGGCAGCATTGAGAATTGAGTGCAGGGCTCTCT | 4169 |
| | TGTCATG <u>A</u> CTATCCTCC | 4170 |
| | GGAGGATAGTCA <u>T</u> GACA | 4171 |
| Alzheimer disease His163Arg CAT-CGT | CTTTTAAAGGGTTGTGGGACCTGTTAATTATATTGAAATGCTTT CTTTTCTAGGTCATCC <u>A</u> TGCCTGGCTTATTATATCATCTCTATT GTTGCTGTTCTTTTTTTCATTCACTTACTTGGG | 4172 |
| | CCCAAGTAAATGAATGAAAAAAGAACAGCAACAATAGAGAT GATATAATAAGCCAGGCATGGATGACCTAGAAAAGAAAGCAT TTCAATATAATTAACAGGTCCCACAACCCTTAAAAAG | 4173 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | GGTCATCC <u>A</u> TGCCTGGC | 4174 |
| | GCCAGGCATGGATGACC | 4175 |
| Alzheimer disease His163Tyr cCAT-TAT | ACTTTTTAAGGGTTGTGGGACCTGTTAATTATATTGAAATGCT TTCTTTTCTAGGTCATCC <u>A</u> TGCCTGGCTTATTATATCATCTCTA TTGTTGCTGTTCTTTTTTTCATTCATTTACTTGG | 4176 |
| | CCAAGTAAATGAATGAAAAAAGAACAGCAACAATAGAGATGA TATAATAAGCCAGGCAT <u>G</u> GATGACCTAGAAAAGAAAGCATTTC AATATAATTAACAGGTCCCACAACCCTTAAAAAGT | 4177 |
| | AGGTCATCCATGCCTGG | 4178 |
| | CCAGGCAT <u>G</u> GATGACCT | 4179 |
| Alzheimer disease Trp165Cys TGGc-TGC | AGGGTTGTGGGACCTGTTAATTATATTGAAATGCTTTCTTTTC TAGGTCATCCATGCCTG <u>G</u> CTTATTATATCATCTCTATTGTTGCT GTTCTTTTTTTCATTCATTTACTTGGGGTAAGTT | 4180 |
| | AACCTACCCCAAGTAAATGAATGAAAAAAGAACAGCAACAAT AGAGATGATATAATAAG <u>C</u> CAGGCATGGATGACCTAGAAAAGA AAGCATTTCAATATAATTAACAGGTCCCACAACCCT | 4181 |
| | CATGCCTG <u>G</u> CTTATTAT | 4182 |
| | ATAATAAG <u>C</u> CAGGCATG | 4183 |
| Alzheimer disease Ser169Leu TCA-TTA | ACCTGTTAATTATATTGAAATGCTTTCTTTTCTAGGTCATCCAT GCCTGGCTTATTATAT <u>C</u> ATCTCTATTGTTGCTGTTCTTTTTTTC ATTCATTTACTTGGGGTAAGTTGTGAAATTTTT | 4184 |
| | AAAAATTTCACAACTTACCCCAAGTAAATGAATGAAAAAAGA ACAGCAACAATAGAGAT <u>G</u> ATATAATAAGCCAGGCATGGATGA CCTAGAAAAGAAAGCATTTCATATAATTAACAGGT | 4185 |
| | TATTATAT <u>C</u> ATCTCTAT | 4186 |
| | ATAGAGAT <u>G</u> ATATAATA | 4187 |
| Alzheimer disease Leu171Pro CTA-CCA | TAATTATATTGAAATGCTTTCTTTTCTAGGTCATCCATGCCTGG CTTATTATATCATCTC <u>T</u> ATTGTTGCTGTTCTTTTTTTCATTCATT TACTTGGGGTAAGTTGTGAAATTTTTGGTCTG | 4188 |
| | CAGACCAAAAATTTCACAACTTACCCCAAGTAAATGAATGAAA AAAAGAACAGCAACAAT <u>A</u> AGAGATGATATAATAAGCCAGGCAT GGATGACCTAGAAAAGAAAGCATTTCATATAATTA | 4189 |
| | ATCATCTC <u>T</u> ATTGTTGC | 4190 |
| | GCAACAAT <u>A</u> GAGATGAT | 4191 |
| Alzheimer disease Leu173Trp TTG-TGG | TATTGAAATGCTTTCTTTTCTAGGTCATCCATGCCTGGCTTATT ATATCATCTCTATTGT <u>T</u> GCTGTTCTTTTTTTCATTCATTTACTTG GGGTAAGTTGTGAAATTTTTGGTCTGTCTTTC | 4192 |
| | GAAAGACAGACCAAAAATTTCACAACTTACCCCAAGTAAATGA ATGAAAAAAGAACAGCA <u>A</u> ACAATAGAGATGATATAATAAGCCA GGCATGGATGACCTAGAAAAGAAAGCATTTCATA | 4193 |
| | TCTATTGT <u>T</u> GCTGTTCT | 4194 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| | AGAACAGCAACAATAGA | 4195 |
| Alzheimer disease Gly209Arg gGGA-AGA | TATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGAATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGA | 4196 |
| | TCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAATCATTCCACCACACCAAAATTCCAGATCAGGAGTGCAACAGTAATGTAGTCCACAGCAACGTTATA | 4197 |
| | GTGTGGTGGGAATGATT | 4198 |
| | AATCATTCCACCACAC | 4199 |
| | | |
| Alzheimer disease Gly209Val GGA-GTA | ATAACGTTGCTGTGGACTACATTACTGTTGCACTCCTGATCTGGAATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGAT | 4200 |
| | ATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCAGTGAATGGAAATCATTCCACCACACCAAAATTCCAGATCAGGAGTGCAACAGTAATGTAGTCCACAGCAACGTTAT | 4201 |
| | TGTGGTGGGAATGATT | 4202 |
| | AAATCATTCCACCACA | 4203 |
| | | |
| Alzheimer disease Ile213Thr ATT-ACT | TGGACTACATTACTGTTGCACTCCTGATCTGGAATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGATTAGTGCCCTCAT | 4204 |
| | ATGAGGGGCACTAATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAATCATTCCACCACACCAAAATTCCAGATCAGGAGTGCAACAGTAATGTAGTCCA | 4205 |
| | GATTTCCATTCACTGGA | 4206 |
| | TCCAGTGAATGGAAATC | 4207 |
| | | |
| Alzheimer disease Leu219Pro CTT-CCT | CACTCCTGATCTGGAATTTTGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATATGATTAGTGCCCTCATGGCCCTGGTGTATCAA | 4208 |
| | TTGATAAACACCAGGGCCATGAGGGCACTAATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAATCATTCCACCACACCAAAATTCCAGATCAGGAGTG | 4209 |
| | AGGTCCACTTCGACTCC | 4210 |
| | GGAGTCGAAGTGGACCT | 4211 |
| | | |
| Alzheimer disease Ala231Thr tGCC-ACC | ATTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCAATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTATCAAGTACCTCCCTGAATGGACTGCGTGGCTCATCTTGG | 4212 |
| | CCAAGATGAGCCACGCAGTCCATTGAGGGAGGTACTTGATAAACACCAGGGCCATGAGGGCACTAATCATAATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAAT | 4213 |
| | TGATTAGTGCCCTCATG | 4214 |
| | CATGAGGGCACTAATCA | 4215 |
| | | |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| Alzheimer disease Ala231Val GCC-GTC | TTTCCATTCACTGGAAAGGTCCACTTCGACTCCAGCAGGCAT ATCTCATTATGATTAGTGCCCTCATGGCCCTGGTGTTCATCAA GTACCTCCCTGAATGGACTGCGTGGCTCATCTTGGC | 4216 |
| | GCCAAGATGAGCCACGCAGTCCATTGAGGGAGGTACTTGATA AACACCAGGGCCATGAGGGCACTAATCATAATGAGATATGCC TGCTGGAGTCGAAGTGGACCTTTCCAGTGAATGGAAA | 4217 |
| | GATTAGTGCCCTCATGG | 4218 |
| | CCATGAGGGCACTAATC | 4219 |
| Alzheimer disease Met233Thr ATG-ACG | TTCAGTGGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCA TTATGATTAGTGCCCTCATGGCCCTGGTGTTCATCAAGTACCT CCCTGAATGGACTGCGTGGCTCATCTTGGCTGTGAT | 4220 |
| | ATCACAGCCAAGATGAGCCACGCAGTCCATTGAGGGAGGTAC TTGATAAACACCAGGGCCATGAGGGCACTAATCATAATGAGA TATGCCTGCTGGAGTCGAAGTGGACCTTTCCAGTGAA | 4221 |
| | TGCCCTCATGGCCCTGG | 4222 |
| | CCAGGGCCATGAGGGCA | 4223 |
| Alzheimer disease Leu235Pro CTG-CCG | GGAAAGGTCCACTTCGACTCCAGCAGGCATATCTCATTATGA TTAGTGCCCTCATGGCCCTGGTGTTCATCAAGTACCTCCCTG AATGGACTGCGTGGCTCATCTTGGCTGTGATTTAGT | 4224 |
| | ACTGAAATCACAGCCAAGATGAGCCACGCAGTCCATTGAGGG AGGTACTTGATAAACACCAGGGCCATGAGGGCACTAATCATA ATGAGATATGCCTGCTGGAGTCGAAGTGGACCTTTCC | 4225 |
| | CATGGCCCTGGTGTTC | 4226 |
| | TAAACACCAGGGCCATG | 4227 |
| Alzheimer disease Ala246Glu GCG-GAG | TCATTATGATTAGTGCCCTCATGGCCCTGGTGTTCATCAAGTA CCTCCCTGAATGGACTGCGTGGCTCATCTTGGCTGTGATTTG AGTATATGGTAAAACCCAAGACTGATAATTTGTTG | 4228 |
| | CAAACAAATTATCAGTCTTGGGTTTTACCATATACTGAAATCA CAGCCAAGATGAGCCACGCAGTCCATTGAGGGAGGTACTTGA TAAACACCAGGGCCATGAGGGCACTAATCATAATGA | 4229 |
| | ATGGACTGCGTGGCTCA | 4230 |
| | TGAGCCACGCAGTCCAT | 4231 |
| Alzheimer disease Leu250Ser TTG-TCG | GTGCCCTCATGGCCCTGGTGTTCATCAAGTACCTCCCTGAAT GGACTGCGTGGCTCATCTTGGCTGTGATTTAGTATATGGTA AAACCCAAGACTGATAATTTGTTTGTACAGGAATGC | 4232 |
| | GCATTCCTGTGACAAACAAATTATCAGTCTTGGGTTTTACCAT ATACTGAAATCACAGCCAGATGAGCCACGCAGTCCATTGAG GGAGGTACTTGATAAACACCAGGGCCATGAGGGCAC | 4233 |
| | GCTCATCTTGGCTGTGA | 4234 |
| | TCACAGCCAGATGAGC | 4235 |
| Alzheimer disease Ala260Val GCT-GTT | AGTTTAGCCCATACATTTTATTAGATGTCTTTTATGTTTTCTTT TTCTAGATTTAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCG TATGCTGGTTGAAACAGCTCAGGAGAGAAATGA | 4236 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| | TCATTTCTCTCCTGAGCTGTTTCAACCAGCATACGAAGTGGAC CTTTCGGACACAAAACA <u>G</u> CCACTAAATCTAGAAAAAGAAAAAC ATAAAAGACATCTAATAAAATGTATGGGCTAAACT | 4237 |
| | TTTAGTGGCTGTTTTGT | 4238 |
| | ACAAAACA <u>G</u> CCACTAAA | 4239 |
| Alzheimer disease Leu262Phe TTGt-TTC | CCCATACATTTTATTAGATGTCTTTTATGTTTTCTTTTTCTAGA TTTAGTGGCTGTTTT <u>G</u> TGTCCGAAAGGTCCACTTCGTATGCTG GTTGAAACAGCTCAGGAGAGAAATGAAACGCTT | 4240 |
| | AAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCATACGA AGTGGACCTTTTCGGACACA <u>A</u> AAACAGCCACTAAATCTAGAAAA AGAAAAACATAAAAGACATCTAATAAAATGTATGGG | 4241 |
| | GCTGTTTT <u>G</u> TGTCCGAA | 4242 |
| | TTCGGACACA <u>A</u> AAACAGC | 4243 |
| Alzheimer disease Cys263Arg gTGT-CGT | CCATACATTTTATTAGATGTCTTTTATGTTTTCTTTTTCTAGAT TTAGTGGCTGTTTTG <u>T</u> GTCGAAAGGTCCACTTCGTATGCTG GTTGAAACAGCTCAGGAGAGAAATGAAACGCTTT | 4244 |
| | AAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCATACG AAGTGGACCTTTTCGGACA <u>A</u> AAACAGCCACTAAATCTAGAAA AAGAAAAACATAAAAGACATCTAATAAAATGTATGG | 4245 |
| | CTGTTTTG <u>T</u> GTCGAAA | 4246 |
| | TTTCGGACA <u>A</u> AAACAG | 4247 |
| Alzheimer disease Pro264Leu CCG-CTG | ACATTTTATTAGATGTCTTTTATGTTTTCTTTTTCTAGATTTAG TGGCTGTTTTGTGTCC <u>G</u> AAAGGTCCACTTCGTATGCTGGTTG AAACAGCTCAGGAGAGAAATGAAACGCTTTTTCC | 4248 |
| | GGAAAAAGCGTTTCATTTCTCTCCTGAGCTGTTTCAACCAGCA TACGAAGTGGACCTTTCC <u>G</u> GACACAAAACAGCCACTAAATCTA GAAAAAGAAAAACATAAAAGACATCTAATAAAATGT | 4249 |
| | TTTGTGTCC <u>G</u> AAAGGTC | 4250 |
| | GACCTTTC <u>G</u> GACACAAA | 4251 |
| Alzheimer disease Arg269Gly tCGT-GGT | GTCTTTTATGTTTTCTTTTTCTAGATTTAGTGGCTGTTTTGTG TCCGAAAGGTCCACTTC <u>G</u> TATGCTGGTTGAAACAGCTCAGGA GAGAAATGAAACGCTTTTTCCAGCTCTCATTACT | 4252 |
| | AGTAAATGAGAGCTGGAAAAAGCGTTTCATTTCTCTCCTGAGC TGTTCACCAGCATAC <u>G</u> AAGTGGACCTTTTCGGACACAAAAC AGCCACTAAATCTAGAAAAAGAAAAACATAAAAGAC | 4253 |
| | GTCCACTTC <u>G</u> TATGCTG | 4254 |
| | CAGCATAC <u>G</u> AAGTGGAC | 4255 |
| Alzheimer disease Arg269His CGT-CAT | TCTTTTATGTTTTCTTTTTCTAGATTTAGTGGCTGTTTTGTGTC CGAAAGGTCCACTTC <u>G</u> TATGCTGGTTGAAACAGCTCAGGAGA GAAATGAAACGCTTTTTCCAGCTCTCATTACTC | 4256 |
| | GAGTAAATGAGAGCTGGAAAAAGCGTTTCATTTCTCTCCTGA GCTGTTTCAACCAGCATAC <u>G</u> AAGTGGACCTTTTCGGACACAAA ACAGCCACTAAATCTAGAAAAAGAAAAACATAAAAGA | 4257 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|---|---|------------|
| | TCCACTTC <u>G</u> TATGCTGG | 4258 |
| | CCAGCATAC <u>G</u> AAGTGA | 4259 |
| Alzheimer disease Arg278Thr AGA-ACA | TAGTGGCTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGG TTGAAACAGCTCAGGAGAG <u>G</u> AAATGAAACGCTTTTTCCAGCTCT CATTTACTCCTGTAAGTATTTGAGAATGATATTGAA | 4260 |
| | TTCAATATCATTCTCAAATACTTACAGGAGTAAATGAGAGCTG GAAAAAGCGTTTCATTT <u>C</u> TCTCCTGAGCTGTTTCAACCAGCAT ACGAAGTGGACCTTTCGGACACAAAACAGCCACTA | 4261 |
| | TCAGGAGAG <u>G</u> AAATGAAA | 4262 |
| | TTTCATTT <u>C</u> TCTCCTGA | 4263 |
| Alzheimer disease Glu280Ala GAA-GCA | CTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAAC AGCTCAGGAGAGAAATG <u>A</u> AACGCTTTTTCCAGCTCTCATTTAC TCCTGTAAGTATTTGAGAATGATATTGAATTAGTA | 4264 |
| | TACTAATTCAATATCATTCTCAAATACTTACAGGAGTAAATGAG AGCTGGAAAAAGCGTTT <u>C</u> ATTTCTCTCCTGAGCTGTTTCAACC AGCATACGAAGTGGACCTTTCGGACACAAAACAG | 4265 |
| | GAGAAATG <u>A</u> AACGCTTT | 4266 |
| | AAAGCGTTT <u>C</u> ATTTCTC | 4267 |
| Alzheimer disease Glu280Gly GAA-GGA | CTGTTTTGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAAC AGCTCAGGAGAGAAATG <u>A</u> AACGCTTTTTCCAGCTCTCATTTAC TCCTGTAAGTATTTGAGAATGATATTGAATTAGTA | 4268 |
| | TACTAATTCAATATCATTCTCAAATACTTACAGGAGTAAATGAG AGCTGGAAAAAGCGTTT <u>C</u> ATTTCTCTCCTGAGCTGTTTCAACC AGCATACGAAGTGGACCTTTCGGACACAAAACAG | 4269 |
| | GAGAAATG <u>A</u> AACGCTTT | 4270 |
| | AAAGCGTTT <u>C</u> ATTTCTC | 4271 |
| Alzheimer disease Leu282Arg CTT-CGT | TGTGTCCGAAAGGTCCACTTCGTATGCTGGTTGAAACAGCTC AGGAGAGAAATGAAACGCTTTTTCCAGCTCTCATTTACTCCTG TAAGTATTTGAGAATGATATTGAATTAGTAATCAGT | 4272 |
| | ACTGATTACTAATTCAATATCATTCTCAAATACTTACAGGAGTA AATGAGAGCTGGAAAA <u>A</u> GCGTTTCATTTCTCTCCTGAGCTGTT TCAACCAGCATACGAAGTGGACCTTTCGGACACA | 4273 |
| | TGAAACGCTTTTTCCAG | 4274 |
| | CTGGAAAA <u>A</u> GCGTTTCA | 4275 |
| Alzheimer disease Ala285Val GCT-GTT | AAGGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAA ATGAAACGCTTTTTCCAG <u>C</u> TCTCATTTACTCCTGTAAGTATTTG AGAATGATATTGAATTAGTAATCAGTGTAGAATTT | 4276 |
| | AAATTCTACACTGATTACTAATTCAATATCATTCTCAAATACTT ACAGGAGTAAATGAGAG <u>G</u> CTGGAAAAAGCGTTTCATTTCTCTC CTGAGCTGTTTCAACCAGCATACGAAGTGGACCTT | 4277 |
| | TTTTCCAG <u>C</u> TCTCATTT | 4278 |
| | AAATGAGAG <u>G</u> CTGGAAAA | 4279 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Alzheimer disease Leu286Val tCTC-GTC | GGTCCACTTCGTATGCTGGTTGAAACAGCTCAGGAGAGAAAT GAAACGCTTTTTCCAGCTCTCATTACTCCTGTAAGTATTTGA GAATGATATTGAATTAGTAATCAGTGTAGAATTTAT | 4280 |
| | ATAAATTCTACACTGATTACTAATTCAATATCATTCTCAAATAC TTACAGGAGTAAATGAGAGCTGGAAAAAGCGTTTCATTTCTCT CCTGAGCTGTTTCAACCAGCATACGAAGTGGACC | 4281 |
| | TTCCAGCTCTCATTAC | 4282 |
| | GTAAATGAGAGCTGGAA | 4283 |
| Alzheimer disease Gly384Ala GGA-GCA | GTGACCAACTTTTTAATATTTGTAACCTTTCCTTTTAGGGGGA GTAAACTTGGATTGGGAGATTTTCTACAGTGTCTGG TTGGTAAAGCCTCAGCAACAGCCAGTGGAGACTG | 4284 |
| | CAGTCTCCACTGGCTGTTGCTGAGGCTTTACCAACCAGAACA CTGTAGAAAATGAAATCTCCCAATCCAAGTTTTACTCCCCCTA AAAAGGAAAGGTTACAAATATTAAGGTTGGTCAC | 4285 |
| | TGGATTGGGAGATTTCA | 4286 |
| | TGAAATCTCCCAATCCA | 4287 |
| Alzheimer disease Ser390Ile AGT-ATT | TTTGTAACCTTTCCTTTTAGGGGGAGTAAACTTGGATTGGG AGATTTTCTACAGTGTTCTGGTTGGTAAAGCCTCAGCA ACAGCCAGTGGAGACTGGAACACAACCATAGCCTG | 4288 |
| | CAGGCTATGGTTGTGTTCCAGTCTCCACTGGCTGTTGCTGAG GCTTTACCAACCAGAACACTGTAGAAAATGAAATCTCCCAATC CAAGTTTTACTCCCCCTAAAAGGAAAGGTTACAAA | 4289 |
| | TTTCTACAGTGTTCTGG | 4290 |
| | CCAGAACACTGTAGAAA | 4291 |
| Alzheimer disease Leu392Val tCTG-GTG | AACCTTTCCTTTTAGGGGGAGTAAACTTGGATTGGGAGATT TCATTTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAACAGC CAGTGGAGACTGGAACACAACCATAGCCTGTTTCG | 4292 |
| | CGAAACAGGCTATGGTTGTGTTCCAGTCTCCACTGGCTGTTG CTGAGGCTTTACCAACCAGAACACTGTAGAAAATGAAATCTCC CAATCCAAGTTTTACTCCCCCTAAAAGGAAAGGTT | 4293 |
| | ACAGTGTCTGGTTGGT | 4294 |
| | ACCAACCAGAACACTGT | 4295 |
| Alzheimer disease Asn405Ser AAC-AGC | ATTCATTTTCTACAGTGTCTGGTTGGTAAAGCCTCAGCAAC AGCCAGTGGAGACTGGAACACAACCATAGCCTGTTTCGTAGC CATATTAATTGTAAGTATACATAATAAGAATGTGT | 4296 |
| | ACACATTCTTATTAGTGTATACTTACAATTAATATGGCTACGAA ACAGGCTATGGTTGTGTTCCAGTCTCCACTGGCTGTTGCTGA GGCTTTACCAACCAGAACACTGTAGAAAATGAAAT | 4297 |
| | AGACTGGAACACAACCA | 4298 |
| | TGGTTGTGTTCCAGTCT | 4299 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|--|------------|
| Alzheimer disease Ala409Thr aGCC-ACC | TACAGTGTCTGGTTGGTAAAGCCTCAGCAACAGCCAGTGGA GACTGGAACACAACCATAGCCTGTTTCGTAGCCATATTAATTG TAAGTATACTAATAAGAATGTGTCAGAGCTCTTA | 4300 |
| | TAAGAGCTCTGACACATTCTTATTAGTGTATACTTACAATTAAT ATGGCTACGAAACAGGCATATGGTTGTGTTCCAGTCTCCACTG GCTGTTGCTGAGGCTTTACCAACCAGAACACTGTA | 4301 |
| | CAACCATAGCCTGTTTC | 4302 |
| | GAAACAGGCATATGGTTG | 4303 |
| Alzheimer disease Cys410Tyr TGT-TAT | GTGTTCTGGTTGGTAAAGCCTCAGCAACAGCCAGTGGAGACT GGAACACAACCATAGCCTGTTTCGTAGCCATATTAATTGTAAG TATACTAATAAGAATGTGTCAGAGCTCTTAATGT | 4304 |
| | ACATTAAGAGCTCTGACACATTCTTATTAGTGTATACTTACAAT TAATATGGCTACGAAACAGGCTATGGTTGTGTTCCAGTCTCCA CTGGCTGTTGCTGAGGCTTTACCAACCAGAACAC | 4305 |
| | CATAGCCTGTTTCGTAG | 4306 |
| | CTACGAAACAGGCTATG | 4307 |
| Alzheimer disease Ala426Pro tGCC-CCC | TGTGAATGTGTGTCTTTCCCATCTTCTCCACAGGGTTTGTGCC TTACATTATTACTCCTTGCCATTTTCAAGAAAGCATTGCCAGC TCTTCCAATCTCCATCACCTTTGGGCTTGTCT | 4308 |
| | AGAAAACAAGCCCAAAGGTGATGGAGATTGGAAGAGCTGGC AATGCTTTCTTGAAAATGGCAAGGAGTAATAATGTAAGGCACA AACCCTGTGGAGAAGATGGGAAAGACACACATTCACA | 4309 |
| | TACTCCTTGCCATTTTC | 4310 |
| | GAAAATGGCAAGGAGTA | 4311 |
| Alzheimer disease Pro436Gln CCA-CAA | AGGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGAA AGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTCTACTTTGCCACAGATTATCTTGACAGCCTTT | 4312 |
| | AAAGGCTGTACAAGATAATCTGTGGCAAAGTAGAAAACAAGC CCAAAGGTGATGGAGATTGGAAGAGCTGGCAATGCTTTCTTG AAAATGGCAAGGAGTAATAATGTAAGGCACAAACCCT | 4313 |
| | AGCTCTTCCAATCTCCA | 4314 |
| | TGGAGATTGGAAGAGCT | 4315 |
| Alzheimer disease Pro436Ser tCCA-TCA | CAGGGTTTGTGCCTTACATTATTACTCCTTGCCATTTTCAAGA AAGCATTGCCAGCTCTTCCAATCTCCATCACCTTTGGGCTTGT TTTCTACTTTGCCACAGATTATCTTGACAGCCTT | 4316 |
| | AAGGCTGTACAAGATAATCTGTGGCAAAGTAGAAAACAAGCC CAAAGGTGATGGAGATTGGAAGAGCTGGCAATGCTTTCTTG AAATGGCAAGGAGTAATAATGTAAGGCACAAACCCTG | 4317 |
| | CAGCTCTTCCAATCTCC | 4318 |
| | GGAGATTGGAAGAGCTG | 4319 |

EXAMPLE 26

Alzheimer's Disease - presenilin-2 (PSEN2)

[0241] The attached table discloses the correcting oligonucleotide base sequences for the PSEN2 oligonucleotides of the invention.

Table 28

5

PSEN2 Mutations And Genome-Correcting Oligos

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Alzheimer disease Arg62His CGC-CAC | GATGTGGTTTCCACAGAGAAGCCAGGAGAACGAGGAGGAC GGTGAGGAGGACCCTGACC <u>G</u> CTATGTCTGTAGTGGGGTTCC CGGGCGGCCGCCAGGCCTGGAGGAAGAGCTGACCCTCAA | 4320 |
| | TTGAGGGTCAGCTCTTCTCCAGGCCTGGCGGCCGCCCGGG AACCCCACTACAGACATAGC <u>G</u> GGTCAGGGTCCTCCTACCGTC CTCCTCGTTCTCTGGCTTCTCTGTGGGAAACCAATC | 4321 |
| | CCCTGACC <u>G</u> CTATGTCT | 4322 |
| | AGACATAGC <u>G</u> GGTCAGGG | 4323 |
| Alzheimer disease Thr122Pro cACG-CCG | GCCTCGAGGAGCAGTCAGGGCCGGGAGCATCAGCCCTTTGC CTTCTCCCTCAGCATCTAC <u>A</u> CGACATTCACTGAGGACACACC CTCGGTGGGCCAGCGCCTCCTCAACTCCGTGCTGAACA | 4324 |
| | TGTTCAACACGGAGTTGAGGAGGCGCTGGCCCACCGAGGGT GTGTCTCAGTGAATGTCTG <u>T</u> GTAGATGCTGAGGGAGAAGGCA AAGGGCTGATGCTCCCGGCCCTGACTGCTCCTCGAGGC | 4325 |
| | GCATCTAC <u>A</u> CGACATTC | 4326 |
| | GAATGTCG <u>T</u> GTAGATGC | 4327 |
| Alzheimer disease Asn141Ile AAC-ATC | ACACGCCATTCACTGAGGACACACCCTCGGTGGGCCAGCGC CTCCTCAACTCCGTGCTGA <u>A</u> CACCCTCATCATGATCAGCGTC ATCGTGGTTATGACCATCTTCTTGGTGGTGTCTCTACAA | 4328 |
| | TTGTAGAGCACCACCAAGAAGATGGTCATAACCACGATGACG CTGATCATGATGAGGGTGT <u>T</u> CAGCACGGAGTTGAGGAGGCG CTGGCCCACCGAGGGTGTGTCCTCAGTGAATGGCGTGT | 4329 |
| | CGTGCTGA <u>A</u> CACCCTCA | 4330 |
| | TGAGGGTGT <u>T</u> CAGCACG | 4331 |
| Alzheimer disease Met239Ile ATGg-ATA | CCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTCAT CATGATCAGTGCCTCAT <u>G</u> CCCTAGTGTTTCATCAAGTACCTC CCAGAGTGGTCCGCGTGGGTCATCCTGGGCGCCATC | 4332 |
| | GATGGCGCCCAGGATGACCCACGCGGACCACTCTGGGAGGT ACTTGTGAACACTAGGGC <u>C</u> ATGAGCGCACTGATCATGATGA GGTAGGCCTGCTGCAGCACCAAGAGGGCCCTTCCAGTGG | 4333 |
| | GCGCTCAT <u>G</u> CCCTAGT | 4334 |
| | ACTAGGGC <u>C</u> ATGAGCGC | 4335 |

| Clinical Phenotype & Mutation | Correcting Oligos | SEQ ID NO: |
|--|---|------------|
| Alzheimer disease Met239Val cATG-GTG | ATCCACTGGAAGGGCCCTCTGGTGCTGCAGCAGGCCTACCTC ATCATGATCAGTGCCTC <u>A</u> TGGCCCTAGTGTTCAAGTAC CTCCAGAGTGGTCCGCGTGGGTCATCCTGGGCGCCA | 4336 |
| | TGGCGCCAGGATGACCCACGCGGACCACTCTGGGAGGTAC TTGATGAACACTAGGGCCA <u>T</u> GAGCGCACTGATCATGATGAGG TAGGCCTGCTGCAGCACCAGAGGGCCCTTCCAGTGGAT | 4337 |
| | GTGCGCTC <u>A</u> TGGCCCTA | 4338 |
| | TAGGGCCAT <u>G</u> AGCGCAC | 4339 |

Example 26
Engineering herbicide resistant plants

[242] Chemical weed control is an important tool of modern agriculture and many herbicides have been developed for this purpose. Their use has resulted in substantial increases in the yields of many crops, including, for example, maize, soybeans, and cotton. Thus while the use of fertilizers and new high-yielding crop varieties have contributed greatly to the "green revolution," chemical weed control has also been at the forefront of technological achievement.

[243] Herbicides having broad-spectrum activity are particularly useful because they obviate the need for multiple herbicides targeting different classes of weeds. The problem with such herbicides is that they typically also affect crops which are exposed to the herbicide. One way to overcome this is to generate plants which are resistant to one or more broad-spectrum herbicides. Such herbicide-tolerant plants may reduce the need for tillage to control weeds, thereby effectively reducing soil erosion and can reduce the quantity and number of different herbicides applied in the field.

[244] Common herbicides used, for example, include those that inhibit the enzyme 5-enolpyruvyl-3-phosphoshikimic acid synthase (EPSPS), for example N-phosphonomethyl-glycine (e.g. glyphosate), those that inhibit acetolactate synthase (ALS) activity, for example the sulfonylureas and related herbicides, and those that inhibit dihydropteroate synthase, for example methyl[(4-amino-phenyl)sulfonyl]carbamate (e.g. Asulam). Herbicide-tolerant plants can be produced by several methods, including, for example, introducing into the genome of the plant the ability to degrade the herbicide, the capacity to produce a higher level of the targeted enzyme, and/or expressing an herbicide-tolerant allele of the enzyme.

[245] The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes that confer herbicide resistance.

Table 28
Genome-Altering Oligos Conferring Glyphosate Resistance

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Glyphosate Resistance EPSPS <i>Arabidopsis thaliana</i> Gly97Ala GGC-GCC | AAGCGTCGGAGATTGTACTTCAACCCATTAGAGAAATCTCCGGTC TTATTAAGCTTCCTG <u>C</u> CTCCAAGTCTCTATCAAATCGGATCCTGC TTCTCGCTGCTCTGTCTGAGGTATATATCAC | 4341 |
| | GTGATATATACCTCAGACAGAGCAGCGAGAAGCAGGATCCGATT TGATAGAGACTTGGAG <u>G</u> CAGGAAGCTTAATAAGACCGGAGATT CTCTAATGGGTTGAAGTACAATCTCCGACGCTT | 4342 |
| | GCTTCCTG <u>C</u> CTCCAAGT | 4343 |
| | ACTTGGAG <u>G</u> CAGGAAGC | 4344 |
| Glyphosate Resistance EPSPS <i>Brassica napus</i> Gly93Ala GGA-GCA | AAGCTTCAGAGATTGTGCTTCAACCAATCAGAGAAATCTCGGGTC TCATTAAGCTACCCG <u>C</u> ATCCAAATCTCTCTCCAATCGGATCCTCC TTCTTGCCGCTCTATCTGAGGTACATATACT | 4345 |
| | AGTATATGTACCTCAGATAGAGCGGCAAGAAGGAGGATCCGATT GGAGAGAGATTTGGAT <u>G</u> CGGGTAGCTTAATGAGACCCGAGATT CTCTGATTGGTTGAAGCACAATCTCTGAAGCTT | 4346 |
| | GCTACCCG <u>C</u> ATCCAAAT | 4347 |
| | ATTTGGAT <u>G</u> CGGGTAGC | 4348 |
| Glyphosate Resistance EPSPS 1 <i>Nicotiana tabacum</i> Gly95Ala GGT-GCT | AGCCCAACGAGATTGTGCTGCAACCCATCAAAGATATATCAGGC ACTGTTAAATTGCCTG <u>C</u> TTCTAAATCCCTTTCCAAATCGTATTCTCC TTCTTGCTGCCCTTTCTAAGGGAAGGACTGT | 4349 |
| | ACAGTCCTTCCCTTAGAAAGGGCAGCAAGAAGGAGAATACGATT GGAAAGGGATTTAGAA <u>G</u> CAGGCAATTTAACAGTGCCTGATATATC TTTGATGGGTTGCAGCACAATCTCGTTGGGCT | 4350 |
| | ATTGCCTG <u>C</u> TTCTAAAT | 4351 |
| | ATTTAGAA <u>G</u> CAGGCAAT | 4352 |
| Glyphosate Resistance EPSPS 2 <i>Nicotiana tabacum</i> Gly62Ala GGA-GCA | ATTGTTTCCTTGGTACGAAATGTCCTCCTGTTCAATTGTCAGCA AGGGAGGCCTTCCCG <u>C</u> AGGGAAGGTAAAGCTCTCTGGATCAATT AGCAGCCAGTACTTGACTGCTCTGCTTATGGC | 4353 |
| | GCCATAAGCAGAGCAGTCAAGTACTGGCTGCTAATTGATCCAGA GAGCTTTACCTTCCCT <u>G</u> CGGGAAGGCCTCCCTTGCTGACAATTC GAACAGGAGGACATTTCTGTACCAAGGAAACAAT | 4354 |
| | CCTTCCCG <u>C</u> AGGGAAGG | 4355 |
| | CCTTCCCT <u>G</u> CGGGAAGG | 4356 |
| Glyphosate Resistance EPSPS <i>Zea mays</i> Gly168Ala GGT-GCT | ATTGTTTCCTTGGCACTGACTGCCACCTGTTCTGTCAATGGAA TCGGAGGGCTACCTG <u>C</u> TGGCAAGGTCAAGCTGTCTGGCTCCATC AGCAGTCAGTACTTGAGTGCCTTGCTGATGGC | 4357 |
| | GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAGCCAGA CAGCTTGACCTTGCCAG <u>G</u> CAGGTAGCCCTCCGATTCCATTGACAC GAACAGGTGGGCAGTCAGTGCCAAGGAAACAAT | 4358 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | GCTACCTG <u>C</u> TGGCAAGG | 4359 |
| | CCTTGCCAG <u>C</u> CAGGTAGC | 4360 |
| Glyphosate Resistance EPSPS <i>Oryza sativa</i> Gly115Ala GGT-GCT | ACTGTTTCCTTGGCACTGAATGCCCACCTGTTTCGTGTCAAGGGA ATTGGAGGACTTCCTG <u>C</u> TGGCAAGGTTAAGCTCTCTGGTTCCAT CAGCAGTCAGTACTTGAGTGCCTTGCTGATGGC | 4361 |
| | GCCATCAGCAAGGCACTCAAGTACTGACTGCTGATGGAACCAGA GAGCTTAACCTTGCCAGCAGGAAGTCCTCCAATTCCTTGACAC GAACAGGTGGGCATTCACTGCCAAGGAAACAGT | 4362 |
| | ACTTCCTG <u>C</u> TGGCAAGG | 4363 |
| | CCTTGCCAG <u>C</u> CAGGAAGT | 4364 |
| Glyphosate Resistance EPSPS <i>Petunia x hybrida</i> Gly93Ala GGC-GCC | AGCCTTCTGAGATAGTGTTGCAACCCATTAAAGAGATTTCAAGGCA CTGTTAAATTGCCTG <u>C</u> CTCTAAATCATTATCTAATAGAATTCTCCT TCTTGCTGCCTTATCTGAAGGAACAACGT | 4365 |
| | ACAGTTGTTCCCTCAGATAAGGCAGCAAGAAGGAGAATTCTATTA GATAATGATTTAGAG <u>G</u> CAGGCAATTTAACAGTGCCTGAAATCTCT TTAATGGGTTGCAACACTATCTCAGAAGGCT | 4366 |
| | ATTGCCTG <u>C</u> CTCTAAAT | 4367 |
| | ATTTAGAG <u>G</u> CAGGCAAT | 4368 |
| Glyphosate Resistance EPSPS <i>Lycopersicon esculentum</i> Gly97Ala GGT-GCT | AACCCCATGAGATTGTGCTAGNACCCATCAAAGATATATCTGGTA CTGTTAAATTACCCG <u>C</u> TTCGAAATCCCTTTCCAATCGTATTCTCCT TCTTGCTGCCCTTTCTGAGGGAAGGACTGT | 4369 |
| | ACAGTCCTTCCCTCAGAAAGGGCAGCAAGAAGGAGAATACGATT GGAAAGGGATTTGAA <u>G</u> CGGGTAATTTAACAGTACCAGATATATC TTTGATGGGTNCTAGCACAATCTCATGGGGTT | 4370 |
| | ATTACCCG <u>C</u> TTCGAAAT | 4371 |
| | ATTTGAA <u>G</u> CGGGTAAT | 4372 |
| Glyphosate Resistance EPSPS <i>Lolium rigidum</i> Gly107Ala GGT-GCT | ATTGTTTCCTTGGCACTGACTGCCCACCTGTTTCGKATCAACGGCA TTGGAGGGCTACCTG <u>C</u> TGGCAAGGTTAAGCTGTCTGGTTCCATC AGCAGCCAATACTTGAGTTCCCTTGCTGATGGC | 4373 |
| | GCCATCAGCAAGGAACTCAAGTATTGGCTGCTGATGGAACCAGA CAGCTTAACCTTGCCAG <u>C</u> CAGGTAGCCCTCCAATGCCGTTGATCG AACAGGTGGGCAGTCAGTGCCAAGGAAACAAT | 4374 |
| | GCTACCTG <u>C</u> TGGCAAGG | 4375 |
| | CCTTGCCAG <u>C</u> CAGGTAGC | 4376 |

Table 29
Genome-Altering Oligos Conferring Imidazolinone and Sulfonylurea Herbicide Resistance

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Sulfonylurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Ser CCT-TCT | AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCTCTTGTAGCA ATCACAGGACAAGTCTCTCGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT | 4377 |
| | AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGAGAGACTTGTCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT | 4378 |
| | GACAAGTCTCTCGTCGT | 4379 |
| | ACGACGAGAGACTTGTC | 4380 |
| Sulfonylurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Gln CCT-CAG | AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCTCTTGTAGCA ATCACAGGACAAGTCCAGCGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT | 4381 |
| | AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGCTGGACTTGTCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT | 4382 |
| | ACAAGTCCAGCGTCGTC | 4383 |
| | TACGACGCTGGACTTGT | 4384 |
| Sulfonylurea Resistance ALS <i>Arabidopsis thaliana</i> Pro197Gln CCT-CAA | AGCGGATTAGCCGATGCGTTGTTAGATAGTGTTCTCTTGTAGCA ATCACAGGACAAGTCCAAACGTCGTATGATTGGTACAGATGCGTTT CAAGAGACTCCGATTGTTGAGGTAACGCGTT | 4385 |
| | AACGCGTTACCTCAACAATCGGAGTCTCTTGAAACGCATCTGTAC CAATCATACGACGTTGGACTTGTCTGTGATTGCTACAAGAGGAA CACTATCTAACAACGCATCGGCTAATCCGCT | 4386 |
| | ACAAGTCCAAACGTCGTA | 4387 |
| | TACGACGTTGGACTTGT | 4388 |
| Imidazolinone Resistance ALS <i>Arabidopsis thaliana</i> Ser653Asn AGT-AAC | GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT TGCCGATGATCCCGAAGCGGTGGCACTTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT | 4389 |
| | ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGT TGAAAGTGCCACCGTTTCGGGATCATCGGCAACACATGTTCTTGGT GCGGACAAATCACATCCAACAGGTAAGGTC | 4390 |
| | GATCCCGAAGCGGTGGCA | 4391 |
| | TGCCACCGTTTCGGGATC | 4392 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Imidazolinone Resistance ALS <i>Arabidopsis thaliana</i> Ser653Asn AGT-AAT | GACCTTACCTGTTGGATGTGATTTGTCCGCACCAAGAACATGTGT TGCCGATGATCCCGAATGGTGGCACTTTCAACGATGTCATAACGG AAGGAGATGGCCGGATTAAATACTGAGAGAT | 4393 |
| | ATCTCTCAGTATTTAATCCGGCCATCTCCTTCCGTTATGACATCGT TGAAAGTGCCACCATTCTGGGATCATCGGCAACACATGTTCTTGGT GCGGACAAATCACATCCAACAGGTAAGGTC | 4394 |
| | GATCCCGAATGGTGGCA | 4395 |
| | TGCCACCATTCTGGGATC | 4396 |
| Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Ser CCC-TCC | TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGGCCAGGTCTCCCGCCGCATGATCGGCACCGACGCCT TCCAGGAGACGCCCATAGTCGAGGTCACCCGCT | 4397 |
| | AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG CCGATCATGCGGCGGGAGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA | 4398 |
| | GCCAGGTCTCCCGCCGC | 4399 |
| | GCGGCGGGAGACCTGGC | 4400 |
| Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAA | CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC ATCACGGGGCCAGGTCCAAAGCGCCGCATGATCGGCACCGACGCCTT CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC | 4401 |
| | GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGTTGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG | 4402 |
| | CCAGGTCCAAAGCGCCGA | 4403 |
| | TGCGGCGTTGGACCTGG | 4404 |
| Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAG | CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC ATCACGGGGCCAGGTCCAGCGCCGCATGATCGGCACCGACGCCTT CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC | 4405 |
| | GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCGTTGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG | 4406 |
| | CCAGGTCCAGCGCCGA | 4407 |
| | TGCGGCGTTGGACCTGG | 4408 |
| Imidazolinone Resistance ALS <i>Oryza sativa</i> Ile627Asn ATT-AAT | GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC TGCCTATGATCCCAAATGGGGGGCGCATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT | 4409 |
| | ATAGATTAATACACAGTCCTGCCATCACCATCCAGGATCATGTCCT TGAATGCGCCCCCATTTGGGATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATATCCAACAAGTATGGCC | 4410 |
| | GATCCCAAATGGGGGCG | 4411 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | CGCCCCCA <u>T</u> TTGGGATC | 4412 |
| Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Ser CCG-TCG | TCCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGC CATCACGGGACAGGTG <u>T</u> CGCGACGCATGATTGGCACCGACGCCT TCCAGGAGACGCCCATCGTCGAGGTCACCCGCT | 4413 |
| | AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGGT GCCAATCATGCGTCGCG <u>A</u> CACCTGTCCCGTGATGGCGACCATGG GGACGGAATCGAGCAGCGCGTCGGCGAGCGCGGA | 4414 |
| | GACAGGTG <u>T</u> CGCGACGC | 4415 |
| | GCGTCGCG <u>A</u> CACCTGTC | 4416 |
| Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Gln CCG-CAG | CCGCGCTCGCCGACGCGCTGCTCGATTCCGTCCCCATGGTCGCC ATCACGGGACAGGTG <u>C</u> AGCGACGCATGATTGGCACCGACGCCTT CCAGGAGACGCCCATCGTCGAGGTCACCCGCTC | 4417 |
| | GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCGG TGCCAATCATGCGTCGCG <u>I</u> GCACCTGTCCCGTGATGGCGACCATG GGGACGGAATCGAGCAGCGCGTCGGCGAGCGCGG | 4418 |
| | ACAGGTG <u>C</u> AGCGACGCA | 4419 |
| | TGCGTCGCG <u>I</u> GCACCTGT | 4420 |
| Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAT | GGCCGTACCTCTTGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTA <u>A</u> TGGTGGGGCTTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA | 4421 |
| | TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCT TGAAAGCCCCACC <u>A</u> TAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC | 4422 |
| | GATCCCTA <u>A</u> TGGTGGGG | 4423 |
| | CCCCACC <u>A</u> TAGGGATC | 4424 |
| Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAC | GGCCGTACCTCTTGATATAATCGTCCCACACCAGGAGCATGTGT TGCCTATGATCCCTA <u>A</u> CGGTGGGGCTTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTACTGATCTAA | 4425 |
| | TTAGATCAGTACACAGTCCTGCCATCACCATCCAGGATCATATCCT TGAAAGCCCCACC <u>G</u> TAGGGATCATAGGCAACACATGCTCCTGGT GTGGGACGATTATATCCAAGAGGTACGGCC | 4426 |
| | GATCCCTA <u>A</u> CGGTGGGG | 4427 |
| | CCCCACC <u>G</u> TAGGGATC | 4428 |
| Sulfonylurea Resistance ALS <i>Lolium multiflorum</i> Pro167Ser CCG-TCG | TCCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGC CATCACGGGGCAGGTG <u>C</u> CGCGCCGCATGATCGGCACGGACGCCT TCCAGGAGACGCCCATCGTCGAGGTCACCCGCT | 4429 |
| | AGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCGTG CCGATCATGCGGCGCG <u>A</u> GACCTGCCCCGTGATGGCCACCATGG GGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGGA | 4430 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | GGCAGGTCTCGCGCCGC | 4431 |
| | GCGGCGCGAGACCTGCC | 4432 |
| Sulfonylurea Resistance ALS <i>Lolium multiflorum</i> Pro167Gln CCG-CAG | CCGCGCTCGCCGACGCCCTCCTCGACTCCATCCCCATGGTGGCC ATCACGGGGCAGGTCCAGCGCCGCATGATCGGCACGGACGCCTT CCAGGAGACGCCCATCGTCGAGGTCACCCGCTC | 4433 |
| | GAGCGGGTGACCTCGACGATGGGCGTCTCCTGGAAGGCGTCCGT GCCGATCATGCGGCGCTGGACCTGCCCGTGATGGCCACCATGG GGATGGAGTCGAGGAGGGCGTCGGCGAGCGCGG | 4434 |
| | GCAGGTCCAGCGCCGCA | 4435 |
| | TGCGGCGCTGGACCTGC | 4436 |
| Imidazolinone Resistance ALS <i>Lolium multiflorum</i> Ser623Asn AGC-AAC | CTGGGCCATACTTGTGGATATCATCGTCCCTCACCAGGAGCATG TGCTGCCTATGATCCCTAACGGTGCTTTCAAGGACATTATCA TGGAAGGTGATGGCAGGATTCGTATTAAAC | 4437 |
| | GTTTAATACGAAATCCTGCCATCACCTTCCATGATAATGTCCTTGA AAGCACCACCGTAGGGATCATAGGCAGCACATGCTCCTGGTGA GGGACGATGATATCCAACAAGTATGGCCAG | 4438 |
| | GATCCCTAACGGTGCTG | 4439 |
| | CACCACCGTAGGGATC | 4440 |
| Sulfonylurea Resistance ALS <i>Hordeum vulgare</i> Pro68Ser CCA-TCA | TCCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGC CATCACGGGCCAGGTCTCACGCCGCATGATCGGCACGGACGCGT TCCAGGAGACGCCCATAGTGAGGTCACGCGCT | 4441 |
| | AGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGTG CCGATCATGCGGCGTGAGACCTGGCCCGTGATGGCGACCATGG GGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGGA | 4442 |
| | GCCAGGTCTCACGCCGC | 4443 |
| | GCGGCGTGAGACCTGGC | 4444 |
| Sulfonylurea Resistance ALS <i>Hordeum vulgare</i> Pro68Gln CCA-CAA | CCGCGCTCGCCGACGCTCTCCTCGACTCCATCCCCATGGTCGCC ATCACGGGCCAGGTCCAGCGCCGCATGATCGGCACGGACGCGTT CCAGGAGACGCCCATAGTGAGGTCACGCGCTC | 4445 |
| | GAGCGCGTGACCTCCACTATGGGCGTCTCCTGGAACGCGTCCGT GCCGATCATGCGGCGTGGACCTGGCCCGTGATGGCGACCATGG GGATGGAGTCGAGGAGAGCGTCGGCGAGCGCGG | 4446 |
| | CCAGGTCCAGCGCCGCA | 4447 |
| | TGCGGCGTGGACCTGG | 4448 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| Imidazolinone Resistance ALS <i>Hordeum vulgare</i> Ser524Asn AGC-AAC | CCCAGGGCCGTACCTGCTGGATATCATTGTCCC GCATCAGGAGC ACGTGCTGCCTATGATCCCAA <u>A</u> CGGTGGTGCTTTCAAGGACATGA TCATGGAGGGTGATGGCAGGACCTCGTACTGA | 4449 |
| | TCAGTACGAGGTCCCTGCCATCACCTCCATGATCATGTCCTTGAA AGCACCACCG <u>I</u> TTGGGATCATAGGCAGCACGTGCTCCTGATGCG GGACAATGATATCCAGCAGGTACGGCCCTGGG | 4450 |
| | GATCCCAA <u>A</u> CGGTGGTG | 4451 |
| | CACCACCG <u>I</u> TTGGGATC | 4452 |
| Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Ser CCT-TCT | AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCG ATCACTGGTCAAGTCTCTCGTCGGATGATCGGTACCGATGCTTTC CAGGAACTCCAATTGTTGAGGTAACAAGGT | 4453 |
| | ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTAC CGATCATCCGACGAGAGACTTGACCAGTGATCGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCACT | 4454 |
| | GTCAAGTCTCTCGTCGG | 4455 |
| | CCGACGAGAGACTTGAC | 4456 |
| Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAA | GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCC <u>A</u> ACGTTCGGATGATCGGTACCGATGCTTTC AGGAACTCCAATTGTTGAGGTAACAAGGTC | 4457 |
| | GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACG <u>T</u> TGGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC | 4458 |
| | TCAAGTCC <u>A</u> ACGTTCGGA | 4459 |
| | TCCGACG <u>T</u> TGGACTTGA | 4460 |
| Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAG | GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCC <u>A</u> ACGTTCGGATGATCGGTACCGATGCTTTC AGGAACTCCAATTGTTGAGGTAACAAGGTC | 4461 |
| | GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACG <u>C</u> TGGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC | 4462 |
| | TCAAGTCC <u>A</u> ACGTTCGGA | 4463 |
| | TCCGACG <u>C</u> TGGACTTGA | 4464 |
| Imidazolinone Resistance ALS <i>Gossypium hirsutum</i> Ser642Asn AGT-AAT | GACCTTACTTGTTGGATGTGATTGTCCACATCAAGAACATGTCCT GCCTATGATCCCCA <u>A</u> TGGAGGCGCTTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACACAATATTGACCTCA | 4465 |
| | TGAGGTCAATATTGTGTTCTTCCATCACCTCTGTGATCACATCTT TGAAAGCGCCTCCAT <u>T</u> TGGGGATCATAGGCAGGACATGTTCTTGAT GTGGGACAATCACATCCAACAAGTAAGGTC | 4466 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | GATCCCCA <u>A</u> TGGAGGCG | 4467 |
| | CGCCTCCA <u>T</u> TGGGGATC | 4468 |
| Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Ser CCC-TCC | TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA TTACTGGGCAAGTT <u>I</u> CCCGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACGAT | 4469 |
| | ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACC AATCATACGCCGGG <u>A</u> AACCTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAGA | 4470 |
| | GGCAAGTT <u>I</u> CCCGGCGT | 4471 |
| | ACGCCGGG <u>A</u> AACCTTGCC | 4472 |
| Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Gln CCC-CAA | CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT TACTGGGCAAGTTCA <u>A</u> ACGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACGATC | 4473 |
| | GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCG <u>T</u> TGAACCTTGCCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAG | 4474 |
| | GCAAGTTC <u>A</u> ACGGCGTA | 4475 |
| | TACGCCG <u>T</u> TGAACCTTGC | 4476 |
| Sulfonylurea Resistance ALS <i>Amaranthus retroflexus</i> Pro192Gln CCC-CAG | CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT TACTGGGCAAGTTCA <u>A</u> CGGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACGATC | 4477 |
| | GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCG <u>C</u> TGAACCTTGCCCAGTAATGGCGACAAGAGGG ACTGAGTCAAGAAGTGCATCAGCAAGACCAG | 4478 |
| | GCAAGTTC <u>A</u> CGGGCGTA | 4479 |
| | TACGCCG <u>C</u> TGAACCTTGC | 4480 |
| Imidazolinone Resistance ALS <i>Amaranthus retroflexus</i> Ser652Asn AGC-AAC | GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGC TGCCTATGATCCCTA <u>A</u> CGGTGCCGCCTTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT | 4481 |
| | ACCAACTAATAAGCCCTTCTTCCATCACCCCTCTGTTATGGTGTCT TGAAGGCGGCACCG <u>T</u> TAGGGATCATAGGCAGCACATGCTCCTGA TGTGGTACGATTACATCCAGCAGATACGGTC | 4482 |
| | GATCCCTA <u>A</u> CGGTGCCG | 4483 |
| | CGGCACCG <u>T</u> TAGGGATC | 4484 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Sulfonylurea Resistance ALS 1 <i>Nicotiana tabacum</i> Pro194Ser CCA-TCA | AGCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGC TATAACAGGTCAAGTGTCACGTAGGATGATAGGTACTGATGCTTTT CAGGAAACTCCTATTGTTGAGGTAAGTAGAT | 4485 |
| | ATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTACC TATCATCCTACGTGACACTTGACCTGTTATAGCAACAATGGGGAC GCTATCCAGTAGCGCGTCAGCGAGGCCGCT | 4486 |
| | GTCAAGTGTCACGTAGG | 4487 |
| | CCTACGTGACACTTGAC | 4488 |
| Sulfonylurea Resistance ALS 1 <i>Nicotiana tabacum</i> Pro194Gln CCA-CAA | GCGGCCTCGCTGACGCGCTACTGGATAGCGTCCCCATTGTTGCT ATAACAGGTCAAGTGCAACGTAGGATGATAGGTACTGATGCTTTT CAGGAAACTCCTATTGTTGAGGTAAGTAGATC | 4489 |
| | GATCTAGTTACCTCAACAATAGGAGTTTCCTGAAAAGCATCAGTAC CTATCATCCTACGTGCACTTGACCTGTTATAGCAACAATGGGGA CGCTATCCAGTAGCGCGTCAGCGAGGCCGC | 4490 |
| | TCAAGTGCAACGTAGGA | 4491 |
| | TCCTACGTGCACTTGGA | 4492 |
| Imidazolinone Resistance ALS 1 <i>Nicotiana tabacum</i> Ser650Asn AGT-AAT | GGCCATACTTGTTGGATGTGATTGTACCTCATCAGGAACATGTTTT ACCTATGATTCCCAATGGCGGAGCTTTCAAAGATGTGATCACAGA GGGTGACGGGAGAAAGTTCTATTGAGTTTG | 4493 |
| | CAAACCTCAATAGGAACTTCTCCCGTCACCCTCTGTGATCACATCTT TGAAAGCTCCGCCATTGGGAATCATAGGTAAAACATGTTCTTGAT GAGGTACAATCACATCCAACAAGTATGGCC | 4494 |
| | GATTCCCAATGGCGGAG | 4495 |
| | CTCCGCCATTGGGAATC | 4496 |
| Sulfonylurea Resistance ALS 2 <i>Nicotiana tabacum</i> Pro191Ser CCA-TCA | AGTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGC TATAACCGGTCAAGTGTCACGTAGGATGATCGGTACTGATGCTTT TCAGGAAACTCCGATTGTTGAGGTAAGTAGAT | 4497 |
| | ATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTACC GATCATCCTACGTGACACTTGACCGGTTATAGCAACAATGGGGAC GCTATCCAGTAGGGCGTCCGCGAGGCCACT | 4498 |
| | GTCAAGTGTCACGTAGG | 4499 |
| | CCTACGTGACACTTGAC | 4500 |
| Sulfonylurea Resistance ALS 2 <i>Nicotiana tabacum</i> Pro191Gln CCA-CAA | GTGGCCTCGCGGACGCCCTACTGGATAGCGTCCCCATTGTTGCT ATAACCGGTCAAGTGCAACGTAGGATGATCGGTACTGATGCTTTT CAGGAAACTCCGATTGTTGAGGTAAGTAGATC | 4501 |
| | GATCTAGTTACCTCAACAATCGGAGTTTCCTGAAAAGCATCAGTAC CGATCATCCTACGTGCACTTGACCGGTTATAGCAACAATGGGGA CGCTATCCAGTAGGGCGTCCGCGAGGCCAC | 4502 |
| | TCAAGTGCAACGTAGGA | 4503 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | TCCTACGT <u>I</u> GCACTTGA | 4504 |
| Imidazolinone Resistance ALS 2 <i>Nicotiana tabacum</i> Ser647Asn AGT-AAT | GGCCATACTTGTGGATGTGATTGTACCTCATCAGGAACATGTTCT ACCTATGATTCCCA <u>A</u> TGGCGGGGCTTTCAAAGATGTGATCACAGA GGGTGACGGGAGAAGTTCTATTGACTTTG | 4505 |
| | CAAAGTCAATAGGAACTTCTCCCGTCACCCTCTGTGATCACATCTT TGAAAGCCCCGCCA <u>T</u> TGGGAATCATAGGTAGAACATGTTCTGAT GAGGTACAATCACATCCAACAAGTATGGCC | 4506 |
| | GATTCCCA <u>A</u> TGGCGGGG | 4507 |
| | CCCCGCCA <u>T</u> TGGGAATC | 4508 |
| Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Ser CCC-TCC | AGTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTA TTACTGGTCAAGTT <u>I</u> CCAGGAGAATGATTGGAACAGATGCGTTTC AAGAAACCCCTATTGTTGAGGTAACACGTT | 4509 |
| | AACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTCC AATCATTCTCCTGG <u>A</u> AACTTGACCAGTAATAGCAACCATTGGAACA CTGTCTAATAAAGCATCAGCAAGACCACT | 4510 |
| | GTCAAGTT <u>I</u> CCAGGAGA | 4511 |
| | TCTCCTGG <u>A</u> AACTTGAC | 4512 |
| Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Gln CCC-CAA | GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTAT TACTGGTCAAGTT <u>C</u> AAAGGAGAATGATTGGAACAGATGCGTTTCA AGAAACCCCTATTGTTGAGGTAACACGTTT | 4513 |
| | GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTT CAATCATTCTCCT <u>T</u> TGAACCTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAGCATCAGCAAGACCAC | 4514 |
| | TCAAGTT <u>C</u> AAAGGAGAA | 4515 |
| | TTCTCCT <u>T</u> TGAACCTTGA | 4516 |
| Sulfonylurea Resistance ALS <i>Xanthium</i> spp. Pro175Gln CCC-CAG | GTGGTCTTGCTGATGCTTTATTAGACAGTGTTCCAATGGTTGCTAT TACTGGTCAAGTT <u>C</u> AGAGGAGAATGATTGGAACAGATGCGTTTCA AGAAACCCCTATTGTTGAGGTAACACGTTT | 4517 |
| | GAACGTGTTACCTCAACAATAGGGGTTTCTTGAAACGCATCTGTTT CAATCATTCTCCT <u>C</u> TGAACCTTGACCAGTAATAGCAACCATTGGAAC ACTGTCTAATAAAGCATCAGCAAGACCAC | 4518 |
| | TCAAGTT <u>C</u> AGAGGAGAA | 4519 |
| | TTCTCCT <u>C</u> TGAACCTTGA | 4520 |
| Imidazolinone Resistance ALS <i>Xanthium</i> spp. Ala631Asn GCT-AAT | GGGCCTTACTTGTGGATGTGATCGTGCCCCATCAAGAACATGTG TTGCCCATGATCCCG <u>A</u> ATGGTGAGGTTTCATGGATGTGATCACC GAAGGCGACGGCAGAATGAAATATTGAGCTT | 4521 |
| | AAGCTCAATATTTATTCTGCCGTCGCCTTCGGTGATCACATCCAT GAAACCTCCACCA <u>T</u> TCGGGATCATGGGCAACACATGTTCTTGATG GGGCACGATCACATCCAACAAGTAAGGCC | 4522 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | TGATCCCGAATGGTGA | 4523 |
| | TCCACCATTCGGGATCA | 4524 |
| Sulfonylurea Resistance ALS <i>Bassia scoparia</i> Pro189Ser CCG-TCG | TCCGGGTTTGCTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCG ATCACGGGGCAGGTGTCGCGGCGAATGATTGGGACGGATGCTTT TCAGGAGACTCCTATTGTTGAGGTAACACGGT | 4525 |
| | ACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTCC CAATCATTCGCCGCGACACCTGCCCCGTGATCGCCACCAGTGA ACGGAATCGAGCAAAGCATCAGCAAACCCGGA | 4526 |
| | GGCAGGTGTCGCGGCGA | 4527 |
| | TCGCCGCGACACCTGCC | 4528 |
| Sulfonylurea Resistance ALS <i>Bassia scoparia</i> Pro189Gln CCG-CAG | CCGGGTTTGCTGATGCTTTGCTCGATTCCGTTCCACTGGTGGCGA TCACGGGGCAGGTGCAGCGGCGAATGATTGGGACGGATGCTTTT CAGGAGACTCCTATTGTTGAGGTAACACGGTC | 4529 |
| | GACCGTGTTACCTCAACAATAGGAGTCTCCTGAAAAGCATCCGTC CCAATCATTCGCCGCTGCACCTGCCCCGTGATCGCCACCAGTGG AACGGAATCGAGCAAAGCATCAGCAAACCCGG | 4530 |
| | GCAGGTGCAGCGGCGAA | 4531 |
| | TTCGCCGCTGCACCTGC | 4532 |
| Imidazolinone Resistance ALS <i>Bassia scoparia</i> Ser649Asn AGT-AAT | GACCTTACCTGCTTGATGTGATTGTACCTCATCAGGAGCATGTGC TGCCTATGATTCCCTAATGGTGCAGCCTTCAAGGATATCATTAAACGA AGGTGATGGAAGAACAAGTTATTGATGTTT | 4533 |
| | GAACATCAATAACTTGTCTTCCATCACCTTCGTTAATGATATCCTT GAAGGCTGCACCATTAGGAATCATAGGCAGCACATGCTCCTGATG AGGTACAATCACATCAAGCAGGTAAGGTC | 4534 |
| | GATTCCTAATGGTGCAG | 4535 |
| | CTGCACCATTAGGAATC | 4536 |
| Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Ser CCT-TCT | AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCTTCTTGTCGCC ATTACAGGACAGGTCTCTCGCCGGATGATCGGTACTGACGCCTTC CAAGAGACACCAATCGTTGAGGTAACGAGGT | 4537 |
| | ACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAAGGCGTCAGTAC CGATCATCCGGCGAGAGACCTGTCCTGTAATGGCGACAAGAGGA ACACTGTCAAGCATCGCGTCTGCTAACCCGCT | 4538 |
| | GACAGGTCTCTCGCCGG | 4539 |
| | CCGGCGAGAGACCTGTC | 4540 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Gln CCT-CAA | GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCCTCTTGTCGCCA TTACAGGACAGGTCC A ACGCCGGATGATCGGTACTGACGCCTTC CAAGAGACACCAATCGTTGAGGTAACGAGGTC | 4541 |
| | GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTA CCGATCATCCGGCG T TGGACCTGTCCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACCCGC | 4542 |
| | ACAGGTCC A ACGCCGGA | 4543 |
| | TCCGGCG T TGGACCTGT | 4544 |
| Sulfonylurea Resistance ALS 1 <i>Brassica napus</i> Pro182Gln CCT-CAG | GCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCCTCTTGTCGCCA TTACAGGACAGGTCC A GCGCCGGATGATCGGTACTGACGCCTTC CAAGAGACACCAATCGTTGAGGTAACGAGGTC | 4545 |
| | GACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTA CCGATCATCCGGCG C TGGACCTGTCCTGTAATGGCGACAAGAGG AACACTGTCAAGCATCGCGTCTGCTAACCCGC | 4546 |
| | ACAGGTCC A GCGCCGGA | 4547 |
| | TCCGGCG C TGGACCTGT | 4548 |
| Imidazolinone Resistance ALS 1 <i>Brassica napus</i> Ser638Asn AGT-AAT | GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGT TACCGATGATCCCAA A TGGTGGCACTTTCAAAGATGTAATAACAG AAGGGGATGGTTCGACTAAGTACTGAGAGAT | 4549 |
| | ATCTCTCAGTACTTAGTGCGACCATCCCTTCTGTTATTACATCTTT GAAAGTGCCACCA T TTGGGATCATCGGTAACACATGTTCTTGGTG CGGACATATCACATCCAACAGGTATGGTC | 4550 |
| | GATCCCAA A TGGTGGCA | 4551 |
| | TGCCACCA T TTGGGATC | 4552 |
| Sulfonylurea Resistance ALS 2 <i>Brassica napus</i> Pro126Ser CCC-TCC | CAGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCCTCTTGTCGC CATTACAGGACAGGT T CCTCGCCGGATGATCGGTACTGACGCCTT CCAAGAGACACCAATCGTTGAGGTAACGAGG | 4553 |
| | CCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTACC GATCATCCGGCGAGG A ACCTGTCCTGTAATGGCGACAAGAGGAA CACTGTCAAGCATCGCGTCTGCTAACCCGCTG | 4554 |
| | GGACAGGT T CCTCGCCG | 4555 |
| | CGGCGAGG A ACCTGTCC | 4556 |
| Sulfonylurea Resistance ALS 2 <i>Brassica napus</i> Pro126Gln CCC-CAG | AGCGGGTTAGCAGACGCGATGCTTGACAGTGTTCCCTCTTGTCGCC ATTACAGGACAGGT C ACTCGCCGGATGATCGGTACTGACGCCTTC CAAGAGACACCAATCGTTGAGGTAACGAGGT | 4557 |
| | ACCTCGTTACCTCAACGATTGGTGTCTCTTGGAAGGCGTCAGTAC CGATCATCCGGCGAG T GACCTGTCCTGTAATGGCGACAAGAGGA AACTGTCAAGCATCGCGTCTGCTAACCCGCT | 4558 |
| | GACAGGT C ACTCGCCGG | 4559 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | CCGGCGAG <u>I</u> GACCTGTC | 4560 |
| Imidazolinone Resistance ALS 2 <i>Brassica napus</i> Ser582Asn AGT-AAT | GACCATACCTGTTGGATGTGATATGTCCGCACCAAGAACATGTGT TACCGATGATCCCAA <u>A</u> TGGTGGCACTTTCAAAGATGTAATAACAG AAGGGGATGGTCGCACTAAGTACTGAGAGAT | 4561 |
| | ATCTCTCAGTACTTAGTGCGACCATCCCCTTCTGTTATTACATCTTT GAAAGTGCCACCA <u>T</u> TTGGGATCATCGGTAACACATGTTCTTGGTG CGGACATATCACATCCAACAGGTATGGTC | 4562 |
| | GATCCCAA <u>A</u> TGGTGGCA | 4563 |
| | TGCCACCA <u>T</u> TTGGGATC | 4564 |
| Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Ser CCT-TCT | AGCGGGTTAGCCGACGCGATGCTTGACAGTGTTCTCTCGTCGC CATCACAGGACAGGT <u>C</u> TCTCGCCGGATGATCGGTACTGACGCGT TCCAAGAGACGCCAATCGTTGAGGTAACGAGGT | 4565 |
| | ACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTAC CGATCATCCGGCGAG <u>A</u> GACCTGTCCTGTGATGGCGACGAGAGGA AACTGTCAAGCATCGCGTCGGCTAACCCGCT | 4566 |
| | GACAGGT <u>C</u> TCTCGCCGG | 4567 |
| | CCGGCGAG <u>A</u> GACCTGTC | 4568 |
| Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Gln CCT-CAA | GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCTCTCGTCGCC ATCACAGGACAGGTCC <u>A</u> ACGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC | 4569 |
| | GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA CCGATCATCCGGCG <u>T</u> TGGACCTGTCCTGTGATGGCGACGAGAGG AACTGTCAAGCATCGCGTCGGCTAACCCGC | 4570 |
| | ACAGGTCC <u>A</u> ACGCCGGA | 4571 |
| | TCCGGCG <u>T</u> TGGACCTGT | 4572 |
| Sulfonylurea Resistance ALS 3 <i>Brassica napus</i> Pro179Gln CCT-CAG | GCGGGTTAGCCGACGCGATGCTTGACAGTGTTCTCTCGTCGCC ATCACAGGACAGGTCC <u>A</u> GCGCCGGATGATCGGTACTGACGCGTT CCAAGAGACGCCAATCGTTGAGGTAACGAGGTC | 4573 |
| | GACCTCGTTACCTCAACGATTGGCGTCTCTTGGAACGCGTCAGTA CCGATCATCCGGCG <u>C</u> TGGACCTGTCCTGTGATGGCGACGAGAGG AACTGTCAAGCATCGCGTCGGCTAACCCGC | 4574 |
| | ACAGGTCC <u>A</u> GCGCCGGA | 4575 |
| | TCCGGCG <u>C</u> TGGACCTGT | 4576 |
| Imidazolinone Resistance ALS 3 <i>Brassica napus</i> Ser635Asn AGT-AAT | GACCGTACCTGTTGGATGTCATCTGTCCGCACCAAGAACATGTGT TACCGATGATCCCAA <u>A</u> TGGTGGCACTTTCAAAGATGTAATAACCG AAGGGGATGGTCGCACTAAGTACTGAGAGAT | 4577 |
| | ATCTCTCAGTACTTAGTGCGACCATCCCCTTCGGTTATTACATCTT TGAAAGTGCCACCA <u>T</u> TTGGGATCATCGGTAACACATGTTCTTGGT GCGGACAGATGACATCCAACAGGTACGGTC | 4578 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | GATCCCAA <u>A</u> TGGTGGCA | 4579 |
| | TGCCACCA <u>T</u> TTGGGATC | 4580 |
| Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Ser CCC-TCC | TCCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGC CATCACGGGGCCAGGTCT <u>C</u> CCCGCCGCATGATCGGCACCGACGCCT TCCAGGAGACGCCCATAGTCGAGGTCACCCGCT | 4581 |
| | AGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGTG CCGATCATGCGGCGGG <u>A</u> GACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGGA | 4582 |
| | GCCAGGTCT <u>C</u> CCCGCCGC | 4583 |
| | GCGGCGGG <u>A</u> GACCTGGC | 4584 |
| Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAA | CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC ATCACGGGGCCAGGTCC <u>A</u> ACGCCGCATGATCGGCACCGACGCCTT CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC | 4585 |
| | GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCG <u>T</u> TGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG | 4586 |
| | CCAGGTCC <u>A</u> ACGCCGCA | 4587 |
| | TGCGGCG <u>T</u> TGGACCTGG | 4588 |
| Sulfonylurea Resistance ALS <i>Oryza sativa</i> Pro171Gln CCC-CAG | CCGCGCTCGCCGACGCGCTGCTCGACTCCGTCCCGATGGTCGCC ATCACGGGGCCAGGTCC <u>A</u> AGCGCCGCATGATCGGCACCGACGCCTT CCAGGAGACGCCCATAGTCGAGGTCACCCGCTC | 4589 |
| | GAGCGGGTGACCTCGACTATGGGCGTCTCCTGGAAGGCGTCGGT GCCGATCATGCGGCG <u>C</u> TGGACCTGGCCCGTGATGGCGACCATCG GGACGGAGTCGAGCAGCGCGTCGGCGAGCGCGG | 4590 |
| | CCAGGTCC <u>A</u> AGCGCCGCA | 4591 |
| | TGCGGCG <u>C</u> TGGACCTGG | 4592 |
| Imidazolinone Resistance ALS <i>Oryza sativa</i> Ser627Asn AGT-AAT | GGCCATACTTGTTGGATATCATCGTCCCGCACCAGGAGCATGTGC TGCCTATGATCCCAA <u>A</u> TGGGGGGCGCATTCAAGGACATGATCCTGG ATGGTGATGGCAGGACTGTGTATTAATCTAT | 4593 |
| | ATAGATTAATACACAGTCCTGCCATCACCATCCAGGATCATGTCCT TGAATGCGCCCCCA <u>T</u> TTGGGATCATAGGCAGCACATGCTCCTGGT GCGGGACGATGATATCCAACAAGTATGGCC | 4594 |
| | GATCCCAA <u>A</u> TGGGGGCG | 4595 |
| | CGCCCCCA <u>T</u> TTGGGATC | 4596 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Ser CCG-TCG | TCTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGC CATCACGGGACAGGTGTCGCGACGCATGATTGGCACCGACGCCT TTCAGGAGACGCCCATCGTCGAGGTCACCCGCT | 4597 |
| | AGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGTG CCAATCATGCGTCGCGACACCTGTCCCGTGATGGCGACCATGGG GACGGAGTCGAGCAACGCGTCTGCGAGCGCAGA | 4598 |
| | GACAGGTGTCGCGACGC | 4599 |
| | GCGTCGCGACACCTGTC | 4600 |
| Sulfonylurea Resistance ALS <i>Zea mays</i> Pro165Gln CCG-CAG | CTGCGCTCGCAGACGCGTTGCTCGACTCCGTCCCCATGGTCGCC ATCACGGGACAGGTGACGCGACGCATGATTGGCACCGACGCCTT TCAGGAGACGCCCATCGTCGAGGTCACCCGCTC | 4601 |
| | GAGCGGGTGACCTCGACGATGGGCGTCTCCTGAAAGGCGTCGGT GCCAATCATGCGTCGCTGCACCTGTCCCGTGATGGCGACCATGG GGACGGAGTCGAGCAACGCGTCTGCGAGCGCAG | 4602 |
| | ACAGGTGCAGCGACGCA | 4603 |
| | TGCGTCGCTGCACCTGT | 4604 |
| Imidazolinone Resistance ALS <i>Zea mays</i> Ser621Asn AGT-AAT | GGCCGTACCTCTTGATATAATCGTCCCGCACCAGGAGCATGTGT TGCCATGATCCCTAATGGTGGGGCTTTCAAGGATATGATCCTGG ATGGTGATGGCAGGACTGTGTATTGATCCGT | 4605 |
| | ACGGATCAATACACAGTCCTGCCATCACCATCCAGGATCATATCC TTGAAAGCCCCACCAATTAGGGATCATAGGCAACACATGCTCCTGG TGCGGGACGATTATATCCAAGAGGTACGGCC | 4606 |
| | GATCCCTAATGGTGGGG | 4607 |
| | CCCCACCAATTAGGGATC | 4608 |
| Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Ser CCT-TCT | AGTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGCGG ATCACTGGTCAAGTCTCTCGTCGGATGATCGGTACCGATGCTTTC CAGGAACTCCAATTGTTGAGGTAACAAGGT | 4609 |
| | ACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTAC CGATCATCCGACGAGAGACTTGACCAGTGATCGCCACGAGAGGG ATACTATCGAGCATTGCATCAGCGAGACCACT | 4610 |
| | GTCAAGTCTCTCGTCGG | 4611 |
| | CCGACGAGAGACTTGAC | 4612 |
| Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAA | GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGCGA TCACTGGTCAAGTCCAAACGTCGGATGATCGGTACCGATGCTTTC AGGAACTCCAATTGTTGAGGTAACAAGGTC | 4613 |
| | GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACGTTGGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC | 4614 |
| | TCAAGTCCAAACGTCGGA | 4615 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | TCCGACG <u>TT</u> GGACTTGA | 4616 |
| Sulfonylurea Resistance ALS <i>Gossypium hirsutum</i> Pro186Gln CCT-CAG | GTGGTCTCGCTGATGCAATGCTCGATAGTATCCCTCTCGTGGCGA TCACTGGTCAAGTCC <u>AG</u> CGTCCGATGATCGGTACCGATGCTTTCC AGGAACTCCAATTGTTGAGGTAACAAGGTC | 4617 |
| | GACCTTGTTACCTCAACAATTGGAGTTTCCTGGAAAGCATCGGTA CCGATCATCCGACG <u>CT</u> GGACTTGACCAGTGATCGCCACGAGAGG GATACTATCGAGCATTGCATCAGCGAGACCAC | 4618 |
| | TCAAGTCC <u>AG</u> CGTCCGA | 4619 |
| | TCCGACG <u>CT</u> GGACTTGA | 4620 |
| Imidazolinone Resistance ALS <i>Gossypium hirsutum</i> Ser642Asn AGT-AAT | GACCTTACTTGTTGGATGTGATTGTCCACATCAAGAACATGTCCT GCCTATGATCCCCA <u>AT</u> GGAGGGGCTTTCAAAGATGTGATCACAGA GGGTGATGGAAGAACAACAATATTGACCTCA | 4621 |
| | TGAGGTCAATATTGTGTTCTTCCATCACCTCTGTGATCACATCTT TGAAAGCCCCCTCCA <u>TT</u> GGGGATCATAGGCAGGACATGTTCTTGAT GTGGGACAATCACATCCAACAAGTAAGGTC | 4622 |
| | GATCCCCA <u>AT</u> GGAGGGG | 4623 |
| | CCCCTCCA <u>TT</u> GGGGATC | 4624 |
| Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Ser CCC-TCC | TCTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCA TTACTGGGCAAGTT <u>TT</u> CCCGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACGAT | 4625 |
| | ATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTACC AATCATACGCCGGG <u>AA</u> ACTTGCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAGA | 4626 |
| | GGCAAGTT <u>TT</u> CCCGGCGT | 4627 |
| | ACGCCGGG <u>AA</u> ACTTGCC | 4628 |
| Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Gln CCC-CAA | CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT TACTGGGCAAGTTCA <u>AA</u> CGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACGATC | 4629 |
| | GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCG <u>TT</u> GAACTTGCCAGTAATGGCGACAAGAGGGA CTGAGTCAAGAAGTGCATCAGCAAGACCAG | 4630 |
| | GCAAGTTC <u>AA</u> CGGCGTA | 4631 |
| | TACGCCG <u>TT</u> GAACTTGC | 4632 |
| Sulfonylurea Resistance ALS <i>Amaranthus powellii</i> Pro192Gln CCC-CAG | CTGGTCTTGCTGATGCACTTCTTGACTCAGTCCCTCTTGTCGCCAT TACTGGGCAAGTTCA <u>AG</u> CGGCGTATGATTGGTACTGATGCTTTTCA AGAGACTCCAATTGTTGAGGTAACGATC | 4633 |
| | GATCGAGTTACCTCAACAATTGGAGTCTCTTGAAAAGCATCAGTAC CAATCATACGCCG <u>CT</u> GAACTTGCCAGTAATGGCGACAAGAGGG ACTGAGTCAAGAAGTGCATCAGCAAGACCAG | 4634 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| | GCAAGTTC A GCGGCGTA | 4635 |
| | TACGCCG C TGAACTTGC | 4636 |
| Imidazolinone Resistance ALS <i>Amaranthus powellii</i> Ser652Asn AGC-AAC | GACCGTATCTGCTGGATGTAATCGTACCACATCAGGAGCATGTGC TGCCTATGATCCCTA A CGGTGCCGCCTTCAAGGACACCATAACAG AGGGTGATGGAAGAAGGGCTTATTAGTTGGT | 4637 |
| | ACCAACTAATAAGCCCTTCTTCCATCACCCCTCTGTTATGGTGTCTT TGAAGGCGGCACCG T AGGGATCATAGGCAGCACATGCTCCTGA TGTGGTACGATTACATCCAGCAGATACGGTC | 4638 |
| | GATCCCTA A CGGTGCCG | 4639 |
| | CGGCACCG T AGGGATC | 4640 |
| | | |

Table 30
Genome-Altering Oligos Conferring Porphyric Herbicide Resistance

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Porphyric Herbicide Resistant PPO <i>Arabidopsis thaliana</i> Val365Met GTT-ATG | TCTTGCGCCCTCTTTCTGAATCTGCTGCAAATGCACTCTCAAACT ATATTACCCACCAATGGCAGCAGTATCTATCTCGTACCCGAAAGA AGCAATCCGAACAGAATGTTTGATAGATGG | 4641 |
| | CCATCTATCAAACATTCTGTTGCGATTGCTTCTTTGCGGTACGAGA TAGATACTGCTGCCATTGGTGGGTAATATAGTTTTGAGAGTGCATT TGCAGCAGATTGAGAAAGAGGGCGCAAGA | 4642 |
| | CCCACCAATGGCAGCAG | 4643 |
| | CTGCTGCCATTGGTGGG | 4644 |
| Porphyric Herbicide Resistant PPO <i>Nicotiana tabacum</i> Val376Met GTT-ATG | TATTACGTCCTCTTTGCGTTGCCGAGCAGATGCACTTTCAAATTT CTACTATCCCCCAATGGGAGCAGTCACAATTTTCATATCCTCAAGAA GCTATTCGTGATGAGCGTCTGGTTGATGG | 4645 |
| | CCATCAACCAGACGCTCATCACGAATAGCTTCTTGAGGATATGAA ATTGTGACTGCTCCCATTTGGGGGATAGTAGAAATTTGAAAGTGCA TCTGCTGCGGCAACCGAAAGAGGACGTAATA | 4646 |
| | TCCCCCAATGGGAGCAG | 4647 |
| | CTGCTCCCATTTGGGGGA | 4648 |
| Porphyric Herbicide Resistant PPO <i>Cichorium intybus</i> Val383Met GTT-ATG | TGTTGCGTCCGCTTTTCGTTGGGTGCAGCAGATGCATTGTCAAAT TTTATTATCCTCCGATGGCAGCTGTATCAATTTTCATATCCAAAAGA CGCAATTCGTGCTGACCGGCTGATTGATGG | 4649 |
| | CCATCAATCAGCCGGTCAGCACGAATTGCGTCTTTTGGATATGAA ATTGATACAGCTGCCATCGGAGGATAATAAAATTTTGACAATGCAT CTGCTGCACCCAACGAAAGCGGACGCAACA | 4650 |
| | TCCTCCGATGGCAGCTG | 4651 |
| | CAGCTGCCATCGGAGGA | 4652 |
| Porphyric Herbicide Resistant PPO <i>Spinacia oleracea</i> Val390Met GTT-ATG | TCCTTCGTCCACTTTTCAGATGTCGCCGAGAATCTCTTTCAAAT TCATTATCCACCAATGGCAGCTGTGTCACTTTCTATCCTAAAGAA GCAATTAGATCAGAGTGCTTGATTGACGG | 4653 |
| | CCGTCAATCAAGCACTCTGATCTAATTGCTTCTTTAGGATAGGAAA GTGACACAGCTGCCATTGGTGGATAATGAAATTTTGAAAGAGATT CTGCGGCGACATCTGAAAGTGGACGAAGGA | 4654 |
| | TCCACCAATGGCAGCTG | 4655 |
| | CAGCTGCCATTGGTGGG | 4656 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|------------|
| Porphyric Herbicide Resistant PPO <i>Zea mays</i> Val363Met GTT-ATG | TTTTGCGTCCACTTTCAAGCGATGCTGCAGATGCTCTATCAAGATTCTATTATCCACCGATGGCTGCTGTAAGTGTTCGTATCCAAAGGAA GCAATTAGAAAAGAATGCTTAATTGATGG | 4657 |
| | CCATCAATTAAGCATTCTTTTCTAATTGCTTCCTTTGGATACGAAACAGTTACAGCAGCCATCGGTGGATAATAGAATCTTGATAGAGCATCTGCAGCATCGCTTGAAAGTGGACGCAAAA | 4658 |
| | TCCACCGATGGCTGCTG | 4659 |
| | CAGCAGCCATCGGTGGA | 4660 |
| Porphyric Herbicide Resistant PPO <i>Oryza sativa</i> Val364Met GTT-ATG | TCTTGCGGCCACTTTCAAGTGATGCAGCAGATGCTCTGTCAATATTCTATTATCCACCAATGGCTGCTGTAAGTGTTCATATCCAAAAGAA GCAATTAGAAAAGAATGCTTAATTGACGG | 4661 |
| | CCGTCAATTAAGCATTCTTTTCTAATTGCTTCCTTTGGATATGAAACAGTTACAGCAGCCATTGGTGGATAATAGAATATTGACAGAGCATCTGCTGCATCACTTGAAAGTGGCCGCAAGA | 4662 |
| | TCCACCAATGGCTGCTG | 4663 |
| | CAGCAGCCATTGGTGGGA | 4664 |
| Porphyric Herbicide Resistant PPO <i>Chlamydomonas reinhardtii</i> Val389Met GTG-ATG | CTGGTCAAGGAGCAGGCGCCCGCCGCGCCGAGGCCCTGGGCTCCTTCGACTACCCGCCGATGGGCGCCGTGACGCTGTCGTACCCGCTGAGCGCCGTGCGGGAGGAGCGCAAGGCCTCGG | 4665 |
| | CCGAGGCCTTGCGCTCCTCCCGCACGGCGCTCAGCGGGTACGACAGCGTCACGGCGCCCATCGGCGGGTAGTCGAAGGAGCCCAGGGCCTCGGCGGCGGGCGGGCGCTGCTCCTTGACCAG | 4666 |
| | ACCCGCCGATGGGCGCC | 4667 |
| | GGCGCCCATCGGCGGGT | 4668 |

Table 31
Genome-Altering Oligos Conferring Triazine Resistance

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|------------|
| Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT | AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGATTTTCCAATATGCTACTTTCAACAATTCTCGTTCTTTACATTTCTTCTTAGCGGCTTGGCCGGTAGTAGGTATTTG | 4669 |
| | CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAACGAGAATTGTTGAAAGTAGCATATTGGAAAATCAATCGGCCAAAATAACCGTGAGCAGCTACAATGTTGTAAGTTT | 4670 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | ATATGCTA <u>C</u> TTTCAACA | 4671 |
| | TGTTGAAA <u>G</u> TAGCATAT | 4672 |
| Triazine Resistant D1 Protein <i>Nicotiana tabacum</i> Ser264Thr AGT-ACT | AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4673 |
| | CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAAGTGAACGAA CGAGAGTTGTTGAAA <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT | 4674 |
| | ATATGCTA <u>C</u> TTTCAACA | 4675 |
| | TGTTGAAA <u>G</u> TAGCATAT | 4676 |
| Triazine Resistant D1 Protein <i>Populus deltoides</i> Ser264Thr AGT-ACT | AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTTAACAACCTCTCGCTCTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4677 |
| | CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAG CGAGAGTTGTTAAA <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT | 4678 |
| | ATATGCTA <u>C</u> TTTTAACA | 4679 |
| | TGTTAAA <u>G</u> TAGCATAT | 4680 |
| Triazine Resistant D1 Protein <i>Petunia x hybrida</i> Ser264Thr AGT-ACT | AAACTTATAATATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4681 |
| | CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAAGTGAACGAA CGAGAGTTGTTGAAA <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT | 4682 |
| | ATATGCTA <u>C</u> TTTCAACA | 4683 |
| | TGTTGAAA <u>G</u> TAGCATAT | 4684 |
| Triazine Resistant D1 Protein <i>Magnolia pyramidata</i> Ser264Thr AGT-ACT | AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCCTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4685 |
| | CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAA <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCAGCTACGATATTATAAGTTT | 4686 |
| | ATATGCTA <u>C</u> TTTCAACA | 4687 |
| | TGTTGAAA <u>G</u> TAGCATAT | 4688 |
| Triazine Resistant D1 Protein <i>Medicago sativa</i> Ser264Thr AGT-ACT | AAACCTATAATATTGTAGCAGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCCTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4689 |
| | CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAGTTGTTGAAA <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCTGCTACAATATTATAGGTTT | 4690 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|------------|
| | ATATGCTA <u>C</u> TTTCAACA | 4691 |
| | TGTTGAAA <u>G</u> TAGCATAT | 4692 |
| Triazine Resistant D1 Protein <i>Glycine max</i> Ser264Thr AGT-ACT | AAACCTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCA <u>A</u> CTTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTTG | 4693 |
| | CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAA <u>G</u> TTGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCAGCTACAATATTATAGGTTT | 4694 |
| | ATATGCA <u>A</u> CTTTCAACA | 4695 |
| | TGTTGAAA <u>G</u> TTGCATAT | 4696 |
| Triazine Resistant D1 Protein <i>Brassica napus</i> Gly264Thr GGT-ACT | AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG | 4697 |
| | CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAA <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATGTTGTAAGTTT | 4698 |
| | ATATGCTA <u>C</u> TTTCAACA | 4699 |
| | TGTTGAAA <u>G</u> TAGCATAT | 4700 |
| Triazine Resistant D1 Protein <i>Oryza sativa</i> Ser264Thr AGT-ACT | AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAAAT CTTCCAATATGCTA <u>C</u> TTTTAACAATTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATTTG | 4701 |
| | CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAGAA CGAGAGTTGTTAAAA <u>G</u> TAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCGGCCACAATATTATAAGTTT | 4702 |
| | ATATGCTA <u>C</u> TTTTAACA | 4703 |
| | TGTTAAA <u>G</u> TAGCATAT | 4704 |
| Triazine Resistant D1 Protein <i>Zea mays</i> Ser264Thr AGT-ACT | AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAAAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATCTG | 4705 |
| | CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAGAA CGAGAATTGTTGAAA <u>G</u> TAGCATATTGGAAGATTAATCGACCAAAT AACCGTGAGCAGCCACAATATTATAAGTCT | 4706 |
| | ATATGCTA <u>C</u> TTTCAACA | 4707 |
| | TGTTGAAA <u>G</u> TAGCATAT | 4708 |
| Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT | AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT TTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCTTTACATTTCTTCT AGCGGCTTGGCCGGTAGTAGGTATTTG | 4709 |
| | CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAA <u>G</u> TAGCATATTGGAAAATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT | 4710 |
| | ATATGCTA <u>C</u> TTTCAACA | 4711 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| | TGTTGAAAGTAGCATAT | 4712 |
| Triazine Resistant D1 Protein <i>Nicotiana tabacum</i> Ser264Thr AGT-ACT | AAACTTATAACATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4713 |
| | CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAAGTGTAAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT | 4714 |
| | ATATGCTA <u>C</u> TTTCAACA | 4715 |
| | TGTTGAAAGTAGCATAT | 4716 |
| | | |
| Triazine Resistant D1 Protein <i>Populus deltoides</i> Ser264Thr AGT-ACT | AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTTAACAACCTCTCGCTCTTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4717 |
| | CAGATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAG CGAGAGTTGTTAAAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT | 4718 |
| | ATATGCTA <u>C</u> TTTTAACA | 4719 |
| | TGTTAAAAGTAGCATAT | 4720 |
| | | |
| Triazine Resistant D1 Protein <i>Petunia x hybrida</i> Ser264Thr AGT-ACT | AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4721 |
| | CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAAGTGTAAACGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT | 4722 |
| | ATATGCTA <u>C</u> TTTCAACA | 4723 |
| | TGTTGAAAGTAGCATAT | 4724 |
| | | |
| Triazine Resistant D1 Protein <i>Magnolia pyramidata</i> Ser264Thr AGT-ACT | AAACTTATAATATCGTAGCTGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4725 |
| | CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCAGCTACGATATTATAAGTTT | 4726 |
| | ATATGCTA <u>C</u> TTTCAACA | 4727 |
| | TGTTGAAAGTAGCATAT | 4728 |
| | | |
| Triazine Resistant D1 Protein <i>Medicago sativa</i> Ser264Thr AGT-ACT | AAACCTATAATATTGTAGCAGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4729 |
| | CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCTGCTACAATATTATAGGTTT | 4730 |
| | ATATGCTA <u>C</u> TTTCAACA | 4731 |
| | | |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | TGTTGAAA <u>G</u> TAGCATAT | 4732 |
| Triazine Resistant D1 Protein <i>Glycine max</i> Ser264Thr AGT-ACT | AAACCTATAATATTGTAGCTGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCAA <u>C</u> TTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTTG | 4733 |
| | CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAA <u>G</u> TTGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCAGCTACAATATTATAGGTTT | 4734 |
| | ATATGCAA <u>C</u> TTTCAACA | 4735 |
| | TGTTGAAA <u>G</u> TTGCATAT | 4736 |
| Triazine Resistant D1 Protein <i>Brassica napus</i> Gly264Thr GGT-ACT | AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCTTTACATTTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG | 4737 |
| | CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAA <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATGTTGTAAGTTT | 4738 |
| | ATATGCTA <u>C</u> TTTCAACA | 4739 |
| | TGTTGAAA <u>G</u> TAGCATAT | 4740 |
| Triazine Resistant D1 Protein <i>Oryza sativa</i> Ser264Thr AGT-ACT | AAACTTATAATATTGTGGCCGCTCATGGTTATTTTGGCCGATTAAAT CTTCCAATATGCTA <u>C</u> TTTTAACAATTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATTTG | 4741 |
| | CAAATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTAAAA <u>G</u> TAGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCGGCCACAATATTATAAGTTT | 4742 |
| | ATATGCTA <u>C</u> TTTTAACA | 4743 |
| | TGTTAAA <u>G</u> TAGCATAT | 4744 |
| Triazine Resistant D1 Protein <i>Zea mays</i> Ser264Thr AGT-ACT | AGACTTATAATATTGTGGCTGCTCACGGTTATTTTGGTCGATTAAAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGGATCTG | 4745 |
| | CAGATCCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAATTGTTGAAA <u>G</u> TAGCATATTGGAAGATTAATCGACCAAAT AACCGTGAGCAGCCACAATATTATAAGTCT | 4746 |
| | ATATGCTA <u>C</u> TTTCAACA | 4747 |
| | TGTTGAAA <u>G</u> TAGCATAT | 4748 |
| Triazine Resistant D1 Protein <i>Arabidopsis thaliana</i> Ser264Thr AGT-ACT | AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT TTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGTTCTTTACATTTCTTCTT AGCGGCTTGGCCGGTAGTAGGTATTTG | 4749 |
| | CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAA <u>G</u> TAGCATATTGGAATCAATCGGCCAAAAT AACCGTGAGCAGCTACAATGTTGTAAGTTT | 4750 |
| | ATATGCTA <u>C</u> TTTCAACA | 4751 |
| | TGTTGAAA <u>G</u> TAGCATAT | 4752 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Triazine Resistant D1 Protein <i>Picea abies</i> Ser264Thr AGT-ACT | AAACCTACAATATTGTGGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAGTATGCTA <u>C</u> TTTCAACAACCTCCCGTTCTTTACATTTCTTCT TAGCTGCTTGGCCCGTAGCAGGTATCTG | 4753 |
| | CAGATACCTGCTACGGGCCAAGCAGCTAAGAAGAAATGTAAAGAA CGGGAGTTGTTGAAAGTAGCATACTGGAAGATCAATCGGCCGAAA TAACCGTGAGCAGCCACAATATTGTAGGTTT | 4754 |
| | GTATGCTA <u>C</u> TTTCAACA | 4755 |
| | TGTTGAAAGTAGCATAC | 4756 |
| Triazine Resistant D1 Protein <i>Vicia faba</i> Ser264Thr AGT-ACT | AAACCTATAATATTGTAGCTGCTCACGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAATTCTCGCTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4757 |
| | CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAG CGAGAATTGTTGAAAGTAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATATTATAGGTTT | 4758 |
| | ATATGCTA <u>C</u> TTTCAACA | 4759 |
| | TGTTGAAAGTAGCATAT | 4760 |
| Triazine Resistant D1 Protein <i>Hordeum vulgare</i> Ser264Thr AGT-ACT | AGACTTATAATATTGTGGCTGCTCATGGTTATTTGGCCGATTAAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGAATCTG | 4761 |
| | CAGATTCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAA TAACCATGAGCAGCCACAATATTATAAGTCT | 4762 |
| | ATATGCTACTTTCAACA | 4763 |
| | TGTTGAAAGTAGCATAT | 4764 |
| Triazine Resistant D1 Protein <i>Triticum aestivum</i> Ser264Thr AGT-ACT | AACTTATAATATTGTGGCTGCTCATGGTTATTTGGCCGATTAAT CTTCCAATATGCTA <u>C</u> TTTCAACAACCTCTCGTTCTTTACACTTCTTCT TGGCTGCTTGGCCTGTAGTAGGAATCTG | 4765 |
| | CAGATTCCTACTACAGGCCAAGCAGCCAAGAAGAAGTGTAAAGAA CGAGAGTTGTTGAAAGTAGCATATTGGAAGATTAATCGGCCAAAA TAACCATGAGCAGCCACAATATTATAAGTTT | 4766 |
| | ATATGCTA <u>C</u> TTTCAACA | 4767 |
| | TGTTGAAAGTAGCATAT | 4768 |
| Triazine Resistant D1 Protein <i>Vigna unguiculata</i> Ser264Thr AGT-ACT | AACTTATAATATTGTAGCTGCTCATGGTTATTTGGCCGATTAATC TTCCAATATGCA <u>C</u> TTTCAACAATTCTCGTTCTTTACATTTCTTCCT AGCTGCTTGGCCTGTAGTAGGTATTTG | 4769 |
| | CAAATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAA CGAGAATTGTTGAAAGTTGCATATTGGAAGATTAATCGGCCAAAAT AACCATGAGCAGCTACAATATTATAAGTTT | 4770 |
| | ATATGCA <u>C</u> TTTCAACA | 4771 |
| | TGTTGAAAGTTGCATAT | 4772 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Triazine Resistant D1 Protein <i>Lotus japonicus</i> Ser264Thr AGT-ACT | AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCAAC <u>CTTT</u> CAACAACCTCTCGTTCTTTACACTTCTTCT TAGCTGCTTGGCCTGTTGTAGGTATCTG | 4773 |
| | CAGATACCTACAACAGGCCAAGCAGCTAAGAAGAAGTGTAAGAA CGAGAGTTGTTGAAAG <u>GTTG</u> CATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATATTATAGGTTT | 4774 |
| | ATATGCAAC <u>CTTT</u> CAACA | 4775 |
| | TGTTGAAAG <u>GTTG</u> CATAT | 4776 |
| Triazine Resistant D1 Protein <i>Sinapis alba</i> Ser264Thr AGT-ACT | AAACTTACAACATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTAC <u>CTTT</u> CAACAATTCTCGTTCTTTACATTTCTTCT TAGCGGCTTGGCCGGTAGTAGGTATTTG | 4777 |
| | CAAATACCTACTACCGGCCAAGCCGCTAAGAAGAAATGTAAAGAA CGAGAATTGTTGAAAG <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATGTTGTAAGTTT | 4778 |
| | ATATGCTAC <u>CTTT</u> CAACA | 4779 |
| | TGTTGAAAG <u>G</u> TAGCATAT | 4780 |
| Triazine Resistant D1 Protein <i>Pisum sativum</i> Ser264Thr AGT-ACT | AAACCTATAATATTGTAGCTGCTCACGGTTATTTTGGCCGATTGAT CTTCCAATATGCTAC <u>CTTT</u> CAACAATTCTCGCTCTTTACATTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4781 |
| | CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAATGTAAAGAG CGAGAATTGTTGAAAG <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCGTGAGCAGCTACAATATTATAGGTTT | 4782 |
| | ATATGCTAC <u>CTTT</u> CAACA | 4783 |
| | TGTTGAAAG <u>G</u> TAGCATAT | 4784 |
| Triazine Resistant D1 Protein <i>Spinacia oleracea</i> Ser264Thr AGT-ACT | AAACTTATAATATCGTAGCTGCTCATGGTTATTTTGGTCGATTGAT CTTCCAATATGCTAC <u>CTTT</u> CAACAACCTCTCGTTCTTTACACTTCTTCT TAGCTGCTTGGCCTGTAGTAGGTATTTG | 4785 |
| | CAAATACCTACTACAGGCCAAGCAGCTAAGAAGAAGTGTAAGAA CGAGAGTTGTTGAAAG <u>G</u> TAGCATATTGGAAGATCAATCGACCAAAA TAACCATGAGCAGCTACGATATTATAAGTTT | 4786 |
| | ATATGCTAC <u>CTTT</u> CAACA | 4787 |
| | TGTTGAAAG <u>G</u> TAGCATAT | 4788 |
| Triazine Resistant D1 Protein <i>Nicotiana debneyi</i> Ser264Thr AGT-ACT | AAACTTATAACATCGTAGCCGCTCATGGTTATTTTGGCCGATTGAT CTTCCAATATGCTAC <u>CTTT</u> CAACAACCTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4789 |
| | CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAAAG <u>G</u> TAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT | 4790 |
| | ATATGCTAC <u>CTTT</u> CAACA | 4791 |
| | TGTTGAAAG <u>G</u> TAGCATAT | 4792 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Triazine Resistant D1 Protein <i>Solanum nigrum</i> Ser264Thr AGT-ACT | AAACTTATAATATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4793 |
| | CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAA <u>A</u> GTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATATTATAAGTTT | 4794 |
| | ATATGCTA <u>C</u> TTTCAACA | 4795 |
| | TGTTGAA <u>A</u> GTAGCATAT | 4796 |
| Triazine Resistant D1 Protein <i>Nicotiana plumbaginifolia</i> Ser264Thr AGT-ACT | AAACTTATAACATCGTAGCCGCTCATGGTTATTTGGCCGATTGAT CTTCCAATATGCTA <u>C</u> TTTCAACAACTCTCGTTCGTTACACTTCTTCC TAGCTGCTTGGCCTGTAGTAGGTATCTG | 4797 |
| | CAGATACCTACTACAGGCCAAGCAGCTAGGAAGAAGTGTAACGAA CGAGAGTTGTTGAA <u>A</u> GTAGCATATTGGAAGATCAATCGGCCAAAA TAACCATGAGCGGCTACGATGTTATAAGTTT | 4798 |
| | ATATGCTA <u>C</u> TTTCAACA | 4799 |
| | TGTTGAA <u>A</u> GTAGCATAT | 4800 |

Example 27
Engineering male- or female-sterile plants

[246] Flower development in distantly related dicot plant species is increasingly better understood and appears to be regulated by a family of genes which encode regulatory proteins. These genes include, for example, *AGAMOUS* (*AG*), *APETALA1* (*AP1*), and *APETALA3* (*AP3*) and *PISTILLATA* (*PI*) in *Arabidopsis thaliana*, and *DEFICIENS A* (*DEFA*), *GLOBOSA* (*GLO*), *SQUAMOSA* (*SQUA*), and *PLENA* (*PLE*) in *Antirrhinum majus*. Genetic studies have shown that the *DEFA*, *GLO* and *AP3* genes are essential for petal and stamen development. Sequence analysis of these genes revealed that the gene products contain a conserved MADS box region, a DNA-binding domain. Using these clones as probes, MADS box genes have also been isolated from other species including tomato, tobacco, petunia, *Brassica napus*, and maize.

[247] Altering the expression of these genes results in altered floral morphology. For example, mutations in *AP3* and *PI* result in male-sterile flowers because petals develop in place of stamens.

[248] The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer altered floral structures in plants.

Table 32
Oligonucleotides to produce male-sterile plants

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|------------|
| Male-sterile AP3 <i>Arabidopsis thaliana</i> Arg3Term AGA-TGA | TTGTCCTCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAG AGAAGAATATGGCGTIGAGGGAAGATCCAGATCAAGAGGATAGAGA ACCAGACAAACAGACAAGTGACGTATTCAA | 4801 |
| | TTGAATACGTCACCTTGTCTGTTTGTCTGGTTCTCTATCCTCTTGATC TGGATCTTCCCTCA A CGCCATATTCTTCTCTCTTTGTTTAATCTTTTT GTTGAAGAGATTTGGTGGAGAGGACAA | 4802 |
| | ATATGGCGTIGAGGGAAG | 4803 |
| | CTTCCCTCA A CGCCATAT | 4804 |
| Male-sterile AP3 <i>Arabidopsis thaliana</i> Lys5Term AAG-TAG | TCTCCACCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGA ATATGGCGAGAGGGTIGATCCAGATCAAGAGGATAGAGAACCAGA CAAACAGACAAGTGACGTATTCAAAGAGAA | 4805 |
| | TTCTCTTTGAATACGTCACCTTGTCTGTTTGTCTGGTTCTCTATCCTC TTGATCTGGATCT A CCCTCTCGCCATATTCTTCTCTCTTTGTTTAAT CTTTTTGTTGAAGAGATTTGGTGGAGA | 4806 |

| | | |
|---|--|------|
| | CGAGAGGGTAGATCCAG | 4807 |
| | CTGGATCTACCCTCTCG | 4808 |
| Male-sterile AP3 <i>Arabidopsis thaliana</i> Gln7Term CAG-TAG | CCAAATCTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGG CGAGAGGGAAGATCTAGATCAAGAGGATAGAGAACCAGACAAACA GACAAGTGACGTATTCAAAGAGAAGGAATG | 4809 |
| | CATTCCTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGGTTCTCT ATCCTCTTGATCTAGATCTTCCCTCTCGCCATATTCTTCTCTCTTTG TTTAATCTTTTTGTTGAAGAGATTTGG | 4810 |
| | GGAAGATCTAGATCAAG | 4811 |
| | CTTGATCTAGATCTTCC | 4812 |
| Male-sterile AP3 <i>Arabidopsis thaliana</i> Lys9Term AAG-TAG | CTCTTCAACAAAAAGATTAAACAAAGAGAGAAGAATATGGCGAGAG GGAAGATCCAGATCTAGAGGATAGAGAACCAGACAAACAGACAAG TGACGTATTCAAAGAGAAGGAATGGTTTAT | 4813 |
| | ATAAACCATTCTTCTCTTTGAATACGTCACTTGTCTGTTTGTCTGG TTCTCTATCCTCTAGATCTGGATCTTCCCTCTCGCCATATTCTTCTC TCTTTGTTAATCTTTTTGTTGAAGAG | 4814 |
| | TCCAGATCTAGAGGATA | 4815 |
| | TATCCTCTAGATCTGGA | 4816 |
| Male-sterile AP3 <i>Brassica oleracea</i> Lys23Term AAG-TAG | AGAGGGAAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCG ACAAGTGACGTATTCTTAGAGAAGAAATGGTTTGTTCAGAAAGCT CACGAGCTTACAGTTTTATGTGATGCTAGGG | 4817 |
| | CCCTAGCATCACATAAACTGTAAGCTCGTGAGCTTTCTTGAACAA ACCATTTCTTCTCTAGAATACGTCACTTGTCTGGTTGGTCTGGTTC TCTATCCTCTTGATCTGGATCTTCCCTCT | 4818 |
| | CGTATTCTTAGAGAAGA | 4819 |
| | TCTTCTCTAGAATACG | 4820 |
| Male-sterile AP3 <i>Brassica oleracea</i> Arg24Term AGA-TGA | GGGAAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAA GTGACGTATTCTAAGTGAAGAAATGGTTTGTTCAGAAAGCTCACG AGCTTACAGTTTTATGTGATGCTAGGGTTT | 4821 |
| | AAACCCTAGCATCACATAAACTGTAAGCTCGTGAGCTTTCTTGAA CAAACCATTTCTTCACTTAGAATACGTCACTTGTCTGGTTGGTCTGG TTCTCTATCCTCTTGATCTGGATCTTCCC | 4822 |
| | ATTCTAAGTGAAGAAAT | 4823 |
| | ATTTCTTCACTTAGAAT | 4824 |
| Male-sterile AP3 <i>Brassica oleracea</i> Arg25Term AGA-TGA | AAGATCCAGATCAAGAGGATAGAGAACCAGACCAACCGACAAAGTG ACGTATTCTAAGAGATGAAATGGTTTGTTCAGAAAGCTCACGAGC TTACAGTTTTATGTGATGCTAGGGTTTCGA | 4825 |
| | TCGAAACCCTAGCATCACATAAACTGTAAGCTCGTGAGCTTTCTT GAACAAACCATTTCTATCTCTTAGAATACGTCACTTGTCTGGTTGGTC TGGTTCTCTATCCTCTTGATCTGGATCTT | 4826 |
| | CTAAGAGATGAAATGGT | 4827 |
| | ACCATTTCTATCTCTTAG | 4828 |

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| Male-sterile AP3 <i>Brassica oleracea</i> Leu28Term TTG-TAG | TCAAGAGGATAGAGAACCAGACCAACCGACAAGTGACGTATTCTA AGAGAAGAAATGGTTAGTTCAAGAAAGCTCACGAGCTTACAGTTTT ATGTGATGCTAGGGTTTCGATTATCATGTT | 4829 |
| | AACATGATAATCGAAACCCTAGCATCACATAAACTGTAAGCTCGT GAGCTTTCTTGAACTAACCATTTCTTCTCTTAGAATACGTCACCTTGT CGGTTGGTCTGGTTCTCTATCCTCTTGA | 4830 |
| | AAATGGTTAGTTCAAGA | 4831 |
| | TCTTGAACTAACCATTT | 4832 |
| Male-sterile AP3 <i>Brassica napus</i> Tyr21Term TAC-TAG | GGCTCGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAA CAGGCAGGTCACCTAGTCCAAGAGAAGAAATGGTTTGTTCAGAA AGCACACGAGCTCTCTGTTCTCTGTGATGCT | 4833 |
| | AGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAAACC ATTTCTTCTCTTGGACTAGGTGACCTGCCTGTTTGTGGTTCTCTA TCCTCTTAATCTGGATCTTCCCTCGAGCC | 4834 |
| | GTCACCTAGTCCAAGAG | 4835 |
| | CTCTTGGACTAGGTGAC | 4836 |
| Male-sterile AP3 <i>Brassica napus</i> Lys23Term AAG-TAG | CGAGGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGG CAGGTCACCTACTCCTAGAGAAGAAATGGTTTGTTCAGAAAGCAC ACGAGCTCTCTGTTCTCTGTGATGCTAAAG | 4837 |
| | CTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAACAA ACCATTTCTTCTCTAGGAGTAGGTGACCTGCCTGTTTGTGGTTTCT TCTATCCTCTTAATCTGGATCTTCCCTCG | 4838 |
| | CCTACTCCTAGAGAAGA | 4839 |
| | TCTTCTCTAGGAGTAGG | 4840 |
| Male-sterile AP3 <i>Brassica napus</i> Arg24Term AGA-TGA | GGGAAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAG GTCACCTACTCCAAGTGAAGAAATGGTTTGTTCAGAAAGCACACG AGCTCTCTGTTCTCTGTGATGCTAAAGTTT | 4841 |
| | AAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTTGAA CAAACCATTTCTTCACTTGGAGTAGGTGACCTGCCTGTTTGTGG TTCTCTATCCTCTTAATCTGGATCTTCCC | 4842 |
| | ACTCCAAGTGAAGAAAT | 4843 |
| | ATTTCTTCACTTGGAGT | 4844 |
| Male-sterile AP3 <i>Brassica napus</i> Arg25Term AGA-TGA | AAGATCCAGATTAAGAGGATAGAGAACCAAACAAACAGGCAGGTC ACCTACTCCAAGAGATGAAATGGTTTGTTCAGAAAGCACACGAG CTCTCTGTTCTCTGTGATGCTAAAGTTTCCA | 4845 |
| | TGGAACTTTAGCATCACAGAGAACAGAGAGCTCGTGTGCTTTCTT GAACAAACCATTTCATCTCTTGGAGTAGGTGACCTGCCTGTTTGT TGGTTCTCTATCCTCTTAATCTGGATCTT | 4846 |
| | CCAAGAGATGAAATGGT | 4847 |
| | ACCATTTCACTCTTGG | 4848 |

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| Male-sterile DEFA <i>Antirrhinum majus</i> Arg3Term CGA-TGA | GGAGAGAAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGG TAGTGGTTCGATGGCTT <u>G</u> AGGGGAAGATCCAGATTAAGAGGATAGA GAACCAAACAACAGGCAGGTCACCTACTCCA | 4849 |
| | TGGAGTAGGTGACCTGCCTGTTTGGTTCTCTATCCTCTTAAT CTGGATCTTCCCTC <u>A</u> AGCCATCGAACCCTACCCTACTGCTCTTG TTTTCTTCTTCCAGCTTTCTTTCTCTCC | 4850 |
| | CGATGGCTT <u>G</u> AGGGAAG | 4851 |
| | CTTCCCTC <u>A</u> AGCCATCG | 4852 |
| Male-sterile DEFA <i>Antirrhinum majus</i> Lys5Term AAG-TAG | AAAGGAAAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGT TCGATGGCTCGAGGGT <u>T</u> AGATCCAGATTAAGAGGATAGAGAACCAA ACAAACAGGCAGGTCACCTACTCCAAGAGAA | 4853 |
| | TTCTCTTGGAGTAGGTGACCTGCCTGTTTGGTTCTCTATCCT CTTAATCTGGATCT <u>A</u> CCCTCGAGCCATCGAACCCTACCCTACTG CTCTTGTTTTCTTCTTCCAGCTTTCTTT | 4854 |
| | CTCGAGGGT <u>T</u> AGATCCAG | 4855 |
| | CTGGATCT <u>A</u> CCCTCGAG | 4856 |
| Male-sterile DEFA <i>Antirrhinum majus</i> Gln7Term CAG-TAG | AAGCTGGAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATG GCTCGAGGGAAGATC <u>T</u> AGATTAAGAGGATAGAGAACCAAACAAC AGGCAGGTCACCTACTCCAAGAGAAGAAATG | 4857 |
| | CATTTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGGTTCTC TATCCTCTTAATCT <u>A</u> GATCTTCCCTCGAGCCATCGAACCCTACCA CTACTGCTCTTGTTTTCTTCTTCCAGCTT | 4858 |
| | GGAAGATC <u>T</u> AGATTAAG | 4859 |
| | CTTAATCT <u>A</u> GATCTTCC | 4860 |
| Male-sterile DEFA <i>Antirrhinum majus</i> Lys9Term AAG-TAG | GAAGAAGAAAACAAGAGCAGTAGTGGTAGTGGTTCGATGGCTCGA GGGAAGATCCAGATT <u>T</u> AGAGGATAGAGAACCAAACAACAGGCAG GTCACCTACTCCAAGAGAAGAAATGGTTTGT | 4861 |
| | ACAAACCATTCTTCTCTTGGAGTAGGTGACCTGCCTGTTTGGTTG GTTCTCTATCCTCT <u>A</u> AATCTGGATCTTCCCTCGAGCCATCGAACCA CTACCACTACTGCTCTTGTTTTCTTCTTC | 4862 |
| | TCCAGATT <u>T</u> AGAGGATA | 4863 |
| | TATCCTCT <u>A</u> AATCTGGA | 4864 |
| Male-sterile AP3 <i>Nicotiana tabacum</i> Lys5Term AAG-TAG | TCAGTAATTCTTAAGATCTCAAACTTTGAGCAAAAAGAAAAAAAAAAC TATGGCTCGTGGGT <u>T</u> AGATCCAGATCAAGAGAATAGAGAACCAAAC AAACAGACAAGTCACTTATTCTAAGAGAA | 4865 |
| | TTCTCTTAGAATAAGTGACTTGTCTGTTTGGTTCTCTATTCTC TTGATCTGGATCT <u>A</u> CCACGAGCCATAGTTTTTTTTCTTTTGCTC AAAGTTTGAGATCTTAAGAATTACTGA | 4866 |
| | CTCGTGGGT <u>T</u> AGATCCAG | 4867 |
| | CTGGATCT <u>A</u> CCACGAG | 4868 |

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| Male-sterile AP3 <i>Nicotiana tabacum</i> Gln7Term CAG-TAG | ATTCTTAAGATCTCAAACCTTTGAGCAAAAAGAAAAAAACTATGGC TCGTGGGAAGATCTAGATCAAGAGAATAGAGAACCAAACAAACAG ACAAGTCACTTATTCTAAGAGAAGAAATG | 4869 |
| | CATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGGTTCTCT ATTCTCTTGATCTAGATCTCCACGAGCCATAGTTTTTTTTCTTT TTGCTCAAAGTTTGAGATCTTAAGAAT | 4870 |
| | GGAAGATCTAGATCAAG | 4871 |
| | CTTGATCTAGATCTTCC | 4872 |
| Male-sterile AP3 <i>Nicotiana tabacum</i> Lys9Term AAG-TAG | AAGATCTCAAACCTTTGAGCAAAAAGAAAAAAACTATGGCTCGTG GGAAGATCCAGATCTAGAGAATAGAGAACCAAACAAACAGACAAG TCACTTATTCTAAGAGAAGAAATGGACTTT | 4873 |
| | AAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGG TTCTCTATTCTCTAGATCTGGATCTTCCACGAGCCATAGTTTTTT TTCTTTTGCTCAAAGTTTGAGATCTT | 4874 |
| | TCCAGATCTAGAGAATA | 4875 |
| | TATTCTCTAGATCTGGA | 4876 |
| Male-sterile AP3 <i>Nicotiana tabacum</i> Arg10Term AGA-TGA | ATCTCAAACCTTTGAGCAAAAAGAAAAAAACTATGGCTCGTGGA AGATCCAGATCAAGTGAATAGAGAACCAAACAAACAGACAAGTCA CTTATTCTAAGAGAAGAAATGGACTTTTCA | 4877 |
| | TGAAAAGTCCATTTCTTCTCTTAGAATAAGTGACTTGTCTGTTTGT TGGTTCTCTATTCACTTGATCTGGATCTTCCACGAGCCATAGTTT TTTTTCTTTTGCTCAAAGTTTGAGAT | 4878 |
| | AGATCAAGTGAATAGAG | 4879 |
| | CTCTATTCACTTGATCT | 4880 |
| Male-sterile AP3 <i>Medicago sativa</i> Tyr21Term TAC-TAG | GGCTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAA CAGACAAGTAACTTAGTCAAAACGAAGGGATGGTCTTTTCAAGAAG GCCAATGAGCTCACTGTTCTTTGTGATGCT | 4881 |
| | AGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGACCA TCCCTTCGTTTTGACTAAGTTACTTGTCTGTTTCGTTGTGTTCTCTAT TCTCTTGATCTGGATCTTCTCGAGCC | 4882 |
| | GTAACCTAGTCAAAACG | 4883 |
| | CGTTTTGACTAAGTTAC | 4884 |
| Male-sterile AP3 <i>Medicago sativa</i> Ser22Term TCA-TGA | CTCGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACA GACAAGTAACTTACTGAAAACGAAGGGATGGTCTTTTCAAGAAGG CCAATGAGCTCACTGTTCTTTGTGATGCTAA | 4885 |
| | TTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAGAC CATCCCTTCGTTTTAGTAAGTTACTTGTCTGTTTCGTTGTGTTCTCT ATTCTCTTGATCTGGATCTTCTCGAG | 4886 |
| | AACTTACTGAAAACGAA | 4887 |
| | TTCGTTTTAGTAAGTT | 4888 |

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| Male-sterile AP3 <i>Medicago sativa</i> Lys23Term AAA-TAA | CGAGGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGA CAAGTAACTTACTCAT <u>A</u> ACGAAGGGATGGTCTTTTCAAGAAGGCCA ATGAGCTCACTGTTCTTTGTGATGCTAAGG | 4889 |
| | CCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAAAAG ACCATCCCTTCGTT <u>A</u> TGAGTAAGTTACTTGTCTGTTGTTGTTCT CTATTCTCTTGATCTGGATCTTTCCTCG | 4890 |
| | CTTACTCAT <u>A</u> ACGAAGG | 4891 |
| | CCTTCGTT <u>A</u> TGAGTAAG | 4892 |
| Male-sterile AP3 <i>Medicago sativa</i> Arg24Term CGA-TGA | GGAAAGATCCAGATCAAGAGAATAGAGAACACAACGAACAGACAA GTAACCTTACTCAAAATGAAGGGATGGTCTTTTCAAGAAGGCCAATG AGCTCACTGTTCTTTGTGATGCTAAGGTTT | 4893 |
| | AAACCTTAGCATCACAAAGAACAGTGAGCTCATTGGCCTTCTTGAA AAGACCATCCCTTC <u>A</u> TTTTGAGTAAGTTACTTGTCTGTTGTTGTT TCTCTATTCTCTTGATCTGGATCTTTC | 4894 |
| | ACTCAAAATGAAGGGAT | 4895 |
| | ATCCCTTC <u>A</u> TTTTGAGT | 4896 |
| Male-sterile DEF4 <i>Solanum tuberosum</i> Tyr21Term TAT-TAG | GGCTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAAT AGGCAAGTGACTTAGTCAAAGAGAAGAAATGGGCTATTCAAGAAG GCTAATGAACCTACAGTTCTTTGTGATGCT | 4897 |
| | AGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCCCA TTTCTTCTCTTTG <u>A</u> CTAAGTCACCTGCCTATTTGTTTGTTTTCTATT TTCTTGATCTGGATCTTACCACGAGCC | 4898 |
| | GTGACTTAGTCAAAGAG | 4899 |
| | CTCTTTG <u>A</u> CTAAGTCAC | 4900 |
| Male-sterile DEF4 <i>Solanum tuberosum</i> Ser22Term TCA-TGA | CTCGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAG GCAAGTGACTTATTGAAAGAGAAGAAATGGGCTATTCAAGAAGGC TAATGAACCTACAGTTCTTTGTGATGCTAA | 4901 |
| | TTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAGCC CATTTCTTCTCTTT <u>C</u> AATAAGTCACCTGCCTATTTGTTTGTTTTCTA TTTTCTTGATCTGGATCTTACCACGAG | 4902 |
| | GACTTATTGAAAGAGAA | 4903 |
| | TTCTCTTT <u>C</u> AATAAGTC | 4904 |
| Male-sterile DEF4 <i>Solanum tuberosum</i> Lys23Term AAG-TAG | CGTGGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGG CAAGTGACTTATTCA <u>T</u> AGAGAAGAAATGGGCTATTCAAGAAGGCTA ATGAACCTACAGTTCTTTGTGATGCTAAAG | 4905 |
| | CTTTAGCATCACAAAGAACTGTAAGTTCATTAGCCTTCTTGAATAG CCCATTTCTTCTCT <u>A</u> TGAATAAGTCACCTGCCTATTTGTTTGTTTT CTATTTCTTGATCTGGATCTTACCACG | 4906 |
| | CTTATTCATAGAGAAGA | 4907 |
| | TCTTCTCT <u>A</u> TGAATAAG | 4908 |

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| Male-sterile DEF4 <i>Solanum tuberosum</i> Arg24Term AGA-TGA | GGTAAGATCCAGATCAAGAAAATAGAAAACCAAACAAATAGGCAA GTGACTTATTCAAAGTGAAGAAATGGGCTATTCAAGAAGGCTAATG AACTTACAGTTCTTTGTGATGCTAAAGTTT | 4909 |
| | AACTTTAGCATCACAAAGAAGTGTAAAGTTTCATTAGCCTTCTTGAAT AGCCCATTTCTTCACTTTGAATAAGTCACTTGCCTATTTGTTTGGTT TTCTATTTTCTTGATCTGGATCTTACC | 4910 |
| | ATTCAAAGTGAAGAAAT | 4911 |
| | ATTTCTTCACTTTGAAT | 4912 |
| Male-sterile AP3 <i>Lycopersicon esculentum</i> Gly27Term GGA-TGA | GCTAATGAACCTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTAT GATTTCTAGTACTTGAAAACCTTCATGAGTTTATAAGTCCCTCTATCA CGACCAAACAATTGTTTCGATCTGTACC | 4913 |
| | GGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTATAAA CTCATGAAGTTTTCAAGTACTAGAAATCATAACAATTGAACTTTAG CATCACAAAGAACAGTAAGTTCATTAGC | 4914 |
| | CTAGTACTTGAAAACCTT | 4915 |
| | AAGTTTTCAAGTACTAG | 4916 |
| Male-sterile AP3 <i>Lycopersicon esculentum</i> Lys28Term AAA-TAA | AATGAACCTACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGAT TTCTAGTACTGGATAAAGTTCATGAGTTTATAAGTCCCTCTATCACGA CCAAACAATTGTTTCGATCTGTACCAGA | 4917 |
| | TCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGAGGGACTTAT AAACTCATGAAGTTATCCAGTACTAGAAATCATAACAATTGAACTT TAGCATCACAAAGAACAGTAAGTTCATT | 4918 |
| | GTAAGTTAAGTTCAT | 4919 |
| | ATGAAGTTATCCAGTAC | 4920 |
| Male-sterile AP3 <i>Lycopersicon esculentum</i> Glu31Term GAG-TAG | ACTGTTCTTTGTGATGCTAAAGTTTCAATTGTTATGATTTCTAGTAC TGAAAACCTTCATTAGTTTATAAGTCCCTCTATCACGACCAAACAAT TGTTTCGATCTGTACCAGAAGACTATTG | 4921 |
| | CAATAGTCTTCTGGTACAGATCGAACAATTGTTTGGTCGTGATAGA GGGACTTATAAACTAATGAAGTTTCCAGTACTAGAAATCATAACA ATTGAACTTTAGCATCACAAAGAACAGT | 4922 |
| | AACTTCATTAGTTTATA | 4923 |
| | TATAAACTAATGAAGTT | 4924 |
| Male-sterile AP3 <i>Lycopersicon esculentum</i> Lys40Term AAA-TAA | ATTGTTATGATTTCTAGTACTGAAAACCTTCATGAGTTTATAAGTCC CTCTATCACGACCTAACAATTGTTTCGATCTGTACCAGAAGACTATT GGAGTTGATATTTGGACTACTCACTATG | 4925 |
| | CATAGTGAGTAGTCCAAATATCAACTCCAATAGTCTTCTGGTACAG ATCGAACAATTGTTAGGTCGTGATAGAGGGACTTATAAACTCATGA AGTTTTCCAGTACTAGAAATCATAACAAT | 4926 |
| | TCACGACCTAACAATTG | 4927 |
| | CAATTGTTAGGTCGTGA | 4928 |

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| Male-sterile AP3 <i>Triticum aestivum</i> Tyr21Term TAC-TAG | GGGGCGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCA ACAGGCAGGTGACCTAGTCCAAGCGCCGGTCGGGGATCATGAAG AAGGCGCGGGAGCTCACCCTGCTCTGCGACGCC | 4929 |
| | GGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATGATCC CCGACCGGCGCTTGGAGTAGGTCACCTGCCTGTTGGTGGCGTTCT CGATCCGCTTTATCTCAATCTTCCCCCGCCCC | 4930 |
| | GTGACCTAGTCCAAGCG | 4931 |
| | CGCTTGGAGTAGGTCAC | 4932 |
| Male-sterile AP3 <i>Triticum aestivum</i> Lys23Term AAG-TAG | CGGGGAAGATTGAGATAAAGCGGATCGAGAACGCCACCAACAG GCAGGTGACCTACTCCTAGCGCCGGTCGGGGATCATGAAGAAGG CGCGGGAGCTCACCCTGCTCTGCGACGCCAGG | 4933 |
| | CCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGCCTTCTTCATG ATCCCCGACCGGCGCTAGGAGTAGGTCACCTGCCTGTTGGTGGC GTTCTCGATCCGCTTTATCTCAATCTTCCCCG | 4934 |
| | CCTACTCCTAGCGCCGG | 4935 |
| | CCGGCGCTAGGAGTAGG | 4936 |
| Male-sterile AP3 <i>Triticum aestivum</i> Ser26Term TCG-TAG | TTGAGATAAAGCGGATCGAGAACGCCACCAACAGGCAGGTGACCT ACTCCAAGCGCCGGTAGGGGATCATGAAGAAGGCGCGGGAGCTC ACCGTGCTCTGCGACGCCAGGTGCGCATCAT | 4937 |
| | ATGATGGCGACCTGGGCGTCGCAGAGCACGGTGAGCTCCCGCGC CTTCTTCATGATCCCCTACCGGCGCTTGGAGTAGGTCACCTGCCT GTTGGTGGCGTTCTCGATCCGCTTTATCTCAA | 4938 |
| | GCGCCGGTAGGGGATCA | 4939 |
| | TGATCCCCTACCGGCGC | 4940 |
| Male-sterile AP3 <i>Triticum aestivum</i> Lys30Term AAG-TAG | CGGATCGAGAACGCCACCAACAGGCAGGTGACCTACTCCAAGCG CCGGTCGGGGATCATGTAGAAGGCGCGGGAGCTCACCCTGCTCT GCGACGCCAGGTGCGCATCATGTTCTCCT | 4941 |
| | AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTG AGCTCCCGCGCCTTCTACATGATCCCCGACCGGCGCTTGGAGTAG GTCACCTGCCTGTTGGTGGCGTTCTCGATCCG | 4942 |
| | GGATCATGTAGAAGGCG | 4943 |
| | CGCCTTCTACATGATCC | 4944 |
| Male-sterile Silky1 <i>Zea mays</i> Tyr21Term TAC-TAG | GGGGCGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCA ACCGCCAGGTGACCTAGTCCAAGCGCCGGACGGGGATCATGAAG AAGGCACGCGAGCTCACCCTGCTCTGCGACGCC | 4945 |
| | GGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTTCATGATCCC CGTCCGGCGCTTGGAGTAGGTCACCTGGCGGTTGGTGGCGTTCT CGATCCGCTTGATCTCGATCTTGCCGCGCCCC | 4946 |
| | GTGACCTAGTCCAAGCG | 4947 |
| | CGCTTGGAGTAGGTCAC | 4948 |

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| Male-sterile Silky1 <i>Zea mays</i> Lys23Term AAG-TAG | CGCGGCAAGATCGAGATCAAGCGGATCGAGAACGCCACCAACCG CCAGGTGACCTACTCCTAGCGCCGGACGGGGATCATGAAGAAGG CACGCGAGCTCACCGTGCTCTGCGACGCCCAGG | 4949 |
| | CCTGGGCGTCGCAGAGCACGGTGAGCTCGCGTGCCTTCTTCATG ATCCCCGTCCGGCGCTAGGAGTAGGTCACCTGGCGGTTGGTGGC GTTCTCGATCCGCTTGATCTCGATCTTGCCGCG | 4950 |
| | CCTACTCCTAGCGCCGG | 4951 |
| | CCGGCGCTAGGAGTAGG | 4952 |
| Male-sterile Silky1 <i>Zea mays</i> Lys30Term AAG-TAG | CGGATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCG CCGGACGGGGATCATGTAGAAGGCACGCGAGCTCACCGTGCTCT GCGACGCCCAGGTCGCCATCATCATGTTCTCCT | 4953 |
| | AGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACGGTG AGCTCGCGTGCCTTCTACATGATCCCCGTCCGGCGCTTGAGTAG GTCACCTGGCGGTTGGTGGCGTTCTCGATCCG | 4954 |
| | GGATCATGTAGAAGGCA | 4955 |
| | TGCCTTCTACATGATCC | 4956 |
| Male-sterile Silky1 <i>Zea mays</i> Lys31Term AAG-TAG | ATCGAGAACGCCACCAACCGCCAGGTGACCTACTCCAAGCGCCG GACGGGGATCATGAAGTAGGCACGCGAGCTCACCGTGCTCTGCG ACGCCCAGGTCGCCATCATCATGTTCTCCTCCA | 4957 |
| | TGGAGGAGAACATGATGATGGCGACCTGGGCGTCGCAGAGCACG GTGAGCTCGCGTGCCTACTTCATGATCCCCGTCCGGCGCTTGAG TAGGTACCTGGCGGTTGGTGGCGTTCTCGAT | 4958 |
| | TCATGAAGTAGGCACGC | 4959 |
| | GCGTGCCTACTTCATGA | 4960 |
| Male-sterile AP3 <i>Oryza sativa</i> Lys5Term AAG-TAG | GCTAGCTGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGC GGCCATGGGGAGGGGCTAGATCGAGATCAAGCGGATCGAGAACG CGACCAACAGGCAGGTGACCTACTCGAAGCGCC | 4961 |
| | GGCGCTTCGAGTAGGTCACCTGCCTGTTGGTTCGCGTTCTCGATCC GCTTGATCTCGATCTAGCCCCTCCCCATGGCCGCCCCCTGCAGCA GCTATCTCTCTCGCCGACAATGCAGCTAGC | 4962 |
| | GGAGGGGCTAGATCGAG | 4963 |
| | CTCGATCTAGCCCCTCC | 4964 |
| Male-sterile AP3 <i>Oryza sativa</i> Glu7Term GAG-TAG | TGCATTGTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCAT GGGGAGGGGCAAGATCTAGATCAAGCGGATCGAGAACGCGACCA ACAGGCAGGTGACCTACTCGAAGCGCCGCACGG | 4965 |
| | CCGTGCGGCGCTTCGAGTAGGTCACCTGCCTGTTGGTTCGCGTTCT CGATCCGCTTGATCTAGATCTTGCCCCTCCCCATGGCCGCCCCCT GCAGCAGCTATCTCTCTCGCCGACAATGCA | 4966 |
| | GCAAGATCTAGATCAAG | 4967 |
| | CTTGATCTAGATCTTGC | 4968 |

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| Male-sterile AP3 <i>Oryza sativa</i> Lys9Term AAG-TAG | GTCCGGCGAGAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGA GGGGCAAGATCGAGATCTAGCGGATCGAGAACGCGACCAACAGG CAGGTGACCTACTCGAAGCGCCGCACGGGGATCA | 4969 |
| | TGATCCCCGTGCGGCGCTTCGAGTAGGTACCTGCCTGTTGGTCG CGTTCTCGATCCGCTAGATCTCGATCTTGCCCCTCCCCATGGCCG CCCCCTGCAGCAGCTATCTCTCTCGCCGGAC | 4970 |
| | TCGAGATCTAGCGGATC | 4971 |
| | GATCCGCTAGATCTCGA | 4972 |
| Male-sterile AP3 <i>Oryza sativa</i> Glu12Term GAG-TAG | GAGAGATAGCTGCTGCAGGGGGCGGCCATGGGGAGGGGCAAGA TCGAGATCAAGCGGATCTAGAACGCGACCAACAGGCAGGTGACCT ACTCGAAGCGCCGCACGGGGATCATGAAGAAGG | 4973 |
| | CCTTCTTCATGATCCCCGTGCGGCGCTTCGAGTAGGTACCTGCC TGTTGGTCGCGTTCTAGATCCGCTTGATCTCGATCTTGCCCCTCCC CATGGCCGCCCCCTGCAGCAGCTATCTCTC | 4974 |
| | AGCGGATCTAGAACGCG | 4975 |
| | CGCGTTCTAGATCCGCT | 4976 |

Table 33
Oligonucleotides to produce male-sterile plants

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Male-sterile AG <i>Arabidopsis thaliana</i> Tyr35Term TAC-TAG | TCTGTACTAATCAAATTTTGGCCTAAACGTTTTTGGCTTTGGAGCA GCAATCACGGCGTAGCAATCGGAGCTAGGAGGAGATTCTCTCC CTTGAGGAAATCTGGGAGAGGAAAGATCGAA | 4977 |
| | TTCGATCTTCTCTCTCCAGATTTCTCAAGGGAGAGGAATCTCCT CCTAGCTCCGATTGCTACGCCGTGATTGCTGCTCCAAAGCCAAA ACGTTTAGGGCAAATTTGATTAGTACAGA | 4978 |
| | ACGGCGTAGCAATCGGA | 4979 |
| | TCCGATTGCTACGCCGT | 4980 |
| Male-sterile AG <i>Arabidopsis thaliana</i> Gln36Term CAA-TAA | CTGTACTAATCAAATTTTGGCCTAAACGTTTTTGGCTTTGGAGCAG CAATCACGGCGTACTAATCGGAGCTAGGAGGAGATTCTCTCCCT TGAGGAAATCTGGGAGAGGAAAGATCGAAA | 4981 |
| | TTTCGATCTTCTCTCTCCAGATTTCTCAAGGGAGAGGAATCTCC TCCTAGCTCCGATTAGTACGCCGTGATTGCTGCTCCAAAGCCAAA AACGTTTAGGGCAAATTTGATTAGTACAG | 4982 |
| | CGGCGTACTAATCGGAG | 4983 |
| | CTCCGATTAGTACGCCG | 4984 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Male-sterile AG <i>Arabidopsis thaliana</i> Ser37Term TCG-TAG | ACTAATCAAATTTTGGCCTAAACGTTTTTGGCTTTGGAGCAGCAAT CACGGCGTACCAATAGGAGCTAGGAGGAGATTCTCTCCCTTGA GGAAATCTGGGAGAGGAAAGATCGAAATCAA | 4985 |
| | TTGATTTGATCTTTCTCTCCAGATTTCTCAAGGGAGAGGAAT CTCCTCCTAGCTCCTATTGGTACGCCGTGATTGCTGCTCCAAAGC CAAAAACGTTTAGGGCAAATTTGATTAGT | 4986 |
| | GTACCAATAGGAGCTAG | 4987 |
| | CTAGCTCCTATTGGTAC | 4988 |
| Male-sterile AG <i>Arabidopsis thaliana</i> Glu38Term GAG-TAG | TAATCAAATTTTGGCCTAAACGTTTTTGGCTTTGGAGCAGCAATCA CGGCGTACCAATCGTAGCTAGGAGGAGATTCTCTCCCTTGAGGA AATCTGGGAGAGGAAAGATCGAAATCAAAC | 4989 |
| | GTTTGATTTGATCTTTCTCTCCAGATTTCTCAAGGGAGAGGA ATCTCCTCCTAGCTACGATTGGTACGCCGTGATTGCTGCTCCAAA GCCAAAACGTTTAGGGCAAATTTGATTA | 4990 |
| | ACCAATCGTAGCTAGGA | 4991 |
| | TCCTAGCTACGATTGGT | 4992 |
| Male-sterile AG <i>Brassica napus</i> Glu3Term GAA-TAA | CTCTCCCACTTCTTTTCGGTGGTTTATTCATTTGGTGACGATATCA CAGAAGCAATGGATTAAAGGTGGGAGTAGTCACGATGCAGAGAGT AGCAAGAAGATAGGTAGAGGGAAGATAGAGA | 4993 |
| | TCTCTATCTTCCCTCTACCTATCTTCTTGCTACTCTCTGCATCGTGA CTACTCCACCTTAATCCATTGCTTCTGTGATATCGTCACCAAATG AATAAACCACCGAAAAGAAGTGGGAGAG | 4994 |
| | CAATGGATTAAAGGTGGG | 4995 |
| | CCCACCTTAATCCATTG | 4996 |
| Male-sterile AG <i>Brassica napus</i> Glu11Term GAG-TAG | TATTCATTTGGTGACGATATCACAGAAGCAATGGATGAAGGTGGG AGTAGTCACGATGCATAGAGTAGCAAGAAGATAGGTAGAGGGAA GATAGAGATAAAGAGGATAGAGAACACAACAA | 4997 |
| | TTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCTCTACCTATC TTCTTGCTACTCTATGCATCGTGACTACTCCACCTTCATCCATTG CTTCTGTGATATCGTCACCAAATGAATA | 4998 |
| | ACGATGCATAGAGTAGC | 4999 |
| | GCTACTCTATGCATCGT | 5000 |
| Male-sterile AG <i>Brassica napus</i> Lys14Term AAG-TAG | GGTGACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCA CGATGCAGAGAGTAGCTAGAAGATAGGTAGAGGGAAGATAGAGA TAAAGAGGATAGAGAACACAACAAATCGTCAAG | 5001 |
| | CTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTCCCT CTACCTATCTTCTAGCTACTCTCTGCATCGTGACTACTCCACCTT CATCCATTGCTTCTGTGATATCGTCACC | 5002 |
| | AGAGTAGCTAGAAGATA | 5003 |
| | TATCTTCTAGCTACTCT | 5004 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Male-sterile AG <i>Brassica napus</i> Lys15Term AAG-TAG | GACGATATCACAGAAGCAATGGATGAAGGTGGGAGTAGTCACGA TGCAGAGAGTAGCAAGTAGATAGGTAGAGGGAAGATAGAGATAAA GAGGATAGAGAACACAACAAATCGTCAAGTAA | 5005 |
| | TACTTGACGATTTGTTGTGTTCTCTATCCTCTTTATCTCTATCTTC CCTCTACCTATCTACTTGCTACTCTCTGCATCGTGACTACTCCCAC CTTCATCCATTGCTTCTGTGATATCGTC | 5006 |
| | GTAGCAAGTAGATAGGT | 5007 |
| | ACCTATCTACTTGCTAC | 5008 |
| Male-sterile AG <i>Lycopersicon esculentum</i> Glu4Term CAA-TAA | CAACCAAAAACTTAAAAATCTTCTCTTTCCTTTCCTTACAAGGTGA AGTAATGGACTTCTAAAGTGATCTAACCAGAGAGATCTCACCACAA AGGAACTAGGAAGGGGAAAATTGAGA | 5009 |
| | TCTCAATTTTCCCCCTTCTAGTTTCCTTGTGGTGAGATCTCTCT GGTTAGATCACTTTAGAAGTCCATTACTTCACCTTGTAAGGAAAGG AAAGAGAAGATTTTTAAGTTTTTGGTTG | 5010 |
| | TGGACTTCTAAAGTGAT | 5011 |
| | ATCACTTTAGAAGTCCA | 5012 |
| Male-sterile AG <i>Lycopersicon esculentum</i> Arg9Term AGA-TGA | AAAATCTTCTCTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCC AAAGTGATCTAACCIGAGAGATCTCACCACAAAGGAACTAGGAA GGGGGAAAATTGAGATCAAAGGATCGAAA | 5013 |
| | TTTCGATCCTTTTGATCTCAATTTCCCCCTTCTAGTTTCCTTGT GGTGAGATCTCTCAGGTTAGATCACTTTGGAAGTCCATTACTTCAC CTTGTAAGGAAAGGAAAGAGAAGATTTT | 5014 |
| | ATCTAACCIGAGAGATC | 5015 |
| | GATCTCTCAGGTTAGAT | 5016 |
| Male-sterile AG <i>Lycopersicon esculentum</i> Glu10Term GAG-TAG | ATCTTCTCTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCCAAA GTGATCTAACCAGATAGATCTCACCACAAAGGAACTAGGAAGGG GGAAAATTGAGATCAAAGGATCGAAAACA | 5017 |
| | TGTTTTCGATCCTTTTGATCTCAATTTCCCCCTTCTAGTTTCCTT TGTGGTGAGATCTATCTGGTTAGATCACTTTGGAAGTCCATTACTT CACCTTGTAAGGAAAGGAAAGAGAAGAT | 5018 |
| | TAACCAGATAGATCTCA | 5019 |
| | TGAGATCTATCTGGTTA | 5020 |
| Male-sterile AG <i>Lycopersicon esculentum</i> Ser12Term TCA-TGA | CTTTCCTTTCCTTACAAGGTGAAGTAATGGACTTCCAAAGTGATCT AACCAGAGAGATCTGACCACAAAGGAACTAGGAAGGGGGAAAA TTGAGATCAAAGGATCGAAAACACGACGAA | 5021 |
| | TTTCGTCGTGTTTTCGATCCTTTTGATCTCAATTTCCCCCTTCTAG TTTCCTTTGTGGTCAGATCTCTCTGGTTAGATCACTTTGGAAGTCC ATTACTTCACCTTGTAAGGAAAGGAAAG | 5022 |
| | AGAGATCTGACCACAAA | 5023 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | TTTGTGGT <u>C</u> AGATCTCT | 5024 |
| Male-sterile NAG1 <i>Nicotiana tabacum</i> Gln4Term CAA-TAA | GTA <u>C</u> TCTCTATTTTCATCTTCCAACCCTTTCTTTCTTACCAGGTGA AAGTATGGACTTCTAAAGTGATCTAACAAGAGAGATCTCTCCACAA AGGAAACTGGGAAGAGGAAAGATTGAGA | 5025 |
| | TCTCAATCTTTCTCTTCCAGTTTCCTTTGTGGAGAGATCTCTCTT GTTAGATCACTTTA <u>G</u> AAGTCCATACTTTACCTGGTAAGGAAAGAA AGGGTTGGAAGATGAAAATAGAGAGTAC | 5026 |
| | TGGACTTCTAAAGTGAT | 5027 |
| | ATCACTTTA <u>G</u> AAGTCCA | 5028 |
| Male-sterile NAG1 <i>Nicotiana tabacum</i> Arg9Term AGA-TGA | ATCTTCCAACCCTTTCTTTCTTACCAGGTGAAAGTATGGACTTCC AAAGTGATCTAACA <u>T</u> GAGAGATCTCTCCACAAAGGAAACTGGGAA GAGGAAAGATTGAGATCAAACGGATCGAAA | 5029 |
| | TTTCGATCCGTTTGATCTCAATCTTCTCTTCCAGTTTCCTTTGT GGAGAGATCTCTCA <u>T</u> GTTAGATCACTTTGGAAGTCCATACTTTCAC CTGGTAAGGAAAGAAAGGGTTGGAAGAT | 5030 |
| | ATCTAACA <u>T</u> GAGAGATC | 5031 |
| | GATCTCTCA <u>T</u> GTTAGAT | 5032 |
| Male-sterile NAG1 <i>Nicotiana tabacum</i> Glu10Term GAG-TAG | TTCCAACCCTTTCTTTCTTACCAGGTGAAAGTATGGACTTCCAAA GTGATCTAACAAGATAGATCTCTCCACAAAGGAAACTGGGAAGAG GAAAGATTGAGATCAAACGGATCGAAAACA | 5033 |
| | TGTTTTCGATCCGTTTGATCTCAATCTTCTCTTCCAGTTTCCTT TGTGGAGAGATCTA <u>T</u> CTTTGTTAGATCACTTTGGAAGTCCATACTTT CACCTGGTAAGGAAAGAAAGGGTTGGAA | 5034 |
| | TAACAAGATAGATCTCT | 5035 |
| | AGAGATCTA <u>T</u> CTTTGTTA | 5036 |
| Male-sterile NAG1 <i>Nicotiana tabacum</i> Gln14Term CAA-TAA | CTTTCCTTACCAGGTGAAAGTATGGACTTCCAAAGTGATCTAACA GAGAGATCTCTCCATAAAGGAAACTGGGAAGAGGAAAGATTGAGA TCAAACGGATCGAAAACACAACGAATCGTC | 5037 |
| | GACGATTGTTGTGTTTTCGATCCGTTTGATCTCAATCTTCTCTT CCCAGTTTCCTTTA <u>T</u> GAGAGATCTCTCTTGTAGATCACTTTGGA AGTCCATACTTTCACCTGGTAAGGAAAG | 5038 |
| | TCTCTCCA <u>T</u> AAAGGAAA | 5039 |
| | TTTCCTTTA <u>T</u> GAGAGAGA | 5040 |
| Male-sterile AG <i>Rosa hybrida</i> Gly22Term GGA-TGA | GCCTATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCCAA AGAAGATTGGGAAGGTGAAAGATCGAGATCAAGCGGATCGAAAA CACCACCAATCGTCAAGTCACCTTCTGCAAAA | 5041 |
| | TTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTCGATCCGCT TGATCTCGATCTTTCACCTTCCAATCTTCTTTGGGCATCAGCGTC CAGGACCGTGTTGGGTTGTTTTCATAGGC | 5042 |
| | TGGGAAGGTGAAAGATC | 5043 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | GATCTTTCACCTTCCCA | 5044 |
| Male-sterile AG <i>Rosa hybrida</i> Lys23Term AAG-TAG | TATGAAAACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGA AGATTGGGAAGGGGATAGATCGAGATCAAGCGGATCGAAAACAC CACCAATCGTCAAGTCACCTTCTGCAAAAGGC | 5045 |
| | GCCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTCGATCC GCTTGATCTCGATCTATCCCCTTCCAATCTTCTTTGGGCATCAGC GTCCAGGACCGTGTTGGGTTTGTTCATA | 5046 |
| | GAAGGGGATAGATCGAG | 5047 |
| | CTCGATCTATCCCCTTC | 5048 |
| Male-sterile AG <i>Rosa hybrida</i> Glu25Term GAG-TAG | AACAAACCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTG GGAAGGGGAAAGATCTAGATCAAGCGGATCGAAAACACCACCAA TCGTCAAGTCACCTTCTGCAAAAGGCGCAATG | 5049 |
| | CATTGCGCTTTTGCAGAAGGTGACTTGACGATTGGTGGTGTTC CGATCCGCTTGATCTAGATCTTCCCCTTCCAATCTTCTTTGGGC ATCAGCGTCCAGGACCGTGTTGGGTTTGT | 5050 |
| | GAAAGATCTAGATCAAG | 5051 |
| | CTTGATCTAGATCTTTC | 5052 |
| Male-sterile AG <i>Rosa hybrida</i> Lys27 AAG-TAG | CCCAACACGGTCCTGGACGCTGATGCCCAAAGAAGATTGGGAAG GGGAAAGATCGAGATCTAGCGGATCGAAAACACCACCAATCGTCA AGTCACCTTCTGCAAAAGGCGCAATGGTTTGC | 5053 |
| | GCAAACCATTGCGCCTTTTGCAGAAGGTGACTTGACGATTGGTGG TGTTCGATCCGCTAGATCTCGATCTTCCCCTTCCAATCTTCT TTGGGCATCAGCGTCCAGGACCGTGTTGGG | 5054 |
| | TCGAGATCTAGCGGATC | 5055 |
| | GATCCGCTAGATCTCGA | 5056 |
| Male-sterile far <i>Antirrhinum majus</i> Gln7Term CAA-TAA | CAATTGCCTGTTTTATTTTTTCTTTTTGACTAAGTAGAAATGGC GTCTCTAAGCGATTAATCGACCGAGGTATCGCCCGAGAGGAAAT CGGGAGAGGAAAGATCGAGATCAAACGGA | 5057 |
| | TCCGTTTGATCTCGATCTTCTCTCCCGATTTCTCTCGGGCGA TACCTCGGTCGATTAAATCGCTTAGAGACGCCATTTCTACTTAGTCA AAAAGAAAAAATAAAAAACAGGCAATTG | 5058 |
| | TAAGCGATTAAATCGACC | 5059 |
| | GGTCGATTAAATCGCTTA | 5060 |
| Male-sterile far <i>Antirrhinum majus</i> Glu10Term GAG-TAG | GTTTTATTTTTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAG CGATCAATCGACCTAGGTATCGCCCGAGAGGAAATCGGGAGAG GAAAGATCGAGATCAAACGGATCGAAAACA | 5061 |
| | TGTTTCGATCCGTTTGATCTCGATCTTCTCTCCCGATTTCTCTC TCGGGCGATACCTAGGTCGATTGATCGCTTAGAGACGCCATTTCT ACTTAGTCAAAAAGAAAAAATAAAAAAC | 5062 |
| | AATCGACCTAGGTATCG | 5063 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | CGATACCTAGGTCGATT | 5064 |
| Male-sterile far <i>Antirrhinum majus</i> Glu14Term GAG-TAG | TTTCTTTTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGA CCGAGGTATCGCCCAGAGGAAAATCGGGAGAGGAAAGATCGAG ATCAAACGGATCGAAAACAAAACAAATCAAC | 5065 |
| | GTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTTCCTCTC CCGATTTTCCTCTAGGGCGATACCTCGGTGCGATTGATCGCTTAGA GACGCCATTTCTACTTAGTCAAAAAGAAA | 5066 |
| | TATCGCCCTAGAGGAAA | 5067 |
| | TTTCCTCTAGGGCGATA | 5068 |
| Male-sterile far <i>Antirrhinum majus</i> Lys16Term AAA-TAA | TTTGACTAAGTAGAAATGGCGTCTCTAAGCGATCAATCGACCGAG GTATCGCCCGAGAGGTAAATCGGGAGAGGAAAGATCGAGATCAA ACGGATCGAAAACAAAACAAATCAACAGGTTA | 5069 |
| | TAACCTGTTGATTTGTTTTGTTTTCGATCCGTTTGATCTCGATCTTT CCTCTCCCGATTTACCTCTCGGGCGATACCTCGGTGCGATTGATCG CTTAGAGACGCCATTTCTACTTAGTCAAA | 5070 |
| | CCGAGAGGTAAATCGGG | 5071 |
| | CCCGATTTACCTCTCGG | 5072 |
| Male-sterile AG <i>Cucumis sativus</i> Leu21Term TTG-TAG | TGTCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGA AGGAAAGGGTAAGTAGCAAATAAAGGGGATGTTCCAGAATCAAGA AGAGAAGATGTCAGACTCGCCTCAGAGGAA | 5073 |
| | TTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCTGGAACA TCCCCTTTATTTGCTACTTACCCTTTCTTCTTCTTAATCATTCTT GTGAGTGGTGACTGATAATGCTTGACA | 5074 |
| | GGGTAAGTAGCAAATAA | 5075 |
| | TTATTTGCTACTTACCC | 5076 |
| Male-sterile AG <i>Cucumis sativus</i> Gln22Term CAA-TAA | TCCAAGCATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAA GGAAAGGGTAAGTTGTAAATAAAGGGGATGTTCCAGAATCAAGAA GAGAAGATGTCAGACTCGCCTCAGAGGAAGA | 5077 |
| | TCTTCCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATTCTGGAA CATCCCCTTTATTTCAACTTACCCTTTCTTCTTCTTAATCATTCT TTGTGAGTGGTGACTGATAATGCTTGGA | 5078 |
| | GTAAGTTGTAAATAAAG | 5079 |
| | CTTTATTTCAACTTAC | 5080 |
| Male-sterile AG <i>Cucumis sativus</i> Lys24Term AAG-TAG | CATTATCAGTCACCACTCACAAGAATGATTAAGGAAGAAGGAAAG GGTAAGTTGCAAATAAGGGGATGTTCCAGAATCAAGAAGAGAAG ATGTCAGACTCGCCTCAGAGGAAGATGGGAA | 5081 |
| | TTCCCATCTTCTCTGAGGCGAGTCTGACATCTTCTCTTCTTGATT CTGGAACATCCCCTATATTTGCAACTTACCCTTTCTTCTTCTTA TCATTCTTGTGAGTGGTGACTGATAATG | 5082 |
| | TGCAAATATAGGGGATG | 5083 |

[illegible]

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| | CTGCTCCT <u>A</u> GACCTTGG | 5104 |
| Male-sterile AG <i>Zea mays</i> Arg4Term CGA-TGA | TCCTACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACA AGAGCATGCACATCTGAGAAGAGGAGGCTACACCATCCACAGTAA CAGGCATCATGTGACCCCTGACTTCGGCGG | 5105 |
| | CCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGATGGT GTAGCCTCCTCTTCTC <u>A</u> GATGTGCATGCTCTTGTTCTATCACACA GATTTTGAGGTCTGAAGGAGAAAAGGTAGGA | 5106 |
| | TGCACATCTGAGAAGAG | 5107 |
| | CTCTTCTC <u>A</u> GATGTGCA | 5108 |
| | | |
| Male-sterile AG <i>Zea mays</i> Glu5Term GAA-TAA | TACCTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGA GCATGCACATCCGAT <u>A</u> AAGAGGAGGCTACACCATCCACAGTAACAG GCATCATGTGACCCCTGACTTCGGCGGGGC | 5109 |
| | GCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTGGAT GGTGTAGCCTCCTCTT <u>A</u> TCGGATGTGCATGCTCTTGTTCTATCAC ACAGATTTTGAGGTCTGAAGGAGAAAAGGTA | 5110 |
| | ACATCCGAT <u>A</u> AAGAGGAG | 5111 |
| | CTCCTCTT <u>A</u> TCGGATGT | 5112 |
| | | |
| Male-sterile AG <i>Zea mays</i> Glu6Term GAG-TAG | CTTTTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCA TGCACATCCGAGAATAGGAGGCTACACCATCCACAGTAACAGGCA TCATGTGACCCCTGACTTCGGCGGGGCAGC | 5113 |
| | GCTGCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACTGTG GATGGTGTAGCCTCCT <u>A</u> TTCTCGGATGTGCATGCTCTTGTTCTAT CACACAGATTTTGAGGTCTGAAGGAGAAAAG | 5114 |
| | TCCGAGAA <u>T</u> AGGAGGCT | 5115 |
| | AGCCTCCT <u>A</u> TTCTCGGA | 5116 |
| | | |
| Male-sterile AG <i>Zea mays</i> Glu7Term GAG-TAG | TTCTCCTTCAGACCTCAAAATCTGTGTGATAGGAACAAGAGCATG CACATCCGAGAAGAGT <u>A</u> GGCTACACCATCCACAGTAACAGGCATC ATGTGACCCCTGACTTCGGCGGGGCAGCAGA | 5117 |
| | TCTGCTGCCCCGCCGAAGTCAGGGTCGACATGATGCCTGTTACT GTGGATGGTGTAGCCT <u>A</u> CTCTTCTCGGATGTGCATGCTCTTGTTCT CTATCACACAGATTTTGAGGTCTGAAGGAGAA | 5118 |
| | GAGAAGAGT <u>A</u> GGCTACA | 5119 |
| | TGTAGCCT <u>A</u> CTCTTCTC | 5120 |
| | | |
| Male-sterile AG <i>Oryza sativa</i> Lys5Term AAG-TAG | GCTGGGTTCAGGATCGTCGGCGGCGGTGGCGGCGGGGAGCAGC GAGAAGATGGGGAGGGGGT <u>T</u> AGATCGAGATAAAGCGGATCGAGAA CACGACGAACCGGCAGGTGACCTTCTGCAAGCGCC | 5121 |
| | GGCGCTTGACAGAAGGTACCTGCCGTTTCGTCGTGTTCTCGATC CGCTTTATCTCGATCT <u>A</u> CCCCCTCCCCATCTTCTCGCTGCTCCCC GCCGCCACCGCCGCCGACGATCCTGACCCAGC | 5122 |
| | GGAGGGGGT <u>T</u> AGATCGAG | 5123 |
| | | |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | CTCGATCT <u>A</u> CCCCCTCC | 5124 |
| Male-sterile AG <i>Oryza sativa</i> Glu7Term GAG-TAG | TCAGGATCGTCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGA TGGGGAGGGGGAAGATCTAGATAAAGCGGATCGAGAACACGACG AACCGGCAGGTGACCTTCTGCAAGCGCCGCAATG | 5125 |
| | CATTGCGGCGCTTGCAAGAAGGTCACCTGCCGGTTCGTCGTGTTCT CGATCCGCTTTATCTAGATCTTCCCCCTCCCCATCTTCTCGCTGCT CCCCGCCGCCACCGCCGCCGACGATCCTGA | 5126 |
| | GGAAGATCTAGATAAAG | 5127 |
| | CTTTATCTAGATCTTCC | 5128 |
| | | |
| Male-sterile AG <i>Oryza sativa</i> Lys9Term AAG-TAG | TCGTCGGCGGCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGG AGGGGGAAGATCGAGATAAGCGGATCGAGAACACGACGAACCG GCAGGTGACCTTCTGCAAGCGCCGCAATGGCCTCC | 5129 |
| | GGAGGCCATTGCGGCGCTTGCAAGAAGGTCACCTGCCGGTTCGTC GTGTTCTCGATCCGCTATATCTCGATCTTCCCCCTCCCCATCTTCT CGCTGCTCCCCGCCGCCACCGCCGCCGACGA | 5130 |
| | TCGAGATATAGCGGATC | 5131 |
| | GATCCGCTATATCTCGA | 5132 |
| | | |
| Male-sterile AG <i>Oryza sativa</i> Glu12Term GAG-TAG | GCGGTGGCGGCGGGGAGCAGCGAGAAGATGGGGAGGGGGAAG ATCGAGATAAAGCGGATCTAGAACACGACGAACCGGCAGGTGAC CTTCTGCAAGCGCCGCAATGGCCTCCTGAAGAAGG | 5133 |
| | CCTTCTTCAGGAGGCCATTGCGGCGCTTGCAAGAAGGTCACCTGC CGGTTCTGTCGTGTTCTAGATCCGCTTTATCTCGATCTTCCCCCTCC CCATCTTCTCGCTGCTCCCCGCCGCCACCGC | 5134 |
| | AGCGGATCTAGAACACG | 5135 |
| | CGTGTTCTAGATCCGCT | 5136 |
| | | |

Table 34
Oligonucleotides to produce male-sterile plants

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Male-sterile PI <i>Cucumis sativus</i> Tyr21Term TAT-TAG | GGGAAGAGGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAA TAGACAAGTTACATAGTCAAAGAGAAGAAATGGTATCATCAAAAAA GCCAAAGAAATTACTGTTCTTTGCGATGCT | 5137 |
| | AGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATACCAT TTCTTCTCTTTGACTATGTAAGTTGTCTATTGCTTGAGTTCTCTATTC TTTTTATTTCTATTTTCCCTCTTCCC | 5138 |
| | GTTACATAGTCAAAGAG | 5139 |
| | CTCTTTGACTATGTAAC | 5140 |
| Male-sterile PI <i>Cucumis sativus</i> Ser22Term TCA-TGA | GAAGAGGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATA GACAAGTTACATATTCAAAGAGAAGAAATGGTATCATCAAAAAAGC CAAAGAAATTACTGTTCTTTGCGATGCTCA | 5141 |
| | TGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATAC CATTTCTTCTCTTTCAATATGTAAGTTGTCTATTGCTTGAGTTCTCTA TTCTTTTTATTTCTATTTTCCCTCTTC | 5142 |
| | TACATATTGAAAGAGAA | 5143 |
| | TTCTCTTTCAATATGTA | 5144 |
| Male-sterile PI <i>Cucumis sativus</i> Lys23Term AAG-TAG | AGAGGGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGAC AAGTTACATATTCAATAGAGAAGAAATGGTATCATCAAAAAAGCCAA AGAAATTACTGTTCTTTGCGATGCTCAAG | 5145 |
| | CTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATGATA CCATTTCTTCTCTATGAATATGTAAGTTGTCTATTGCTTGAGTTCTC TATTCTTTTTATTTCTATTTTCCCTCT | 5146 |
| | CATATTCAATAGAGAAGA | 5147 |
| | TCTTCTCTATGAATATG | 5148 |
| Male-sterile PI <i>Cucumis sativus</i> Arg24Term AGA-TGA | GGGAAAATAGAAATAAAAAGAATAGAGAACTCAAGCAATAGACAAG TTACATATTCAAAGTGAAGAAATGGTATCATCAAAAAAGCCAAAGA AATTACTGTTCTTTGCGATGCTCAAGTTT | 5149 |
| | AACTTGAGCATCGCAAAGAACAGTAATTTCTTTGGCTTTTTTGATG ATACCATTTCTTCACTTTGAATATGTAAGTTGTCTATTGCTTGAGTT CTCTATTCTTTTTATTTCTATTTTCCC | 5150 |
| | ATTCAAAGTGAAGAAAT | 5151 |
| | ATTTCTTCACTTTGAAT | 5152 |
| Male-sterile PI <i>Malus domestica</i> Tyr21Term TAC-TAG | GGGACGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAA CAGGCAGGTGACCTAGTCCAAGAGGAGGAATGGGATTATCAAGAA GGCAAAGGAGATCACTGTTCTATGTGATGCT | 5153 |
| | AGCATCACATAGAAGAGTGATCTCCTTTGCCTTTTGATAATCCCA TTCTCCTCTTGGACTAGGTACCTGCCTGTTACTTGAGTTCTCAA TCCTCTTGATCTCAACCTTCCCACGTCCC | 5154 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| | GTGACCTAGTCCAAGAG | 5155 |
| | CTCTTGGACTAGGTCAC | 5156 |
| Male-sterile PI <i>Malus domestica</i> Lys23Term AAG-TAG | CGTGGGAAGGTTGAGATCAAGAGGATTGAGAACTCAAGTAACAGG CAGGTGACCTACTCCTAGAGGAGGAATGGGATTATCAAGAAGGCA AAGGAGATCACTGTTCTATGTGATGCTAAAG | 5157 |
| | CTTTAGCATCACATAGAACAGTGATCTCCTTTGCCTTCTTGATAATC CCATTCCTCCTCTAGGAGTAGGTCACCTGCCTGTTACTTGAGTTCT CAATCCTCTTGATCTCAACCTTCCCACG | 5158 |
| | CCTACTCCTAGAGGAGG | 5159 |
| | CCTCCTCTAGGAGTAGG | 5160 |
| Male-sterile PI <i>Malus domestica</i> Lys30Term AAG-TAG | AGGATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGG AGGAATGGGATTATCTAGAAGGCCAAAGGAGATCACTGTTCTATGT GATGCTAAAGTATCTCTTATCATTTATTCTA | 5161 |
| | TAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGTGAT CTCCTTTGCCTTCTAGATAATCCCATTCCCTCCTCTTGGAGTAGGTC ACCTGCCTGTTACTTGAGTTCTCAATCCT | 5162 |
| | GGATTATCTAGAAGGCA | 5163 |
| | TGCCTTCTAGATAATCC | 5164 |
| Male-sterile PI <i>Malus domestica</i> Lys31Term AAG-TAG | ATTGAGAACTCAAGTAACAGGCAGGTGACCTACTCCAAGAGGAGG AATGGGATTATCAAGTAGGCCAAAGGAGATCACTGTTCTATGTGATG CTAAAGTATCTCTTATCATTTATTCTAGCT | 5165 |
| | AGCTAGAATAAATGATAAGAGATACTTTAGCATCACATAGAACAGT GATCTCCTTTGCCTACTTGATAATCCCATTCCCTCCTCTTGGAGTAG GTCACCTGCCTGTTACTTGAGTTCTCAAT | 5166 |
| | TTATCAAGTAGGCCAAAG | 5167 |
| | CTTTGCCTACTTGATAA | 5168 |
| Male-sterile globosa <i>Antirrhinum majus</i> Gly2Term GGA-TGA | CATTTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAA AAACAAAAAATGTGAAGAGGAAAAATTGAGATCAAAAGAATTGAG AACTCAAGCAACAGGCAGGTTACTTACT | 5169 |
| | AGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTGATCTCA ATTTTTCCTCTTACATTTTTTTGTTTTTCTCTCTTGTTTTG | 5170 |
| | TTTGCAGATAACTATTGTAAAAATG | |
| | AAAAAATGTGAAGAGGA | 5171 |
| | TCCTCTTACATTTTTT | 5172 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Male-sterile globosa <i>Antirrhinum majus</i> Arg3Term AGA-TGA | TTTTACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAA CAAAAAATGGGATGAGGAAAAATTGAGATCAAAGAATTGAGAAC TCAAGCAACAGGCAGGTTACTTACTCAA | 5173 |
| | TTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTGATC TCAATTTTCTCTCATCCCATTTTTTTGTTTTGTTTTCTCTCTGTTT TTGTTTGCAGATAACTATTGTA AAA | 5174 |
| | AAATGGGATGAGGAAAA | 5175 |
| | TTTTCCTCATCCCATTT | 5176 |
| Male-sterile globosa <i>Antirrhinum majus</i> Gly4Term GGA-TGA | TACAATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACA AAAAAATGGGAAGATGAAAAATTGAGATCAAAGAATTGAGAACTC AAGCAACAGGCAGGTTACTTACTCAAAGA | 5177 |
| | TCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTTTTG ATCTCAATTTTCTCTCTCCCATTTTTTTGTTTTGTTTTCTCTCTTG TTTTGTTTGCAGATAACTATTGTA | 5178 |
| | TGGGAAGATGAAAAATT | 5179 |
| | AATTTTCTCTTCCCA | 5180 |
| Male-sterile globosa <i>Antirrhinum majus</i> Lys5Term AAA-TAA | AATAGTTATCTGCAAACAAAAACAAGAGAGAAAAACAAAAACAAAA AAATGGGAAGAGGATAAATTGAGATCAAAGAATTGAGAACTCAAG CAACAGGCAGGTTACTTACTCAAAGAGAA | 5181 |
| | TTCTCTTTGAGTAAGTAACCTGCCTGTTGCTTGAGTTCTCAATTCTT TTGATCTCAATTTATCCTCTTCCCATTTTTTTGTTTTGTTTTCTCT CTTGTTTTGTTTGCAGATAACTATT | 5182 |
| | GAAGAGGATAAATTGAG | 5183 |
| | CTCAATTTATCCTCTTC | 5184 |
| Male-sterile PI <i>Zea mays</i> Lys5Term AAG-TAG | GCTGAGCTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGC AGTATGGGGCGCGGCTAGATCAAGATCAAGAGGATCGAGAACTCT ACCAACCGGCAGGTGACCTTCTCCAAGCGCC | 5185 |
| | GGCGCTTGGAGAAGGTCACCTGCCGTTGGTAGAGTTCTCGATCC TCTTGATCTTGATCTAGCCGCGCCCCATACTGCGTTCTCCACTCCC AAACAGATCCAAGGGCAGCAAGAGCTCAGC | 5186 |
| | GGCGCGGCTAGATCAAG | 5187 |
| | CTTGATCTAGCCGCGCC | 5188 |
| Male-sterile PI <i>Zea mays</i> Lys7Term AAG-TAG | CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATG GGGCGCGGCAAGATCTAGATCAAGAGGATCGAGAACTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG | 5189 |
| | CGGCCCGCGCTTGGAGAAGGTCACCTGCCGTTGGTAGAGTTC TCGATCCTCTTGATCTAGATCTTGCCGCGCCCCATACTGCGTTCTC CACTCCCAAACAGATCCAAGGGCAGCAAGAG | 5190 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | GCAAGATC <u>I</u> AGATCAAG | 5191 |
| | CTTGATCT <u>A</u> GATCTTGC | 5192 |
| Male-sterile PI <i>Zea mays</i> Lys9Term AAG-TAG | CTCTTGCTGCCCTTGGATCTGTTTGGGAGTGGAGAACGCAGTATG GGGCGCGGCAAGATC <u>I</u> AGATCAAGAGGATCGAGAACTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG | 5193 |
| | CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGATCT <u>A</u> GATCTTGCCGCGCCCCATACTGCGTTCTC CACTCCCAAACAGATCCAAGGGCAGCAAGAG | 5194 |
| | GCAAGATC <u>I</u> AGATCAAG | 5195 |
| | CTTGATCT <u>A</u> GATCTTGC | 5196 |
| Male-sterile PI <i>Zea mays</i> Glu12Term GAG-TAG | GATCTGTTTGGGAGTGGAGAACGCAGTATGGGGCGCGGCAAGAT CAAGATCAAGAGGATC <u>I</u> AGA AACTCTACCAACCGGCAGGTGACCTT CTCCAAGCGCCGGGCCGGACTGGTCAAGAAGG | 5197 |
| | CCTTCTTGACCAAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGC CGGTTGGTAGAGTTCT <u>A</u> GATCCTCTTGATCTTGATCTTGCCGCGCC CCATACTGCGTTCTCCACTCCCAAACAGATC | 5198 |
| | AGAGGATC <u>I</u> AGA AACTCT | 5199 |
| | AGAGTTCT <u>A</u> GATCCTCT | 5200 |
| Male-sterile PI <i>Zea mays</i> Lys5Term AAG-TAG | GCTGAGCTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGG AGTATGGGGCGCGGCT <u>I</u> AGATCGAGATCAAGAGGATCGAGAACTCT ACCAACCGGCAGGTGACCTTCTCCAAGCGCC | 5201 |
| | GGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTCTCGATCC TCTTGATCTCGATCT <u>A</u> GCCGCGCCCCATACTCCGTTCTCCACTCCC TAACAGATTCAAGGGCAGCAAGAGCTCAGC | 5202 |
| | GGCGCGGCT <u>I</u> AGATCGAG | 5203 |
| | CTCGATCT <u>A</u> GCCGCGCC | 5204 |
| Male-sterile PI <i>Zea mays</i> Glu7Term GAG-TAG | CTCTTGCTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATG GGGCGCGGCAAGATC <u>I</u> AGATCAAGAGGATCGAGAACTCTACCAAC CGGCAGGTGACCTTCTCCAAGCGCCGGGCCG | 5205 |
| | CGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTAGAGTTC TCGATCCTCTTGATCT <u>A</u> GATCTTGCCGCGCCCCATACTCCGTTCTC CACTCCCTAACAGATTCAAGGGCAGCAAGAG | 5206 |
| | GCAAGATC <u>I</u> AGATCAAG | 5207 |
| | CTTGATCT <u>A</u> GATCTTGC | 5208 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Male-sterile PI <i>Zea mays</i> Lys9Term AAG-TAG | CTGCCCTTGAATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCG CGGCAAGATCGAGATCTAGAGGATCGAGAACTCTACCAACCGGCA GGTGACCTTCTCCAAGCGCCGGGCGGACTGG | 5209 |
| | CCAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGCCGGTTGGTA GAGTTCTCGATCCTCTAGATCTCGATCTTGCCGCGCCCCATACTC CGTTCTCCACTCCCTAACAGATTCAAGGGCAG | 5210 |
| | TCGAGATCTAGAGGATC | 5211 |
| | GATCCTCTAGATCTCGA | 5212 |
| Male-sterile PI <i>Zea mays</i> Glu12Term GAG-TAG | AATCTGTTAGGGAGTGGAGAACGGAGTATGGGGCGCGGCAAGAT CGAGATCAAGAGGATCTAGA ACTCTACCAACCGGCAGGTGACCTT CTCCAAGCGCCGGGCGGACTGGTCAAGAAGG | 5213 |
| | CCTTCTTGACAGTCCGGCCCGGCGCTTGGAGAAGGTCACCTGC CGGTTGGTAGAGTTCTAGATCCTCTTGATCTCGATCTTGCCGCGC CCCATACTCCGTTCTCCACTCCCTAACAGATT | 5214 |
| | AGAGGATCTAGA ACTCT | 5215 |
| | AGAGTTCTAGATCCTCT | 5216 |
| Male-sterile PI <i>Oryza sativa</i> Lys5Term AAG-TAG | TTGCTGCTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGG CGGGATGGGGCGCGGGTAGATCGAGATCAAGAGGATCGAGAACT CCACCAACCGCCAGGTGACCTTCTCCAAGCGCA | 5217 |
| | TGCGCTTGAGAAGGTCACCTGGCGGTTGGTGGAGTTCTCGATCC TCTTGATCTCGATCTACCCGCGCCCCATCCCGCCTCCTCCTCCTC CTCCTCCTCCTCCAGCTAGCTTAGCAGCAA | 5218 |
| | GGCGCGGGTAGATCGAG | 5219 |
| | CTCGATCTACCCGCGCC | 5220 |
| Male-sterile PI <i>Oryza sativa</i> Glu7Term GAG-TAG | CTAAGCTAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGCGGGA TGGGGCGCGGGAAGATCTAGATCAAGAGGATCGAGAACTCCACC AACCGCCAGGTGACCTTCTCCAAGCGCAGGAGCG | 5221 |
| | CGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTGGAGTTCT CGATCCTCTTGATCTAGATCTTCCGCGCCCCATCCCGCCTCCTC CTCCTCCTCCTCCTCCTCCAGCTAGCTTAG | 5222 |
| | GGAAGATCTAGATCAAG | 5223 |
| | CTTGATCTAGATCTTCC | 5224 |
| Male-sterile PI <i>Oryza sativa</i> Lys9Term AAG-TAG | TAGCTGGAGGAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGC GCGGGAAGATCGAGATCTAGAGGATCGAGAACTCCACCAACCGC CAGGTGACCTTCTCCAAGCGCAGGAGCGGGATCC | 5225 |
| | GGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGCGGTTGGTG GAGTTCTCGATCCTCTAGATCTCGATCTTCCGCGCCCCATCCCG CCTCCTCCTCCTCCTCCTCCTCCTCCTCCAGCTA | 5226 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | TCGAGATC <u>T</u> AGAGGATC | 5227 |
| | GATCCTCT <u>A</u> GATCTCGA | 5228 |
| Male-sterile PI <i>Oryza sativa</i> Glu12Term GAG-TAG | GAAGGAGGAGGAGGAGGAGGAGGCGGGATGGGGCGCGGGAAG ATCGAGATCAAGAGGATC <u>T</u> AGAACTCCACCAACCGCCAGGTGACC TTCTCCAAGCGCAGGAGCGGGATCCTCAAGAAGG | 5229 |
| | CCTTCTTGAGGATCCCGCTCCTGCGCTTGGAGAAGGTCACCTGGC GGTTGGTGGAGTTCT <u>A</u> GATCCTCTTGATCTCGATCTTCCCGCGCC CCATCCCGCCTCCTCCTCCTCCTCCTCCTTC | 5230 |
| | AGAGGATC <u>T</u> AGAACTCC | 5231 |
| | GGAGTTCT <u>A</u> GATCCTCT | 5232 |

Example 28

Engineering plants for abiotic stress tolerance

[249] Environmental stresses, such as drought, increased soil salinity, soil contamination with heavy metals, and extreme temperature, are major factors limiting plant growth and productivity. The worldwide loss in yield of three major cereal crops, rice, maize, and wheat due to water stress (drought) has been estimated to be over ten billion dollars annually and many currently marginal soils could be brought into cultivation if suitable plant varieties were available.

[250] Physiological and biochemical responses to high levels of ionic or nonionic solutes and decreased water potential have been studied in a variety of plants. It is known, for example, that increasing levels of alcohol dehydrogenase can confer enhanced flooding resistance in plants. There are also several possible mechanisms to enhance plant salt tolerance. For example, one mechanism underlying the adaptation or tolerance of plants to osmotic stresses is the accumulation of compatible, low molecular weight osmolytes such as sugar alcohols, special amino acids, and glycinebetaine. Such accumulation can be engineered, for example, by removing feedback inhibition on 1-pyrroline-t-carboxylate synthetase, which results in accumulation of proline. Additionally, recent experiments suggest that altering the expression or activity of specific sodium or potassium transporters can confer enhanced salt tolerance.

[251] Plant tolerance of contamination by heavy metals such as lead and aluminum in soils has also been investigated and one mechanism underlying tolerance is the production of dicarboxylic acids such as oxalate and citrate. In addition, individual genes involved in heavy metal sensitivity have been identified.

[252] The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that confer stress tolerance in plants.

Table 35
Genome-Altering Oligos Conferring Stress Tolerance

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Salt Tolerance P5CS <i>Arabidopsis thaliana</i> Phe128Ala TTT-GCT | CGTCTTTTTGTGTGGTAGTTGGATGTGACGGTTGCTCAAATGCTT GTGACCGATAGCAGT <u>GCT</u> AGAGATAAGGATTTTCAGGAAGCAACTT AGTGAAACTGTCAAAGCGATGCTGAGGATGA | 5233 |
| | TCATCCTCAGCATCGCTTTGACAGTTTCACTAAGTTGCTTCCTGAA ATCCTTATCTCTAG <u>GCA</u> CTGCTATCGGTCACAAGCATTTGAGCAACC GTCACATCCAACTACCACACAAAAAGACG | 5234 |
| | ATAGCAGT <u>GCT</u> AGAGAT | 5235 |
| | ATCTCTAG <u>GCA</u> CTGCTAT | 5236 |
| Salt Tolerance P5CS 1 <i>Brassica napus</i> Phe128Ala TTC-GCC | GAGACTATGTTTGACCAGCTGGATGTGACGGCTGCTCAGCTGCTG GTGAATGACAGTAGT <u>GCC</u> CAGAGACAAGGAGTTTCAGGAAGCAACTT AATGAGACAGTGAAGTCCATGCTTGATTTGA | 5237 |
| | TCAAATCAAGCATGGACTTCACTGTCTCATTAAAGTTGCTTCCTGAA CTCCTTGTCTCTG <u>GCA</u> CTACTGTCAATCACCAGCAGCTGAGCAGC CGTCACATCCAGCTGGTCAAACATAGTCTC | 5238 |
| | ACAGTAGT <u>GCC</u> CAGAGAC | 5239 |
| | GTCTCTG <u>GCA</u> CTACTGT | 5240 |
| Salt Tolerance P5CS 2 <i>Brassica napus</i> Phe129Ala TTC-GCC | GAGACTATGTTTGACCAGATGGATGTGACGGTGGCTCAAATGCTG GTGACTGATAGCAGT <u>GTC</u> CAGAGATAAGGATTTTCAGGAAGCAACTT AGTGAGACAGTCAAAGCTATGCTGAAAATGA | 5241 |
| | TCATTTTCAGCATAGCTTTGACTGTCTCACTAAGTTGCTTCCTGAA ATCCTTATCTCTGAC <u>CA</u> CTGCTATCAGTCACCAGCATTTGAGCCACC GTCACATCCATCTGGTCAAACATAGTCTC | 5242 |
| | ATAGCAGT <u>GTC</u> CAGAGAT | 5243 |
| | ATCTCTGAC <u>CA</u> CTGCTAT | 5244 |
| Salt Tolerance P5CS <i>Oryza sativa</i> Phe128Ala TTT-GCT | GATATGTTGTTTAACCAACTGGATGTCTCGTCATCTCAACTTCTTG TCACCGACAGTGAT <u>GCT</u> GAGAACCCAAAGTTCCGGGAGCAACTCA CTGAAACTGTTGAGTCATTATTAGATCTTA | 5245 |
| | TAAGATCTAATAATGACTCAACAGTTTCAGTGAGTTGCTCCCGGAA CTTTGGGTTCTCAG <u>GCA</u> TCACTGTGCGGTGACAAGAAGTTGAGATGA CGAGACATCCAGTTGGTTAAACAACATATC | 5246 |
| | ACAGTGAT <u>GCT</u> GAGAAC | 5247 |
| | GTTCTCAG <u>GCA</u> TCACTGT | 5248 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Salt Tolerance P5CS <i>Medicago sativa</i> Phe128Ala TTT-GCT | GATATTTTGTGTTAGTCAGCTGGATGTGACATCTGCTCAGCTTCTTG TACTGACAATGATGCTAGAGACCAAGATTTTAGAAAGCAACTTTC TGAAACTGTGAGATCACTTCTAGCACTAA | 5249 |
| | TTAGTGCTAGAAGTGATCTCACAGTTTCAGAAAGTTGCTTTCTAAA ATCTTGGTCTCTAGCATCATTGTGAGTAACAAGAAGCTGAGCAGAT GTCACATCCAGCTGACTAAACAAAATATC | 5250 |
| | ACAATGATGCTAGAGAC | 5251 |
| | GTCTCTAGCATCATTGT | 5252 |
| Salt Tolerance P5CS <i>Actinidia deliciosa</i> Phe128Ala TTT-GCT | GATACATTGTTTAGTCAGCTGGATGTGACATCAGCTCAGCTACTC GTTACTGATAATGATGCTAGGGATCCAGAATTCAGGAAGCAACTT ACTGAACTGTAGAATCACTATTGAATTTGA | 5253 |
| | TCAAATTCAATAGTGATTCTACAGTTTCAGTAAGTTGCTTCCTGAAT TCTGGATCCCTAGCATCATTATCAGTAACGAGTAGCTGAGCTGAT GTCACATCCAGCTGACTAAACAATGTATC | 5254 |
| | ATAATGATGCTAGGGAT | 5255 |
| | ATCCCTAGCATCATTAT | 5256 |
| Salt Tolerance P5CS <i>Cichorium intybus</i> Phe122Ala TTC-GCC | GACACACTCTTCAGTCAACTGGATGTGACATCAGCACAGCTTCTT GTAACAGATAATGACGCCAGAAAGTCCAGAATTTAGAAAACAACCTTA CTGAAACAGTCGATTCTTTATTATCTTATA | 5257 |
| | TATAAGATAATAAAGAATCGACTGTTTCAGTAAGTTGTTTTCTAAAT TCTGGACTTCTGGCGTCATTATCTGTTACAAGAAGCTGTGCTGAT GTCACATCCAGTTGACTGAAGAGTGTGTC | 5258 |
| | ATAATGACGCCAGAAAGT | 5259 |
| | ACTTCTGGCGTCATTAT | 5260 |
| Salt Tolerance P5CS <i>Lycopersicon esculentum</i> Phe128Ala TTT-GCT | GATTCTTTGTTTCAGTCAGTTGGATGTGACATCAGCTCAGCTTCTGG TGACTGATAATGACGCTAGAGATCCAGATTTTAGGAGACAACCTCA ATGACACAGTAAATTCGTTGCTTTCTCTAA | 5261 |
| | TTAGAGAAAGCAACGAATTTACTGTGTCATTGAGTTGTCTCCTAAA ATCTGGATCTCTAGCGTCATTATCAGTCACCAGAAGCTGAGCTGA TGTCACATCCAACGACTGAACAAAGAATC | 5262 |
| | ATAATGACGCTAGAGAT | 5263 |
| | ATCTCTAGCGTCATTAT | 5264 |
| Salt Tolerance P5CS <i>Vigna unguiculata</i> Phe162Ala TTT-GCT | GATACCATGTTTCAGCCAGCTTGATGTGACTTCTTCCCAACTTCTTG TGAATGATGGATTTGCTAGGGATGCTGGCTTCAGAAAACAACCTT CGGACACAGTGAACGCGTTATTAGATTTAA | 5265 |
| | TTAAATCTAATAACGCGTTCACTGTGTCCGAAAGTTGTTTTCTGAA GCCAGCATCCCTAGCAAATCCATCATTACAAGAAGTTGGGAAGA AGTCACATCAAGCTGGCTGAACATGGTATC | 5266 |
| | ATGGATTTGCTAGGGAT | 5267 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| | ATCCCTAGC GC AAATCCAT | 5268 |
| Salt Tolerance P5CS <i>Mesembryanthemum crystallinum</i> Phe125Ala TTT-GCT | GACACCTTGTTTAGTCAGTTGGATCTGACTGCTGCTCAGCTGCTT GTGACGGACAACGAC GC TAGAGATCCAAGTTTTAGAACACAACCTA ACTGAAACAGTGTATCAGTTGTTGGATCTAA | 5269 |
| | TTAGATCCAACAACCTGATACACTGTTTCAGTTAGTTGTGTTCTAAA ACTTGATCTCTAG CG TCGTTGTCCGTCACAAGCAGCTGAGCAGC AGTCAGATCCAACCTGACTAAACAAGGTGTC | 5270 |
| | ACAACGAC GC TAGAGAT | 5271 |
| | ATCTCTAG CG TCGTTGT | 5272 |
| Salt Tolerance P5CS <i>Vitis vinifera</i> Phe130Ala TTT-GCT | GACACATTATTTAGCCAGCTGGATGTGACATCAGCTCAGCTTCTT GTGACTGATAATGAT GC TAGGGATGAAGCTTTCCGAAATCAACTTA CTCAAACAGTGGATTCAATTGTTAGCTTTGA | 5273 |
| | TCAAAGCTAACAAATGAATCCACTGTTTGAGTAAGTTGATTTCCGAA AGCTTCATCCCTAG GC ATCATTATCAGTCACAAGAAGCTGAGCTGAT GTCACATCCAGCTGGCTAAATAATGTGTC | 5274 |
| | ATAATGAT GC TAGGGAT | 5275 |
| | ATCCCTAG GC ATCATTAT | 5276 |
| Salt Tolerance P5CS <i>Vigna aconitifolia</i> Phe129Ala TTT-GCT | GATACGCTGTTCACTCAGCTCGATGTGACATCGGCTCAGCTTCTT GTGACGGATAACGAT GC TCGAGATAAGGATTTAGGAAGCAGCTT ACTGAGACTGTGAAGTCGCTGTTGGCGCTGA | 5277 |
| | TCAGCGCCAACAGCGACTTCACAGTCTCAGTAAGCTGCTTCCTGA AATCCTTATCTCGAG GC ATCGTTATCCGTCACAAGAAGCTGAGCCG ATGTCACATCGAGCTGAGTGAACAGCGTATC | 5278 |
| | ATAACGAT GC TCGAGAT | 5279 |
| | ATCTCGAG GC ATCGTTAT | 5280 |
| Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Ser207Val TCC-GTC | AGAGATGTTCTTAGTTCCAAAGAAATCTCACCTCTCACTTTCTCCG TCTTCACAACAGTT GT CACGTTTGCAAACCTGCGGATTTGCCCCAC GAATGAGAACATGATCATCTTTGCAAAA | 5281 |
| | TTTTGCGAAAGATGATCATGTTCTCATTCTGTTGGGGACAAATCCGC AGTTTGCAAACGTG ACA AACTGTTGTGAAGACGGAGAAAGTGAGAG GTGAGATTTCTTTGGAACCTAAGAACATCTCT | 5282 |
| | CAACAGTT GT CACGTTT | 5283 |
| | AAACGTG ACA AACTGTTG | 5284 |
| Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Gln237Leu CAA-CTA | CGAATGAGAACATGATCATCTTTGCAAAAACCTCTGGTCTCATCTG GCTCCTAATCCCTC T AGTACTGATGGGAAACACTTTGTTCCCTTGC TTCTTGTTTTGCTCATATGGGGACTTTA | 5285 |
| | TAAAGTCCCCATATGAGCAAAACCAAGAAGCAAGGGGAACAAAGTG TTTCCCATCAGTACT A GAGGGATTAGGAGCCAGATGAGACCAGAG TTTTTGCGAAAGATGATCATGTTCTCATTCTG | 5286 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | AATCCCTCTAGTACTGA | 5287 |
| | TCAGTACTAGAGGGATT | 5288 |
| Salt Tolerance HKT1 <i>Arabidopsis thaliana</i> Asn332Ser AAT-AGT | AGTCTCTAGAAGGAATGAGTTCGTACGAGAAGTTGGTTGGATCGT TGTTTCAAGTGGTGAAGTTCGCGACACACCGGAGAACTATAGTAG ACCTCTCTACACTTTCCCCAGCTATCTTGGT | 5289 |
| | ACCAAGATAGCTGGGGAAAGTGTAGAGAGGTCTACTATAGTTTCT CCGGTGTGTCGCGAACTCACCACCTGAAACAACGATCCAACCAAC TTCTCGTACGAACCTATTCTTCTAGAGACT | 5290 |
| | AGTGGTGAGTTCGCGAC | 5291 |
| | GTCGCGAACTCACCACCT | 5292 |
| Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Ser256Val TCG-GTG | AGAGATGTGCTAAAGAAGAAAGGTCTCAAAATGGTGACCTTTTCC GTCTTCACCACCGTGAGTACCTTTGCCAGTTGTGGGTTTGTCCCG ACCAATGAAAACATGATTATCTTCAGCAAAA | 5293 |
| | TTTTGCTGAAGATAATCATGTTTTATTGGTCGGGACAAACCCACA ACTGGCAAAGGTCAACACGGTGGTGAAGACGGAAAAGGTCACCA TTTTGAGACCTTTCTTCTTTAGCACATCTCT | 5294 |
| | CCACCGTGAGTACCTTT | 5295 |
| | AAAGGTCACACGGTGG | 5296 |
| Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Gln286Leu CAG-CTG | CCAATGAAAACATGATTATCTTCAGCAAAAACCTCTGGCCTCCTCCT GATTCTCATCCCTCTGGCCCTTCTTGGAACATGCTGTTCCCATC GAGCCTACGTTTGACGCTTTGGCTCATCGG | 5297 |
| | CCGATGAGCCAAAGCGTCAAACGTAGGCTCGATGGGAACAGCAT GTTCCCAAGAAGGGCCAGAGGGATGAGAATCAGGAGGAGGCCA GAGTTTTTGCTGAAGATAATCATGTTTTATTGG | 5298 |
| | CATCCCTCTGGCCCTTC | 5299 |
| | GAAGGGCCAGAGGGATG | 5300 |
| Salt Tolerance HKT1 <i>Eucalyptus camaldulensis</i> Asn381Ser AAC-AGC | AATCGTTGAATGGACTAAGCTCCTGTGAGAAAATCGTGGGCGCGC TGTTTCAGTGCGTGAGCAGCAGACATACCGGCGAGACGGTCGTC GATCTGTCCACAGTTGCTCCCGCCATCTTGGT | 5301 |
| | ACCAAGATGGCGGGAGCAACTGTGGACAGATCGACGACCGTCTC GCCGGTATGTCTGCTGCTCACGCACTGAAACAGCGCGCCACGA TTTTCTCACAGGAGCTTAGTCCATTCAACGATT | 5302 |
| | GTGCGTGAGCAGCAGAC | 5303 |
| | GTCTGCTGCTCACGCAC | 5304 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Salt Tolerance HKT1 <i>Oryza sativa</i> Ser238Val TCC-GTC | AAAGCTCCACTGAAGAAGAAAGGGATCAACATTGCACTCTTCTCA TTCTCGGTCACGGTCGCTCTCGTTTGCGAATGTGGGGCTCGTGCC GACAAATGAGAACATGGCAATCTTCTCCAAGA | 5305 |
| | TCTTGAGAAGATTGCCATGTTCTCATTGTGCGGCACGAGCCCCA CATTCGCAAACGAGACGACCGTGACCGAGAATGAGAAGAGTGCA ATGTTGATCCCTTTCTTCTTCAGTGGAGCTTT | 5306 |
| | TCACGGTCGCTCTCGTTT | 5307 |
| | AAACGAGACGACCGTGA | 5308 |
| Salt Tolerance HKT1 <i>Oryza sativa</i> Gln268Leu CAG-CTG | CAAATGAGAACATGGCAATCTTCTCCAAGAACCCGGGCCTCCTCC TCCTGTTTCATCGGCCCTGATTCTTGACGGCAATACACTTTACCCTCT CTTCCTAAGGCTATTGATATGGTTCTCTGGG | 5309 |
| | CCCAGGAACCATATCAATAGCCTTAGGAAGAGAGGGTAAAGTGTA TTGCCTGCAAGAATCAGGCCGATGAACAGGAGGAGGAGGCCCGG GTTCTTGAGAAGATTGCCATGTTCTCATTG | 5310 |
| | CATCGGCCCTGATTCTTG | 5311 |
| | CAAGAATCAGGCCGATG | 5312 |
| Salt Tolerance HKT1 <i>Oryza sativa</i> Asn363Ser AAC-AGC | CAGTCTTTGATGGACTCAGCTCTTACCAGAAGATTATCAATGCATT GTTTCATGGCAGTGAGCGCAAGGCACTCGGGGAGAACTCCATCG ACTGCTCACTCATCGCCCCTGCTGTTCTAGT | 5313 |
| | ACTAGAACAGCAGGGGCGATGAGTGAGCAGTCGATGGAGTTCTC CCCCGAGTGCCCTTGCGCTCACTGCCATGAACAATGCATTGATAAT CTTCTGGTAAGAGCTGAGTCCATCAAAGACTG | 5314 |
| | GGCAGTGAGCGCAAGGC | 5315 |
| | GCCTTGCGCTCACTGCC | 5316 |
| Salt Tolerance HKT1 <i>Triticum aestivum</i> Ala240Val GCC-GTC | GTGCCCCACTGAACAAGAAAGGGATCAACATCGTGCTCTTCTCAC TATCAGTCACCGTTGCTCTCCTGTGCGAATGCAGGACTCGTGCCCA CAAATGAGAACATGGTCATCTTCTCAAAGAA | 5317 |
| | TTCTTTGAGAAGATGACCATGTTCTCATTGTGGGCACGAGTCCT GCATTGCGACAGGAGACAACGGTGACTGATAGTGAGAAGAGCAC GATGTTGATCCCTTTCTTGTTTCAGTGGGGCAC | 5318 |
| | CACCGTTGCTCTCTGTG | 5319 |
| | CACAGGAGACAACGGTG | 5320 |
| Salt Tolerance HKT1 <i>Triticum aestivum</i> Gln270Leu CAG-CTG | CAAATGAGAACATGGTCATCTTCTCAAAGAATTGAGGCCTCTTGTT GCTGCTGAGTGGCCCTGATGCTCGCAGGCAATACATTGTTCCCTCT CTTCCTGAGGCTACTGGTGTGGTTCTCTGGG | 5321 |
| | CCCAGGAACCACACAGTAGCCTCAGGAAGAGAGGGGAACAATGT ATTGCCCTGCGAGCATCAGGCCACTCAGCAGCAACAAGAGGCCTG AATTCTTTGAGAAGATGACCATGTTCTCATTG | 5322 |
| | GAGTGGCCCTGATGCTCG | 5323 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | CGAGCATC <u>A</u> GGCCACTC | 5324 |
| Salt Tolerance HKT1 <i>Triticum aestivum</i> Asn365Ser AAT-AGT | CAGTCTTTGATGGGCTCAGCTCTTATCAGAAGACTGTCAATGCATT CTTCATGGTGGTGAGTGCGAGGCACTCAGGGGAGAATTCCATCG ACTGCTCGCTCATGTCCCCTGCCATTATAGT | 5325 |
| | ACTATAATGGCAGGGGACATGAGCGAGCAGTCGATGGAATTCTCC CCTGAGTGCCTCGCACTCACCACCATGAAGAATGCATTGACAGTC TTCTGATAAGAGCTGAGCCCATCAAAGACTG | 5326 |
| | GGTGGTGAGTGCGAGGC | 5327 |
| | GCCTCGCACTCACCACC | 5328 |
| Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Arg7Term CGA-TGA | TTTTTTTTGTTTTCGTTTTCAAAAACAAAATCTTTGAATTTTATGGCA ACCCGTCTTCTCTGAACAACTTTATCCGGCGATCTTACCGTTTAC CCGCTTTTAGCCCGGTGGGTCCTCCCA | 5329 |
| | TGGGAGGACCCACCGGGCTAAAAGCGGGTAAACGGTAAGATCGC CGGATAAAGTTTGTTCAGAGAAGACGGGTTGCCATAAAATTCAAA GATTTTGTTTTGA AACGAAAACAAAAAAA | 5330 |
| | GTCTTCTCTGAACAAAC | 5331 |
| | GTTTGTTCAAGAGAAGAC | 5332 |
| Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Arg13Term CGA-TGA | TCAAAAACAAAATCTTTGAATTTTATGGCAACCCGTCTTCTCAGAA CAAACCTTTATCCGGTGATCTTACCGTTTACCCGCTTTTAGCCCGGT GGGTCCTCCACCGTGACTGCTTCCACCG | 5333 |
| | CGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGGCTAAAAGC GGGTAAACGGTAAGATCACCGGATAAAGTTTGTTCGAGAAGACG GGTTGCCATAAAATTCAAAGATTTTGTTCGTTTGA | 5334 |
| | TTATCCGGTGATCTTAC | 5335 |
| | GTAAGATCACCGGATAA | 5336 |
| Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Tyr15Term TAC-TAG | AAAATCTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAACTTT ATCCGGCGATCTTAGCGTTTACCCGCTTTTAGCCCGGTGGGTCCT CCCACCGTGACTGCTTCCACCGCCGTCGTC | 5337 |
| | GACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCACCGGG CTAAAAGCGGGTAAACGCTAAGATCGCCGGATAAAGTTTGTTCGG AGAAGACGGGTTGCCATAAAATTCAAAGATTTT | 5338 |
| | CGATCTTAGCGTTTACC | 5339 |
| | GGTAAACGCTAAGATCG | 5340 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Leu17Term TTA-TAA | CTTTGAATTTTATGGCAACCCGTCTTCTCCGAACAACTTTATCCG GCGATCTTACCGTTA ^A ACCCGCTTTTAGCCCGGTGGGTCCTCCCAC CGTGACTGCTTCCACCGCCGTCGTCCCGGA | 5341 |
| | TCCGGGACGACGGCGGTGGAAGCAGTCACGGTGGGAGGACCCA CCGGGCTAAAAGCGGGTTA ^A ACGGTAAGATCGCCGGATAAAGTTT GTTCCGAGAAGACGGGTTGCCATAAAATTCAAAG | 5342 |
| | TTACCGTTA ^A ACCCGCTT | 5343 |
| | AAGCGGGTTA ^A ACGGTAA | 5344 |
| Freezing Tolerance proline oxidase precursor <i>Arabidopsis thaliana</i> Gly42Term GGA-TGA | CCGGTGGGTCCTCCACCGTGACTGCTTCCACCGCCGTCGTCCC GGAGATTCTCTCCTTTT ^T GACAACAAGCACCGGAACCACCTCTTCA CCACCCAAAACCCACCGAGCAATCTCACGATG | 5345 |
| | CATCGTGAGATTGCTCGGTGGGTTTTGGGTGGTGAAGAGGTGGT TCCGGTGCTTGTGTGTC ^A AAAGGAGAGAATCTCCGGGACGACGGC GGTGGAAGCAGTCACGGTGGGAGGACCCACCGG | 5346 |
| | TCTCCTTTT ^T GACAACAA | 5347 |
| | TTGTTGTC ^A AAAGGAGA | 5348 |
| Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Arg4Term CGA-TGA | ACATGAAGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTC AAACTATGAATTTCT ^T GACAAGAGAAGTTTGTAAAGGTCAGTGTTCCA GATTTGTCTCATTGAATTCTAAGTCGTGA | 5349 |
| | TCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCTTAC AAACTTCTCTTGTC ^A AGAAATTCATAGTTTGAGACTAATAAGATTCAA TACAAACAGAGATTTCACTGCTTCATGT | 5350 |
| | TGAATTTCT ^T GACAAGAG | 5351 |
| | CTCTTGTC ^A AGAAATTC | 5352 |
| Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Gln5Term CAA-TAA | TGAAGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAA CTATGAATTTCCGATA ^A AGAGAAGTTTGTAAAGGTCAGTGTTCCAGAT TTGTCTCATTGAATTCTAAGTCGTGAAGC | 5353 |
| | GCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGACCT TACAACTTCTCTT ^A TCGGAAATTCATAGTTTGAGACTAATAAGATT CAATACAAACAGAGATTTCACTGCTTCA | 5354 |
| | ATTCCGATA ^A AGAGAAG | 5355 |
| | CTTCTCTT ^A TCGGAAAT | 5356 |
| Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Glu6Term GAG-TAG | AGCAGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACAT GAATTTCCGACAATA ^A GAGTTTGTAAAGGTCAGTGTTCCAGATTTGT CTCATTGAATTCTAAGTCGTGAAGCTTA | 5357 |
| | TAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACACTGA CCTTACAAACTTCT ^A ATTGTGCGAAATTCATAGTTTGAGACTAATAA GATTCAATACAAACAGAGATTTCACTGCT | 5358 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | TCCGACAATAGAAAGTTT | 5359 |
| | AAACTTCTATTGTCGGA | 5360 |
| Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Lys7Term AAG-TAG | AGTGAAATCTCTGTTTGTATTGAATCTTATTAGTCTCAAACATGAA TTTCCGACAAGAGTAGTTTGTAAGGTCAGTGTTCCAGATTTGTCTC ATTGAATTCTAAGTCGTGAAGCTTAATT | 5361 |
| | AATTAAGCTTCACGACTTAGAATTCAATGAGACAAATCTGGAACAC TGACCTTACAACTACTCTTGTCGGAAATTCATAGTTTGAGACTAA TAAGATTCAATACAAACAGAGATTTCCT | 5362 |
| | GACAAGAGTAGTTTGTA | 5363 |
| | TACAACTACTCTTGTC | 5364 |
| | | |
| Lead Tolerance cyclic nucleotide- regulated ion channel <i>Arabidopsis thaliana</i> Gln12Term CAA-TAA | CATTGAATTCTAAGTCGTGAAGCTTAATTCGATTCTTCTTCACTTTC TCGGATCAGGTTTAAAGATTGGAAGTCGGATAAGACTTCCTCCGA CGTGGAATATTCCGGTAAAAACGAGATTC | 5365 |
| | GAATCTCGTTTTTACCGGAATATTCCACGTCGGAGGAAGTCTTATC CGACTTCCAATCTTAAACCTGATCCGAGAAAGTGAAGAAGAATC GAATTAAGCTTCACGACTTAGAATTCAATG | 5366 |
| | TCAGGTTTAAAGATTGG | 5367 |
| | CCAATCTTAAACCTGA | 5368 |
| | | |
| Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gln5Term CAA-TAA | TGGAAGTCAATCCCCACGTTGAGCAGGTTGATGCATTGGCTAAA GTTATGAATCACCGCTAAGACGAGTTTGTGAGGTTTCAGGATTGG AAATCAGAGAGAAGCTCTGAGGGAAATTTTC | 5369 |
| | GAAAATTTCCCTCAGAGCTTCTCTCTGATTTCGAATCCTGAAACCT CACAACTCGTCTTAGCGGTGATTACATACTTTAGCCAATGCATCA ACCTGCTCAACGTGGGGGATTGACTTCCA | 5370 |
| | ATCACCGCTAAGACGAG | 5371 |
| | CTCGTCTTAGCGGTGAT | 5372 |
| | | |
| Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gly7Term GAG-TAG | TCAATCCCCACGTTGAGCAGGTTGATGCATTGGCTAAAGTTATG AATCACCGCCAAGACTAGTTTGTGAGGTTTCAGGATTGGAAATCA GAGAGAAGCTCTGAGGGAAATTTTCATGCTA | 5373 |
| | TAGCATGAAAATTTCCCTCAGAGCTTCTCTCTGATTTCGAATCCTG AAACCTCACAACTAGTCTTGCGGTGATTACATACTTTAGCCAAT GCATCAACCTGCTCAACGTGGGGGATTGA | 5374 |
| | GCCAAGACTAGTTTGTG | 5375 |
| | CACAACTAGTCTTGGC | 5376 |
| | | |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Gln12Term CAG-TAG | GAGCAGGTTGATGCATTGGCTAAAGTTATGAATCACCGCCAAGAC GAGTTTGTGAGGTTT <u>I</u> AGGATTGGAAATCAGAGAGAAGCTCTGAG GGAAATTTTCATGCTAAAGGTGGAGTCCACC | 5377 |
| | GGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAGCTTCTCTC TGATTTCCAATCCT <u>A</u> AAACCTCACAACTCGTCTTGGCGGTGATTG ATAACTTTAGCCAATGCATCAACCTGCTC | 5378 |
| | TGAGGTTT <u>I</u> AGGATTGG | 5379 |
| | CCAATCCT <u>A</u> AAACCTCA | 5380 |
| Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Trp14Term TGG-TGA | TGATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGT GAGGTTTCAGGATTG <u>T</u> AAATCAGAGAGAAGCTCTGAGGGAAATTT TCATGCTAAAGGTGGAGTCCACCGAAGTAAA | 5381 |
| | TTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGAG CTTCTCTCTGATTT <u>A</u> CAATCCTGAAACCTCACAACTCGTCTTGGC GGTGATTCACTTTAGCCAATGCATCA | 5382 |
| | CAGGATTG <u>T</u> AAATCAGA | 5383 |
| | TCTGATTT <u>A</u> CAATCCTG | 5384 |
| Lead Tolerance cyclic nucleotide- gated calmodulin- binding ion channel (CBP4) <i>Nicotiana Tabacum</i> Lys15Term AAA-TAA | GATGCATTGGCTAAAGTTATGAATCACCGCCAAGACGAGTTTGTG AGGTTTCAGGATTGG <u>I</u> AATCAGAGAGAAGCTCTGAGGGAAATTTT CATGCTAAAGGTGGAGTCCACCGAAGTAAAG | 5385 |
| | CTTTACTTCGGTGGACTCCACCTTTAGCATGAAAATTTCCCTCAGA GCTTCTCTCTGATT <u>A</u> CCAATCCTGAAACCTCACAACTCGTCTTGG CGGTGATTCACTTTAGCCAATGCATC | 5386 |
| | AGGATTGG <u>I</u> AATCAGAG | 5387 |
| | CTCTGATT <u>A</u> CCAATCCT | 5388 |
| Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Glu2Term GAA-TAA | CTTGAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTGCGCTGG TGGAGATAATGATG <u>I</u> AAAGAGAGGACAGATATGTTAGATTTTCAGG ACTGCAAATCAGAGCAATCTGTTATCTCAG | 5389 |
| | CTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCTAACATA TCTGTCCTCTCTTT <u>A</u> CATCATTATCTCCACCAGGCGAACAGTTAGC AGCTAAGAGTGGTAGATCAATTCTTCAAG | 5390 |
| | TAATGATG <u>I</u> AAAGAGAG | 5391 |
| | CTCTCTTT <u>A</u> CATCATTA | 5392 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Arg3Term AGA-TGA | GAAGAATTGATCTACCACTCTTAGCTGCTAACTGTTGCGCTGGTG GAGATAATGATGGAATGAGAGGACAGATATGTTAGATTTTCAGGAC TGCAAATCAGAGCAATCTGTTATCTCAGAGA | 5393 |
| | TCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCTAAC ATATCTGTCCTCTCATTCCATCATTATCTCCACCAGGCGAACAGTT AGCAGCTAAGAGTGGTAGATCAATTCTTC | 5394 |
| | TGATGGAATGAGAGGAC | 5395 |
| | GTCCTCTCATTCCATCA | 5396 |
| Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Glu4Term GAG-TAG | GAATTGATCTACCACTCTTAGCTGCTAACTGTTGCGCTGGTGGAG ATAATGATGGAAAGATAGGACAGATATGTTAGATTTTCAGGACTGC AAATCAGAGCAATCTGTTATCTCAGAGAACG | 5397 |
| | CGTTCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTGAAATCT AACATATCTGTCCTATCTTTCCATCATTATCTCCACCAGGCGAACCA GTTAGCAGCTAAGAGTGGTAGATCAATTC | 5398 |
| | TGGAAAGATAGGACAGA | 5399 |
| | TCTGTCCTATCTTTCCA | 5400 |
| Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Arg6Term AGA-TGA | ATCTACCACTCTTAGCTGCTAACTGTTGCGCTGGTGGAGATAATG ATGGAAAGAGAGGACTGATATGTTAGATTTTCAGGACTGCAAATCA GAGCAATCTGTTATCTCAGAGAACGCAGTTT | 5401 |
| | AACTGCGTTCTCTGAGATAACAGATTGCTCTGATTTGCAGTCCTG AAATCTAACATATCAGTCCTCTCTTTCCATCATTATCTCCACCAGG CGAACAGTTAGCAGCTAAGAGTGGTAGAT | 5402 |
| | GAGAGGACTGATATGTT | 5403 |
| | AACATATCAGTCCTCTC | 5404 |
| Lead Tolerance calmodulin binding transport protein <i>Hordeum vulgare</i> Tyr7Term TAT-TAG | CCACTCTTAGCTGCTAACTGTTGCGCTGGTGGAGATAATGATGGA AAGAGAGGACAGATAGGTTAGATTTTCAGGACTGCAAATCAGAGCA ATCTGTTATCTCAGAGAACGCAGTTTCACCA | 5405 |
| | TGGTGAACTGCGTTCTCTGAGATAACAGATTGCTCTGATTTGCA GTCCTGAAATCTAACCTATCTGTCCTCTCTTTCCATCATTATCTCCA CCAGGCGAACAGTTAGCAGCTAAGAGTGG | 5406 |
| | GACAGATAGGTTAGATT | 5407 |
| | AATCTAACCTATCTGTC | 5408 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Glu2Term GAG-TAG | ATCCTTCTCTGAGAAAAACAACAGATCCGAATTTTATCTTTAATCA GCCGGAAAAAATGTAGAAAGCGATCGAGAGACAACGCGTTCTTCT TGAGCATCTCCGACCTTCTTCTTCTTCTT | 5409 |
| | AAGAAGAAGAAGAGGTCGGAGATGCTCAAGAAGAACGCGTTGT CTCTCGATCGCTTTCTACATTTTTTCCGGCTGATTAAAGATAAAATT CGGATCTGTTGTTTTTCTCAGAGAAGGAT | 5410 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | AAAAAATG <u>T</u> AGAAAGCG | 5411 |
| | CGCTTTCT <u>A</u> CATTTTTT | 5412 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Lys3Term AAA-TAA | CTTCTCTGAGAAAAACAACAGATCCGAATTTTATCTTTAATCAGC CGGAAAAAATGGAG <u>T</u> AAGCGATCGAGAGACAACGCGTTCTTCTTG AGCATCTCCGACCTTCTTCTTCTTCTTCGC | 5413 |
| | GCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGAAGAACGCGT TGTCTCTCGATCGCTT <u>A</u> CTCCATTTTTTCCGGCTGATTAAAGATAA AATTCGGATCTGTTGTTTTTCTCAGAGAAG | 5414 |
| | AAATGGAG <u>T</u> AAGCGATC | 5415 |
| | GATCGCTT <u>A</u> CTCCATT | 5416 |
| | | |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Glu6Term GAG-TAG | GAAAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAA TGGAGAAAGCGATCTAGAGACAACGCGTTCTTCTTGAGCATCTCC GACCTTCTTCTTCTTCTTCGCACAATTACG | 5417 |
| | CGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAAGA AGAACGCGTTGTCTCT <u>A</u> GATCGCTTTCTCCATTTTTTCCGGCTGAT TAAAGATAAAATTCGGATCTGTTGTTTTTC | 5418 |
| | AAGCGATCTAGAGACAA | 5419 |
| | TTGTCTCTAGATCGCTT | 5420 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Arg7Term AGA-TGA | AAAACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGG AGAAAGCGATCGAGT <u>G</u> ACAACGCGTTCTTCTTGAGCATCTCCGAC CTTCTTCTTCTTCTTCGCACAATTACGAGG | 5421 |
| | CCTCGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGCTCAA GAAGAACGCGTTGTCT <u>A</u> CTCGATCGCTTTCTCCATTTTTTCCGGCT GATTAAAGATAAAATTCGGATCTGTTGTTTT | 5422 |
| | CGATCGAGT <u>G</u> ACAACGC | 5423 |
| | GCGTTGTCT <u>A</u> CTCGATCG | 5424 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Arabidopsis thaliana</i> Gln8Term CAA-TAA | ACAACAGATCCGAATTTTATCTTTAATCAGCCGGAAAAAATGGAGA AAGCGATCGAGAGAT <u>A</u> ACGCGTTCTTCTTGAGCATCTCCGACCTT CTTCTTCTTCTTTCGCACAATTACGAGGCTT | 5425 |
| | AAGCCTCGTAATTGTGCGAAGAAGAAGAAGAAGGTCGGAGATGC TCAAGAAGAACGCGTT <u>A</u> TCTCTCGATCGCTTTCTCCATTTTTTCCG GCTGATTAAAGATAAAATTCGGATCTGTTGT | 5426 |
| | TCGAGAGAT <u>A</u> ACGCGTT | 5427 |
| | AACGCGTT <u>A</u> TCTCTCGA | 5428 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| 2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Glu26Term GAA-TAA | GAGAGACAAAGAGTTCTTCTTGAACATCTCCGTCCTTCTTCTTCTT CCTCTCACAGCTTTAAGGCTCTCTCTCTGCTTCAGCTTGCTTGGC TGGGGACAGTGCTGCGTATCAGAGGACCT | 5429 |
| | AGGTCCTCTGATACGCAGCACTGTCCCCAGCCAAGCAAGCTGAA GCAGAGAGAGAGCCTTAAAAGCTGTGAGAGGAAGAAGAAGAAGG ACGGAGATGTTCAAGAAGAACTCTTTGTCTCTC | 5430 |
| | ACAGCTTTAAGGCTCT | 5431 |
| | AGAGCCTTAAAAGCTGT | 5432 |
| 2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Ser32Term TCA-TGA | TTGAACATCTCCGTCCTTCTTCTTCTTCTCTCACAGCTTTGAAGG CTCTCTCTCTGCTTGAGCTTGCTTGGCTGGGGACAGTGCTGCGTA TCAGAGGACCTCTCTCTATGGAGATGATGT | 5433 |
| | ACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGCACTGTCC CCAGCCAAGCAAGCTCAAGCAGAGAGAGAGCCTTCAAAGCTGTG AGAGGAAGAAGAAGAAGGACGGAGATGTTCAA | 5434 |
| | CTCTGCTTGAGCTTGCT | 5435 |
| | AGCAAGCTCAAGCAGAG | 5436 |
| 2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Cys34Term TGC-TGA | TCTCCGTCCTTCTTCTTCTTCTCTCACAGCTTTGAAGGCTCTCTC TCTGCTTCAGCTTGATTGGCTGGGGACAGTGCTGCGTATCAGAG GACCTCTCTCTATGGAGATGATGTAGTCATT | 5437 |
| | AATGACTACATCATCTCCATAGAGAGAGGTCCTCTGATACGCAGC ACTGTCCCCAGCCAATCAAGCTGAAGCAGAGAGAGAGCCTTCAAA GCTGTGAGAGGAAGAAGAAGAAGGACGGAGA | 5438 |
| | TCAGCTTGATTGGCTGG | 5439 |
| | CCAGCCAATCAAGCTGA | 5440 |
| 2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Leu35Term TTG-TAG | TCCGTCCTTCTTCTTCTTCTCTCACAGCTTTGAAGGCTCTCTCTC TGCTTCAGCTTGCTAGGCTGGGGACAGTGCTGCGTATCAGAGGA CCTCTCTCTATGGAGATGATGTAGTCATTGT | 5441 |
| | ACAATGACTACATCATCTCCATAGAGAGAGGTCCTCTGATACGCA GCACTGTCCCCAGCCTAGCAAGCTGAAGCAGAGAGAGAGCCTTC AAAGCTGTGAGAGGAAGAAGAAGAAGGACGGA | 5442 |
| | AGCTTGCTAGGCTGGGG | 5443 |
| | CCCCAGCCTAGCAAGCT | 5444 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| 2,4-DB resistance glyoxysomal beta- ketoacyl-thiolase precursor <i>Brassica napus</i> Tyr42Term TAT-TAG | TCACAGCTTTGAAGGCTCTCTCTCTGCTTCAGCTTGCTTGGCTGG GGACAGTGCTGCGTAGCAGAGGACCTCTCTCTATGGAGATGATGT AGTCATTGTTGCGGCACATAGGACTGCACTA | 5445 |
| | TAGTGCAGTCCTATGTGCCGCAACAATGACTACATCATCTCCATA GAGAGAGGTCCTCTGCTACGCAGCACTGTCCCCAGCCAAGCAAG CTGAAGCAGAGAGAGAGCCTTCAAAGCTGTGA | 5446 |
| | GCTGCGTAGCAGAGGAC | 5447 |
| | GTCCTCTGCTACGCAGC | 5448 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Tyr25Term TAC-TAG | CAACAGACAGCAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTCT TTCTTCTCACAATTAGGAGTCCGCTCTTGCCGCATCAGTATGTGCT GCAGGGGATAGCGCCGCATATCATAGGGCT | 5449 |
| | AGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATGC GGCAAGAGCGGACTCCTAATTGTGAGAAGAAGAATTAGAAGGGC GGAGATGCTGGAGCAACACTTGCTGTCTGTG | 5450 |
| | CACAATTAGGAGTCCGC | 5451 |
| | GCGGACTCCTAATTGTG | 5452 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Glu26Term GAG-TAG | AACAGACAGCAAGTGTTGCTCCAGCATCTCCGCCCTTCTAATTCTT CTTCTCACAATTACTAGTCCGCTCTTGCCGCATCAGTATGTGCTGC AGGGGATAGCGCCGCATATCATAGGGCTT | 5453 |
| | AAGCCCTATGATATGCGGCGCTATCCCCTGCAGCACATACTGATG CGGCAAGAGCGGACTAGTAATTGTGAGAAGAAGAATTAGAAGGG CGGAGATGCTGGAGCAACACTTGCTGTCTGTG | 5454 |
| | ACAATTACTAGTCCGCT | 5455 |
| | AGCGGACTAGTAATTGT | 5456 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Ser32Term TCA-TGA | TCCAGCATCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTC CGCTCTTGCCGCATGAGTATGTGCTGCAGGGGATAGCGCCGCAT ATCATAGGGCTTCTGTTTATGGAGACGATGT | 5457 |
| | ACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGCGCTATCC CCTGCAGCACATACTCATGCGGCAAGAGCGGACTCGTAATTGTGA GAAGAAGAATTAGAAGGGCGGAGATGCTGGA | 5458 |
| | TGCCGCATGAGTATGTG | 5459 |
| | CACATACTCATGCGGCA | 5460 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Cys34Term TGT-TGA | TCTCCGCCCTTCTAATTCTTCTTCTCACAATTACGAGTCCGCTCTT GCCGCATCAGTATGAGCTGCAGGGGATAGCGCCGCATATCATAG GGCTTCTGTTTATGGAGACGATGTGGTGATT | 5461 |
| | AATCACCACATCGTCTCCATAAACAGAAGCCCTATGATATGCGGC GCTATCCCCTGCAGCTCATACTGATGCGGCAAGAGCGGACTCGT AATTGTGAGAAGAAGAATTAGAAGGGCGGAGA | 5462 |
| | TCAGTATGAGCTGCAGG | 5463 |
| | CCTGCAGCTCATACTGA | 5464 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase B <i>Mangifera indica</i> Tyr42Term TAT-TAG | TCACAATTACGAGTCCGCTCTTGCCGCATCAGTATGTGCTGCAGG GGATAGCGCCGCATAGCATAGGGCTTCTGTTTATGGAGACGATGT GGTGATTGTGGCAGCTCATCGTACTGCACTT | 5465 |
| | AAGTGCAGTACGATGAGCTGCCACAATCACCACATCGTCTCCATA AACAGAAGCCCTATGCTATGCGGCGCTATCCCCTGCAGCACATAC TGATGCGGCAAGAGCGGACTCGTAATTGTGA | 5466 |
| | GCCGCATAGCATAGGGC | 5467 |
| | GCCCTATGCTATGCGGC | 5468 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Tyr22Term TAC-TAG | GAAGGCGATCAACAGGCAGAGCATTTTGCTACATCATCTCCGGCC TTCTTCTTCCGCTTAGACAAATGAATCTTCGCTCTCTGCATCGGTT TGTGCAGCTGGGGATAGTGCTTCGTATCAA | 5469 |
| | TTGATACGAAGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTCAATTTGTCTAAGCGGAAGAAGAAGGCCGGAGATGATG TAGCAAAATGCTCTGCCTGTTGATCGCCTTC | 5470 |
| | TCCGCTTAGACAAATGA | 5471 |
| | TCATTTGTCTAAGCGGA | 5472 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Glu25Term GAA-TAA | ATCAACAGGCAGAGCATTTTGCTACATCATCTCCGGCCTTCTTCTT CCGCTTACACAAATTAATCTTCGCTCTCTGCATCGGTTTGTGCAGC TGGGGATAGTGCTTCGTATCAAAGGACAT | 5473 |
| | ATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATTAAATTTGTGTAAGCGGAAGAAGAAGGCCGG AGATGATGTAGCAAAATGCTCTGCCTGTTGAT | 5474 |
| | ACACAAATTAATCTTCG | 5475 |
| | CGAAGATTAAATTTGTGT | 5476 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Ser27Term TCG-TAG | GGCAGAGCATTGCTACATCATCTCCGGCCTTCTTCTCCGCTTACACAAATGAATCTTCTCGCTCTCTGCATCGGTTTGTGCAGCTGGGGA TAGTGCTTCGTATCAAAGGACATCGGTGTT | 5477 |
| | AACACCGATGTCCTTTGATACGAAGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAGCTAAGATTCAATTTGTGTAAGCGGAAGAAGAA GGCCGGAGATGATGTAGCAAAATGCTCTGCC | 5478 |
| | TGAATCTTCTAGCTCTCTG | 5479 |
| | CAGAGAGCTAAGATTCA | 5480 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Ser31Term TCG-TAG | TGCTACATCATCTCCGGCCTTCTTCTCCGCTTACACAAATGAATCTTCTCGCTCTCTGCATAGGTTTGTGCAGCTGGGGATAGTGCTTCGTA TCAAAGGACATCGGTGTTTGGAGATGATGT | 5481 |
| | ACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCACTATCCC CAGCTGCACAAACCTATGCAGAGAGCGAAGATTCATTTGTGTAAG CGGAAGAAGAAGGCCGGAGATGATGTAGCA | 5482 |
| | CTCTGCATAGGTTTGTG | 5483 |
| | CACAAACCTATGCAGAG | 5484 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucumis sativus</i> Cys33Term TGT-TGA | TCATCTCCGGCCTTCTTCTCCGCTTACACAAATGAATCTTCTCGCTC TCTGCATCGGTTTGAAGCAGCTGGGGATAGTGCTTCGTATCAAAGG ACATCGGTGTTTGGAGATGATGTCGTGATT | 5485 |
| | AATCACGACATCATCTCCAAACACCGATGTCCTTTGATACGAAGCA CTATCCCAGCTGCTCAAACCGATGCAGAGAGCGAAGATTCATTT GTGTAAGCGGAAGAAGAAGGCCGGAGATGA | 5486 |
| | TCGGTTTGAAGCAGCTGG | 5487 |
| | CCAGCTGCTCAAACCGA | 5488 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita sp.</i> Tyr22Term TAT-TAG | GAAGGCAATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCC TTCATCTTCGGCTTAGAGCCATGAATCTTCTCGCTCTCTGCATCGGTT TGTGCAGCTGGGGATAGTGCCTCGTATCAA | 5489 |
| | TTGATACGACGCACTATCCCCAGCTGCACAAACCGATGCAGAGAG CGAAGATTCATGGCTCTAAGCCGAAGATGAAGGCCGGAGATGAT GTAGCAGAATGCTCTGCCTGTTGATTGCCTTC | 5490 |
| | TCGGCTTAGAGCCATGA | 5491 |
| | TCATGGCTCTAAGCCGA | 5492 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita</i> sp. Glu25Term GAA-TAA | ATCAACAGGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTT CGGCTTATAGCCATTAAATCTTCGCTCTCTGCATCGGTTTGTGCAGC TGGGGATAGTGCGTCGTATCAAAGAACGT | 5493 |
| | ACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAAACCGATG CAGAGAGCGAAGATTAAATGGCTATAAGCCGAAGATGAAGGCCGG AGATGATGTAGCAGAATGCTCTGCCTGTTGAT | 5494 |
| | ATAGCCATTAAATCTTCG | 5495 |
| | CGAAGATTAAATGGCTAT | 5496 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita</i> sp. Ser27Term TCG-TAG | GGCAGAGCATTCTGCTACATCATCTCCGGCCTTCATCTTCGGCTT ATAGCCATGAATCTTAGCTCTCTGCATCGGTTTGTGCAGCTGGGG ATAGTGCGTCGTATCAAAGAACGTCGGTGTT | 5497 |
| | AACACCGACGTTCTTTGATACGACGCACTATCCCCAGCTGCACAA ACCGATGCAGAGAGCTAAGATTCATGGCTATAAGCCGAAGATGAA GGCCGGAGATGATGTAGCAGAATGCTCTGCC | 5498 |
| | TGAATCTTAGCTCTCTG | 5499 |
| | CAGAGAGCTAAGATTCA | 5500 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita</i> sp. Ser31Term TCG-TAG | TGCTACATCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATC TTCGCTCTCTGCATAGGTTTGTGCAGCTGGGGATAGTGCGTCGTA TCAAAGAACGTCGGTGTTTGGAGATGATGT | 5501 |
| | ACATCATCTCCAAACACCGACGTTCTTTGATACGACGCACTATCCC CAGCTGCACAAACCTATGCAGAGAGCGAAGATTCATGGCTATAAG CCGAAGATGAAGGCCGGAGATGATGTAGCA | 5502 |
| | CTCTGCATAGGTTTGTG | 5503 |
| | CACAAACCTATGCAGAG | 5504 |
| 2,4-DB resistance 3-ketoacyl-CoA thiolase <i>Cucurbita</i> sp. Cys33Term TGT-TGA | TCATCTCCGGCCTTCATCTTCGGCTTATAGCCATGAATCTTCGCTC TCTGCATCGGTTTGAAGCAGCTGGGGATAGTGCGTCGTATCAAAGA ACGTCGGTGTTTGGAGATGATGTCGTGATA | 5505 |
| | TATCACGACATCATCTCCAAACACCGACGTTCTTTGATACGACGCA CTATCCCCAGCTGCTCAAACCGATGCAGAGAGCGAAGATTCATGG CTATAAGCCGAAGATGAAGGCCGGAGATGA | 5506 |
| | TCGGTTTGAAGCAGCTGG | 5507 |
| | CCAGCTGCTCAAACCGA | 5508 |
| 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln5Term CAG-TAG | TCATAGTCTCTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTG CTATGGCAACTCATTAGCAAACGCAACCTCCTTCCGATTTTCCCGC TCTTGCCGATGAAAATTCCCAGATTCCAG | 5509 |
| | CTGGAATCTGGGAATTTTCATCGGCAAGAGCGGGAAAATCGGAA GGAGGTTGCGTTTGCTAATGAGTTGCCATAGCAGCTCACTAACCT TGGAAGAATCCAAGCGGCAAAAGAGACTATGA | 5510 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | CAACTCAT <u>T</u> AGCAAACG | 5511 |
| | CGTTTGCT <u>A</u> ATGAGTTG | 5512 |
| 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln6Term CAA-TAA | TAGTCTCTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTA TGGCAACTCATCAGTAAACGCAACCTCCTTCCGATTTTCCCGCTCT TGCCGATGAAAATTCCAGATTCCAGGTT | 5513 |
| | AACCTGGAATCTGCGAATTTTCATCGGCAAGAGCGGGAAAATCGG AAGGAGGTTGCGTTT <u>A</u> CTGATGAGTTGCCATAGCAGCTCACTAAC CTTGGAAGAATCCAAGCGGCAAAAGAGACTA | 5514 |
| | CTCATCAGTAAACGCAA | 5515 |
| | TTGCGTTT <u>A</u> CTGATGAG | 5516 |
| | | |
| 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln8Term CAA-TAA | CTTTTGCCGCTTGGATTCTTCCAAGGTTAGTGAGCTGCTATGGCA ACTCATCAGCAAACGTAACCTCCTTCCGATTTTCCCGCTCTTGCCG ATGAAAATTTCCAGATTCCAGGTTCAATTT | 5517 |
| | AAATTGAACCTGGAATCTGCGAATTTTCATCGGCAAGAGCGGGAA AATCGGAAGGAGGTT <u>A</u> CGTTTGCTGATGAGTTGCCATAGCAGCTC ACTAACCTTGGAAGAATCCAAGCGGCAAAAG | 5518 |
| | AGCAAACGTAAACCTCCT | 5519 |
| | AGGAGGTT <u>A</u> CGTTTGCT | 5520 |
| | | |
| 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Glu19Term GAA-TAA | GCTGCTATGGCAACTCATCAGCAAACGCAACCTCCTTCCGATTTT CCCGCTCTTGCCGATTAAATTTCCAGATTCCAGGTTCAATTTACA CCTTCTAATCATTATTTCTTAATTTTCTT | 5521 |
| | AAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAATTGAACCTGG AATCTGGGAATTTT <u>A</u> ATCGGCAAGAGCGGGAAAATCGGAAGGAG GTTGCGTTTGCTGATGAGTTGCCATAGCAGC | 5522 |
| | TTGCCGATTAAATTC | 5523 |
| | GGAATTTT <u>A</u> ATCGGCAA | 5524 |
| | | |
| 2,4 DB resistance Pex14 <i>Arabidopsis thaliana</i> Gln22Term CAG-TAG | GCAACTCATCAGCAAACGCAACCTCCTTCCGATTTTCCCGCTCTT GCCGATGAAAATTCCTAGATTCCAGGTTCAATTTACACCTTCTAAT CATTATTTCTTAATTTTCTTTGGTGGATT | 5525 |
| | AATCCACCAAAGAAAAATTAAGAAATAATGATTAGAAGGTGTAAAT TGAACCTGGAATCT <u>A</u> GGAATTTTCATCGGCAAGAGCGGGAAAATC GGAAGGAGGTTGCGTTTGCTGATGAGTTGC | 5526 |
| | AAAATTCCTAGATTCCA | 5527 |
| | TGGAATCT <u>A</u> GGAATTTT | 5528 |
| | | |

Example 29

Production of albino mutants for the analysis of photosynthetic processes

[253] Plant productivity is limited by resources available and the ability of plants to harness these resources. The conversion of light to chemical energy, which is then used to synthesize carbohydrates, fatty acids, sugars, amino acids and other compounds, requires a complex system which combines the light harvesting apparatus of pigments and proteins. The value of light energy to the plant can only be realized when it is efficiently converted into chemical energy by photosynthesis and fed into various biochemical processes. Significant effort has therefore been directed at studying photosynthetic processes in plants in order to improve productivity and/or the efficiency of photosynthesis. The analysis of the photosynthetic process is substantially aided by the ability to produce albino plants.

[254] The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

Table 36
Oligonucleotides to produce albino plants

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| White leaves Immutans <i>Arabidopsis thaliana</i> Ser5Term TCA-TGA | TTCTTTCCTGTGAAATTATCTGCTCAAATCTTTGGTTCCTGACGGAG ATGGCGGCGATTTGAGGCATCTCCTCTGGTACGTTGACGATTTC CGGCCTTTGGTTACTCTTCGACGCTCTAG | 5529 |
| | CTAGAGCGTCGAAGAGTAACCAAAGGCCGTGAAATCGTCAACGTA CCAGAGGAGATGCCTCAAATCGCCGCCATCTCCGTCAGGAACCAA AGATTTGAGCAGATAATTTACAGGAAAGAA | 5530 |
| | GGCGATTTGAGGCATCT | 5531 |
| | AGATGCCTCAAATCGCC | 5532 |
| White leaves Immutans <i>Arabidopsis thaliana</i> Leu12Term TTG-TAG | GCTCAAATCTTTGGTTCCTGACGGAGATGGCGGCGATTTACAGGCA TCTCCTCTGGTACGTAGACGATTTACGGCCTTTGGTTACTCTTCG ACGCTCTAGAGCCGCCGTTTCGTACAGCTC | 5533 |
| | GAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAGAGTAACCAA GGCCGTGAAATCGTCTACGTACCAGAGGAGATGCCTGAAATCGCC GCCATCTCCGTCAGGAACCAAAGATTTGAGC | 5534 |
| | TGGTACGTAGACGATTT | 5535 |
| | AAATCGTCTACGTACCA | 5536 |
| White leaves Immutans <i>Arabidopsis thaliana</i> Ser15Term TCA-TGA | TTTGGTTCCTGACGGAGATGGCGGCGATTTACAGGCATCTCCTCTG GTACGTTGACGATTTGACGGCCTTTGGTTACTCTTCGACGCTCTAG AGCCGCCGTTTCGTACAGCTCCTCTCACCG | 5537 |
| | CGGTGAGAGGAGCTGTACGAAACGGCGGCTCTAGAGCGTCGAAG AGTAACCAAAGGCCGTCAAATCGTCAACGTACCAGAGGAGATGCC TGAAATCGCCGCCATCTCCGTCAGGAACCAA | 5538 |
| | GACGATTTGACGGCCTT | 5539 |
| | AAGGCCGTCAAATCGTC | 5540 |
| White leaves Immutans <i>Arabidopsis thaliana</i> Arg22Term CGA-TGA | GCGGCGATTTACAGGCATCTCCTCTGGTACGTTGACGATTTACGG CCTTTGGTTACTCTTIGACGCTCTAGAGCCGCCGTTTCGTACAGCT CCTCTACCGATTGCTTCATCATCTTCCTC | 5541 |
| | GAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTGTACGAAACG GCGGCTCTAGAGCGTCAAAGAGTAACCAAAGGCCGTGAAATCGTC AACGTACCAGAGGAGATGCCTGAAATCGCCGC | 5542 |
| | TTACTCTTIGACGCTCT | 5543 |
| | AGAGCGTCAAAGAGTAA | 5544 |

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|--|--|------|
| White leaves Immutans <i>Arabidopsis thaliana</i> Arg25Term AGA-TGA | TCAGGCATCTCCTCTGGTACGTTGACGATTTACGGCCTTTGGTTA CTCTTCGACGCTCTTGAGCCGCCGTTTCGTACAGCTCCTCTCACC GATTGCTTCATCATCTTCCTCTCTCTTCTC | 5545 |
| | GAGAAGAGAGAGGAAGATGATGAAGCAATCGGTGAGAGGAGCTG TACGAAACGGCGGCTCAAGAGCGTCGAAGAGTAACCAAAGGCCG TGAAATCGTCAACGTACCAGAGGAGATGCCTGA | 5546 |
| | GACGCTCTTGAGCCGCC | 5547 |
| | GGCGGCTCAAGAGCGTC | 5548 |
| White leaves Immutans <i>Lycopersicon esculentum</i> Gly11Term GGA-TGA | GATTCTTGTGGGAAGGAAGAAGGATCAAGAATGGCGATTTTCGATT TCTGCTATGAGTTTTGAACCTCAGTTTCTTCATATTCTTGTTTTAG AGCTAGGAGTTTTGAGAAGTCATCAGTTT | 5549 |
| | AAACTGATGACTTCTCAAACTCCTAGCTCTAAAACAAGAATATGA AGAACTGAGGTTCAAAACTCATAGCAGAAATCGAAATCGCCATT CTTGATCCTTCTTCCTTCCACAAGAATC | 5550 |
| | TGAGTTTTGAACCTCA | 5551 |
| | TGAGGTTCAAAACTCA | 5552 |
| White leaves Immutans <i>Lycopersicon esculentum</i> Ser13Term TCA-TGA | GTGGGAAGGAAGAAGGATCAAGAATGGCGATTTTCGATTTCTGCTA TGAGTTTTGGAACCTGAGTTTCTTCATATTCTTGTTTTAGAGCTAGG AGTTTTGAGAAGTCATCAGTTTTATGCAA | 5553 |
| | TTGCATAAACTGATGACTTCTCAAACTCCTAGCTCTAAAACAAG AATATGAAGAACTCAGGTTCCAAACTCATAGCAGAAATCGAAAT CGCCATTCTTGATCCTTCTTCCTTCCCAC | 5554 |
| | TGGAACCTGAGTTTCTT | 5555 |
| | AAGAACTCAGGTTCCA | 5556 |
| White leaves Immutans <i>Lycopersicon esculentum</i> Ser16Term TCA-TGA | AAGAAGGATCAAGAATGGCGATTTTCGATTTCTGCTATGAGTTTTGG AACCTCAGTTTCTTGATATTCTTGTTTTAGAGCTAGGAGTTTTGAGA AGTCATCAGTTTTATGCAATTCCCAGAA | 5557 |
| | TTCTGGGAATTGCATAAACTGATGACTTCTCAAACTCCTAGCTC TAAAACAAGAATATCAAGAACTGAGGTTCCAAACTCATAGCAGA AATCGAAATCGCCATTCTTGATCCTTCTT | 5558 |
| | AGTTTCTTGATATTCTT | 5559 |
| | AAGAATATCAAGAACT | 5560 |
| White leaves Immutans <i>Lycopersicon esculentum</i> Tyr17Term TAT-TAG | AGGATCAAGAATGGCGATTTTCGATTTCTGCTATGAGTTTTGGAACC TCAGTTTCTTCATAGTCTTGTTTTAGAGCTAGGAGTTTTGAGAAGTC ATCAGTTTTATGCAATTCCCAGAACCCA | 5561 |
| | TGGGTTCTGGGAATTGCATAAACTGATGACTTCTCAAACTCCTA GCTCTAAAACAAGACTATGAAGAACTGAGGTTCCAAACTCATAG CAGAAATCGAAATCGCCATTCTTGATCCT | 5562 |
| | TCTTCATAGTCTTGTTT | 5563 |
| | AAACAAGACTATGAAGA | 5564 |

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|--|---|------|
| White leaves Immutans <i>Lycopersicon esculentum</i> Cys19Term TGT-TGA | AAGAATGGCGATTTCTGCTATGAGTTTTGGAACCTCAGTT TCTTCATATTCTTGATTTAGAGCTAGGAGTTTTGAGAAGTCATCAGT TTTATGCAATTTCCAGAACCCATGTCGG | 5565 |
| | CCGACATGGGTTCTGGAATTGCATAAACTGATGACTTCTCAAAA CTCCTAGCTCTAAATCAAGAATATGAAGAACTGAGGTTCCAAAAC TCATAGCAGAAATCGAAATCGCCATTCTT | 5566 |
| | TATTCTTGATTTAGAGC | 5567 |
| | GCTCTAAATCAAGAATA | 5568 |
| White leaves Immutans <i>Capsicum annuum</i> Ser13Term TCA-TGA | CGCGTCCGATAAAAAAATCAAGAATGGCGATTTCCATATCTGCTAT GAGTTTTCGAAGTTGAGTTTCTTCTTCATATTCAGCATTTTTGTGCA ATTCCAAGAACCCATTTTGTGTTGAATTC | 5569 |
| | GAATTCAAACAAAATGGGTTCTTGAATTGCACAAAAATGCTGAAT ATGAAGAAGAACTCAAGTTCGAAAACATAGCAGATATGGAAAT CGCCATTCTTGATTTTTTATCGGACGCG | 5570 |
| | TCGAAGTTGAGTTTCTT | 5571 |
| | AAGAACTCAAGTTCTGA | 5572 |
| White leaves Immutans <i>Capsicum annuum</i> Ser17Term TCA-TGA | AAAAATCAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAAC TTCAGTTTCTTCTTGATATTCAGCATTTTTGTGCAATTCCAAGAACC CATTTTGTGTTGAATTCTCTATTTTCACT | 5573 |
| | AGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGAATTGCACA AAAATGCTGAATATCAAGAAGAACTGAAGTTCGAAAACATAGC AGATATGGAAATCGCCATTCTTGATTTTT | 5574 |
| | TTCTTCTTGATATTCAG | 5575 |
| | CTGAATATCAAGAAGAA | 5576 |
| White leaves Immutans <i>Capsicum annuum</i> Ser19Term TCA-TGA | CAAGAATGGCGATTTCCATATCTGCTATGAGTTTTCGAAGTTTCTTCTTCA TATTCTTCTCATATTGAGCATTTTTGTGCAATTCCAAGAACCCATTTT GTTTGAATTCTCTATTTTCACTTAGGAA | 5577 |
| | TTCTAAGTGAAAATAGAGAATTCAAACAAAATGGGTTCTTGAAT TGCACAAAAATGCTCAATATGAAGAAGAACTGAAGTTGAAAAC CATAGCAGATATGGAAATCGCCATTCTTG | 5578 |
| | TTTCATATTGAGCATTTT | 5579 |
| | AAAATGCTCAATATGAA | 5580 |
| White leaves Immutans <i>Capsicum annuum</i> Leu21Term TTG-TAG | CGATTTCCATATCTGCTATGAGTTTTCGAAGTTTCTTCTTCA TATTCAGCATTTTGTGCAATTCCAAGAACCCATTTTGTGTTGAATTC TCTATTTTCACTTAGGAATTCTCATAG | 5581 |
| | CTATGAGAATTCCTAAGTGAAAATAGAGAATTCAAACAAAATGGGT TCTTGAATTGCACTAAAATGCTGAATATGAAGAAGAACTGAAGT TCGAAAACATAGCAGATATGGAAATCG | 5582 |
| | AGCATTTTGTGCAATT | 5583 |
| | AATTGCACTAAAATGCT | 5584 |

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|--|---|------|
| White leaves Immutans <i>Capsicum annuum</i> Cys22Term TGC-TGA | TTCCATATCTGCTATGAGTTTTTCGAACTTCAGTTTCTTCTTCATATT CAGCATTTTTGTGA A AATTCCAAGAACCCATTTGTTTGAATTCTCTA TTTTCACTTAGGAATTCTCATAGAACT | 5585 |
| | AGTTCTATGAGAATTCTAAGTGAAAATAGAGAATTCAAACAAAAT GGGTTCTTGGAATTTCACAAAAATGCTGAATATGAAGAAGAACTG AAGTTCGAAAACATCATAGCAGATATGGAA | 5586 |
| | TTTTTGTGA A AATTCCAA | 5587 |
| | TTGGAATTTCACAAAAA | 5588 |
| White leaves Immutans <i>Oryza sativa</i> Glu22Term GAG-TAG | TTCGGCACGAGGGAGAAGGAGCAGACCGAGGTGGCCGTCGAGG AGTCCTTCCCCTTCAGGTAGACGGCTCCTCCTGACGAGCCACTGG TCACCGCCGAGGAGAGCTGGGTGGTTAAGCTCG | 5589 |
| | CGAGCTTAACCACCCAGCTCTCCTCGGCGGTGACCAGTGGCTCGT CAGGAGGAGCCGTCTA C CTGAAGGGGAAGGACTCCTCGACGGCC ACCTCGGTCTGCTCCTTCTCCCTCGTGCCGAA | 5590 |
| | CCTTCAGGTAGACGGCT | 5591 |
| | AGCCGTCTA C CTGAAGG | 5592 |
| White leaves Immutans <i>Oryza sativa</i> Glu28Term CAG-TAG | GAGCAGACCGAGGTGGCCGTCGAGGAGTCCTTCCCCTTCAGGGA GACGGCTCCTCCTGACTAGCCACTGGTCACCGCCGAGGAGAGCT GGGTGGTTAAGCTCGAGCAGTCCGTGAACATTT | 5593 |
| | AAATGTTACGGACTGCTCGAGCTTAACCACCCAGCTCTCCTCGG CGGTGACCAGTGGCTA G TCAGGAGGAGCCGTCTCCCTGAAGGGG AAGGACTCCTCGACGGCCACCTCGGTCTGCTC | 5594 |
| | CTCCTGACTAGCCACTG | 5595 |
| | CAGTGGCTA G TCAGGAG | 5596 |
| White leaves Immutans <i>Oryza sativa</i> Glu34Term GAG-TAG | GTCGAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGA GCCACTGGTCACCGCCTAGGAGAGCTGGGTGGTTAAGCTCGAGC AGTCCGTGAACATTTTCTCACGGAGTCAGTCA | 5597 |
| | TGACTGACTCCGTGAGGAAAATGTTACGGACTGCTCGAGCTTAA CCACCCAGCTCTCCTA G GGCGGTGACCAGTGGCTCGTCAGGAGGA GCCGTCTCCCTGAAGGGGAAGGACTCCTCGAC | 5598 |
| | TCACCGCCTAGGAGAGC | 5599 |
| | GCTCTCCTA G GGCGGTGA | 5600 |
| White leaves Immutans <i>Oryza sativa</i> Glu35Term GAG-TAG | GAGGAGTCCTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCC ACTGGTCACCGCCGAGTAGAGCTGGGTGGTTAAGCTCGAGCAGT CCGTGAACATTTTCTCACGGAGTCAGTCATCA | 5601 |
| | TGATGACTGACTCCGTGAGGAAAATGTTACGGACTGCTCGAGCT TAACCACCCAGCTCTA C TCGGCGGTGACCAGTGGCTCGTCAGGA GGAGCCGTCTCCCTGAAGGGGAAGGACTCCTC | 5602 |
| | CCGCCGAGTAGAGCTGG | 5603 |
| | CCAGCTCTA C TCGGCGG | 5604 |

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| White leaves Immutans <i>Oryza sativa</i> Trp37Term TGG-TGA | CTTCCCCTTCAGGGAGACGGCTCCTCCTGACGAGCCACTGGTCAC CGCCGAGGAGAGCTGAGTGGTTAAGCTCGAGCAGTCCGTGAACA TTTTCTCACGGAGTCAGTCATCACGATACTT | 5605 |
| | AAGTATCGTGATGACTGACTCCGTGAGGAAAATGTTACGGACTG CTCGAGCTTAACCACTCAGCTCTCCTCGGCGGTGACCAGTGGCTC GTCAGGAGGAGCCGTCTCCCTGAAGGGGAAG | 5606 |
| | GAGAGCTGAGTGGTTAA | 5607 |
| | TTAACCACCTCAGCTCTC | 5608 |
| White leaves Immutans <i>Triticum aestivum</i> Trp22Term TGG-TGA | TCCGGAGGAGGAAGGGGGATTTCGACGAGGAGCTCACCTCGCCG GCGAGGACGGCGACTGAGTCGTCAGATTTCGAGCAGTCCTTCAAC GTATTCCTCACGGATACTGTCATCTTTATACTC | 5609 |
| | GAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAAGGACTG CTCGAATCTGACGACTCAGTCGCCGTCTCGCCGGCGAGGGTGA GCTCCTCGTCGAATCCCCCTTCCTCCTCCGGA | 5610 |
| | GGCGACTGAGTCGTCAG | 5611 |
| | CTGACGACTCAGTCGCC | 5612 |
| White leaves Immutans <i>Triticum aestivum</i> Arg25Term AGA-TGA | GAGGAAGGGGGATTTCGACGAGGAGCTCACCTCGCCGGCGAGG ACGGCGACTGGGTCGTCGATTTCGAGCAGTCCTTCAACGTATTCC TCACGGATACTGTCATCTTTATACTCGATATTC | 5613 |
| | GAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATACGTTGAA GGACTGCTCGAATCAGACGACCCAGTCGCCGTCTCGCCGGCGA GGGTGAGCTCCTCGTCGAATCCCCCTTCCTC | 5614 |
| | GGGTCGTCGATTTCGAG | 5615 |
| | CTCGAATCAGACGACCC | 5616 |
| White leaves Immutans <i>Triticum aestivum</i> Glu27Term GAG-TAG | GGGGGATTTCGACGAGGAGCTCACCTCGCCGGCGAGGACGGCG ACTGGGTCGTCAGATTCTAGCAGTCCTTCAACGTATTCTCACGGA TACTGTCATCTTTATACTCGATATTCTGTATC | 5617 |
| | GATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAATAC GTTGAAGGACTGCTAGAATCTGACGACCCAGTCGCCGTCTCGCC GGCGAGGGTGAGCTCCTCGTCGAATCCCC | 5618 |
| | TCAGATTCTAGCAGTCC | 5619 |
| | GGACTGCTAGAATCTGA | 5620 |
| White leaves Immutans <i>Triticum aestivum</i> Gln28Term CAG-TAG | GGATTTCGACGAGGAGCTCACCTCGCCGGCGAGGACGGCGACTG GGTCGTCAGATTTCGAGTAGTCCTTCAACGTATTCTCACGGATACT GTCATCTTTATACTCGATATTCTGTATCGTG | 5621 |
| | CACGATACAGAATATCGAGTATAAAGATGACAGTATCCGTGAGGAA TACGTTGAAGGACTACTCGAATCTGACGACCCAGTCGCCGTCTC GCCGGCGAGGGTGAGCTCCTCGTCGAATCC | 5622 |
| | GATTTCGAGTAGTCCTTC | 5623 |
| | GAAGGACTACTCGAATC | 5624 |

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| White leaves Immutans <i>Triticum aestivum</i> Tyr46Term TAT-TAG | CGAGCAGTCCTTCAACGTATTCCTCACGGATACTGTCATCTTTATA CTCGATATTCTGTAGCGTGACCGCGACTACGCAAGGTTCTTCGTG CTCGAGACCATCGCCAGGGTGCCCTATTTTC | 5625 |
| | GAAATAGGGCACCCCTGGCGATGGTCTCGAGCACGAAGAACCTTG CGTAGTCGCGGTCACGCTACAGAATATCGAGTATAAAGATGACAG TATCCGTGAGGAATACGTTGAAGGACTGCTCG | 5626 |
| | ATTCTGTAGCGTGACCG | 5627 |
| | CGGTCACGCTACAGAAT | 5628 |

Example 30

Altering amino acid content of plants

[255] Another aim of biotechnology is to generate plants, especially crop plants, with added value traits. An example of such a trait is improved nutritional quality in food crops. For example, lysine, tryptophan and threonine, which are essential amino acids in the diet of humans and many animals, are limiting nutrients in most cereal crops. Consequently, grain-based diets, such as those based on corn, barley, wheat, rice, maize, millet, sorghum, and the like, must be supplemented with more expensive synthetic amino acids or amino-acid-containing oilseed protein meals. Increasing the lysine content of these grains or of any of the feed component crops would result in significant added value.

[256] Naturally occurring mutants of plants that have different levels of particular essential amino acids have been identified. However, these mutants are generally not the result of increased free amino acid, but are instead the result of shifts in the overall protein profile of the grain. For example, in maize, reduced levels of lysine-deficient endosperm proteins (prolamines) are complemented by elevated levels of more lysine-rich proteins (albumins, globulins and glutelins). While nutritionally superior, these mutants are associated with reduced yields and poor grain quality, limiting their agronomic usefulness.

[257] An alternative approach is to generate plants with mutations that render key amino acid biosynthetic enzymes insensitive to feedback inhibition. Many such mutations are known and mutation results in increased free amino acid. The increased production can optionally be coupled to increased expression of an abundant storage protein comprising the chosen amino acid. Alternatively, a normally abundant protein can be engineered to contain more of the target amino acid.

[258] The attached table discloses exemplary oligonucleotide base sequences which can be used to generate site-specific mutations that remove feedback inhibition in plant amino acid biosynthetic enzymes.

Table 37
Genome-Altering Oligos Conferring Amino Acid Overproduction

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| Met Overproduction CGS <i>Arabidopsis thaliana</i> Arg77His CGT-CAT | TATCCTCCAGGATCTTAAGATTTCTCCTAATTTGTCCTCAGCT GAGCATTAAAGCCCATAGAAACTGTAGCAACATCGGTGTTGCACA GATCGTGGCGGCTAAGTGGTCCAACAACCC | 5629 |
| | GGGTTGTTGGACCACTTAGCCGCCACGATCTGTGCAACACCGAT GTTGCTACAGTTTCTATGGGCTTTAATGCTCAGCTGACGGACGAA ATTAGGAGGAAATCTTAAGATCCTGGAGGATA | 5630 |
| | TAAAGCCCATAGAAACT | 5631 |
| | AGTTTCTATGGGCTTTA | 5632 |
| Met Overproduction CGS <i>Arabidopsis thaliana</i> Ser81Asn AGC-AAC | TCTTAAGATTTCTCCTAATTTGTCCTCAGCTGAGCATTAAAGC CCGTAGAAACTGTAAACAACATCGGTGTTGCACAGATCGTGGCGG CTAAGTGGTCCAACAACCCATCCTCCGCGTT | 5633 |
| | AACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCCACGATCTG TGCAACACCGATGTTGTACAGTTTCTACGGGCTTTAATGCTCAGC TGACGGACGAAATTAGGAGGAAATCTTAAGA | 5634 |
| | AAACTGTAAACAACATCG | 5635 |
| | CGATGTTGTACAGTTT | 5636 |
| Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Ser GGT-AGT | TTTCCTCCTAATTTGTCCTCAGCTGAGCATTAAAGCCCGTAGAA ACTGTAGCAACATCAGTGTTGCACAGATCGTGGCGGCTAAGTGGT CCAACAACCCATCCTCCGCGTTACCTTCGG | 5637 |
| | CCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGCC ACGATCTGTGCAACACIGATGTTGCTACAGTTTCTACGGGCTTTAA TGCTCAGCTGACGGACGAAATTAGGAGGAAA | 5638 |
| | GCAACATCAGTGTTGCA | 5639 |
| | TGCAACACIGATGTTGC | 5640 |
| Met Overproduction CGS <i>Arabidopsis thaliana</i> Gly84Asp GGT-GAT | TTTCCTCCTAATTTGTCCTCAGCTGAGCATTAAAGCCCGTAGAAA CTGTAGCAACATCGATGTTGCACAGATCGTGGCGGCTAAGTGGTC CAACAACCCATCCTCCGCGTTACCTTCGGC | 5641 |
| | GCCGAAGGTAACGCGGAGGATGGGTTGTTGGACCACTTAGCCGC CACGATCTGTGCAACATCGATGTTGCTACAGTTTCTACGGGCTTTA ATGCTCAGCTGACGGACGAAATTAGGAGGAA | 5642 |
| | CAACATCGATGTTGCAC | 5643 |
| | GTGCAACATCGATGTTG | 5644 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Met Overproduction CGS <i>Fragraria vesca</i> Arg73His CGC-CAC | TATCGTCACTCATCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGC TCAGCACCAAGGCCCACCGCAACTGCAGCAACATCGGCGTCGCG CAGATCGTCGCGGCTTCGTGGTCCAACAAAGA | 5645 |
| | TCTTTGTTGGACCACGAAGCCGCGACGATCTGCGCGACGCCGAT GTTGCTGCAGTTGCGGTGGGCCTTGGTGCTGAGCTGGCGGACGA AGTTGGGAGGGAAGCGGAGGATGAGTGACGATA | 5646 |
| | CAAGGCCCCACCGCAACT | 5647 |
| | AGTTGCGGTGGGCCTTG | 5648 |
| Met Overproduction CGS <i>Fragraria vesca</i> Ser77Asn AGC-AAC | TCCTCCGCTTCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGG CCCGCCGCAACTGCAACAACATCGGCGTCGCGCAGATCGTCGCG GCTTCGTGGTCCAACAAAGACTCCGACCTTTC | 5649 |
| | GAAAGGTCGGAGTCTTTGTTGGACCACGAAGCCGCGACGATCTG CGCGACGCCGATGTTGTGTCAGTTGCGGCGGGCCTTGGTGCTGA GCTGGCGGACGAAGTTGGGAGGGAAGCGGAGGA | 5650 |
| | CAACTGCAACAACATCG | 5651 |
| | CGATGTTGTGTCAGTTG | 5652 |
| Met Overproduction CGS <i>Fragraria vesca</i> Gly80Ser GGC-AGC | TCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG CAACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCGGCTTCGT GGTCCAACAAAGACTCCGACCTTTCGGCGGTGC | 5653 |
| | GCACCGCCGAAAGGTTCGGAGTCTTTGTTGGACCACGAAGCCGCG ACGATCTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGGGCCTT GGTGCTGAGCTGGCGGACGAAGTTGGGAGGGAA | 5654 |
| | GCAACATCAGCGTCGCG | 5655 |
| | CGCGACGCTGATGTTGC | 5656 |
| Met Overproduction CGS <i>Fragraria vesca</i> Gly80Asp GGC-GAC | TCCCTCCCAACTTCGTCCGCCAGCTCAGCACCAAGGCCCGCCG AACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCGGCTTCGTG GTCCAACAAAGACTCCGACCTTTCGGCGGTGCC | 5657 |
| | GGCACCGCCGAAAGGTTCGGAGTCTTTGTTGGACCACGAAGCCGC GACGATCTGCGCGACGCTCGATGTTGCTGCAGTTGCGGCGGGCCT TGGTGCTGAGCTGGCGGACGAAGTTGGGAGGGA | 5658 |
| | CAACATCAGCGTCGCGC | 5659 |
| | GCGCGACGCTCGATGTTG | 5660 |
| Met Overproduction CGS <i>Glycine max</i> Arg68His CGC-CAC | TCTCCTCCCTCATCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGC TAAGCACCAAGGCGAGCCGCAACTGCAGCAACATCGGCGTCGCG CAAATCGTCGCCGCTTCGTGGTCAACAACAG | 5661 |
| | CTGTTGTTGACCACGAAGCGGCGACGATTTGCGCGACGCCGAT GTTGCTGCAGTTGCGGCTCGCCTTGGTGCTTAGCTGGCGCTGGA AGTTGGGAGGGAAGCGGAGGATGAGGGAGGAGA | 5662 |
| | CCAAGGCGAGCCGCAAC | 5663 |
| | GTTGCGGCTCGCCTTG | 5664 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Met Overproduction CGS <i>Glycine max</i> Ser72Asn AGC-AAC | TCCTCCGCTTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGG CGCGCCGCAACTGCAACAACATCGGCGTCGCGCAAATCGTCGCC GCTTCGTGGTTCGAACAACAGCGACAACCTCTCC | 5665 |
| | GGAGAGTTGTCGCTGTTGTTTCGACCACGAAGCGGCGACGATTTG CGCGACGCCGATGTTGTTGTCAGTTGCGGCGCGCCTTGGTGCTTA GCTGGCGCTGGAAGTTGGGAGGGAAGCGGAGGA | 5666 |
| | CAACTGCAACAACATCG | 5667 |
| | CGATGTTGTTGTCAGTTG | 5668 |
| Met Overproduction CGS <i>Glycine max</i> Gly75Ser GGC-AGC | TTCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCG CAACTGCAGCAACATCAGCGTCGCGCAAATCGTCGCCGCTTCGT GGTCGAACAACAGCGACAACCTCTCCGGCCGCCG | 5669 |
| | CGGCGGCCGGAGAGTTGTCGCTGTTGTTTCGACCACGAAGCGGCG ACGATTTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGCGCCTT GGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGAA | 5670 |
| | GCAACATCAGCGTCGCG | 5671 |
| | CGCGACGCTGATGTTGC | 5672 |
| Met Overproduction CGS <i>Glycine max</i> Gly75Asp GGC-GAC | TCCCTCCCAACTTCCAGCGCCAGCTAAGCACCAAGGCGCGCCGC AACTGCAGCAACATCAGCGTCGCGCAAATCGTCGCCGCTTCGTG GTCGAACAACAGCGACAACCTCTCCGGCCGCCG | 5673 |
| | CCGGCGGCCGGAGAGTTGTCGCTGTTGTTTCGACCACGAAGCGGC GACGATTTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGCGCCT TGGTGCTTAGCTGGCGCTGGAAGTTGGGAGGGA | 5674 |
| | CAACATCAGCGTCGCGC | 5675 |
| | GCGCGACGCTGATGTTG | 5676 |
| Met Overproduction CGS <i>Solanum tuberosum</i> Arg70His AGG-CAC | TGTCTTCTCTGATTTTCAGGTTTCCTCCTAATTTTCGTGAGGCAGCT AAGCATTAAAGGCTCACAGGAATTGCAGCAATATTGGCGTGGCTCA AGTTGTGGCGGCTTCCTGGTCTAACAACCA | 5677 |
| | TGGTTGTTAGACCAGGAAGCCGCCACAACCTTGAGCCACGCCAATA TTGCTGCAATTCCTGTGAGCCTTAATGCTTAGCTGCCTCACGAAAT TAGGAGGAAACCTGAAATCAGAGAAGACA | 5678 |
| | TAAGGCTCACAGGAATT | 5679 |
| | AATTCCTGTGAGCCTTA | 5680 |
| Met Overproduction CGS <i>Solanum tuberosum</i> Ser74Asn AGC-AAC | TTTTCAGGTTTCCTCCTAATTTTCGTGAGGCAGCTAAGCATTAAAGC TAGGAGGAATTGCAACAATATTGGCGTGGCTCAAGTTGTGGCGG CTTCCTGGTCTAACAACCAAGCCGGTCTCTGA | 5681 |
| | TCAGGACCGGCTTGGTTGTTAGACCAGGAAGCCGCCACAACCTTG AGCCACGCCAATATTGTTGCAATTCCTCCTAGCCTTAATGCTTAGC TGCCTCACGAAATTAGGAGGAAACCTGAAAA | 5682 |
| | GAATTGCAACAATATTG | 5683 |
| | CAATATTGTTGCAATTC | 5684 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Met Overproduction CGS <i>Solanum tuberosum</i> Gly77Ser GGC-AGC | TTTCCTCCTAATTTCTGAGGCAGCTAAGCATTAAAGGCTAGGAGG AATTGCAGCAATATTAGCGTGGCTCAAGTTGTGGCGGCTTCCTGG TCTAACAACCAAGCCGGTCCTGAATTCCTC | 5685 |
| | GAGTGAATTCAGGACCGGCTTGTTGTTAGACCAGGAAGCCGCC ACAACCTTGAGCCACGCTAATATTGCTGCAATTCCTCCTAGCCTTAA TGCTTAGCTGCCTCACGAAATTAGGAGGAAA | 5686 |
| | GCAATATTAGCGTGGCT | 5687 |
| | AGCCACGCTAATATTGC | 5688 |
| Met Overproduction CGS <i>Solanum tuberosum</i> Gly77Asp GGC-GAC | TTTCCTCCTAATTTCTGAGGCAGCTAAGCATTAAAGGCTAGGAGGA ATTGCAGCAATATTGACGTGGCTCAAGTTGTGGCGGCTTCCTGGT CTAACAACCAAGCCGGTCCTGAATTCCTC | 5689 |
| | GGAGTGAATTCAGGACCGGCTTGTTGTTAGACCAGGAAGCCGC CACAACCTTGAGCCACGCTCAATATTGCTGCAATTCCTCCTAGCCTTA ATGCTTAGCTGCCTCACGAAATTAGGAGGAA | 5690 |
| | CAATATTGACGTGGCTC | 5691 |
| | GAGCCACGCTCAATATTG | 5692 |
| Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Arg73His CGC-CAC | CTTCCTCTCTTATCCTTCGCTTTCTCCCAACTTTGTCCGTCAGCT CAGCACCAAGGCTCGCCACAACCTGCAGCAACATTGGTGTGCGAC AGGTCGTCGCTGCCTCCTGGTCCAACAACCTC | 5693 |
| | GAGTTGTTGGACCAGGAGGCAGCGACGACCTGTGCGACACCAAT GTTGCTGCAGTTGTGGCGAGCCTTGGTGCTGAGCTGACGGACAA AGTTGGGAGGAAAGCGAAGGATAAGAGAGGAAG | 5694 |
| | GGCTCGCCACAACCTGCA | 5695 |
| | TGCAGTTGTGGCGAGCC | 5696 |
| Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Ser77Asn AGC-AAC | TCCTTCGCTTTCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGG CTCGCCGCAACTGCAACAACATTGGTGTGCGACAGGTCGTCGCT GCCTCCTGGTCCAACAACCTCCGATGCCGGCGC | 5697 |
| | GCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGCGACGACCT GTGCGACACCAATGTTGTGTCAGTTGCGGCGAGCCTTGGTGCTG AGCTGACGGACAAAGTTGGGAGGAAAGCGAAGGA | 5698 |
| | CAACTGCAACAACATTG | 5699 |
| | CAATGTTGTGTCAGTTG | 5700 |
| Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Gly80Ser GGT-AGT | TTTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGC AACTGCAGCAACATTAGTGTGCGACAGGTCGTCGCTGCCTCCTG GTCCAACAACCTCCGATGCCGGCGCCACCTCTT | 5701 |
| | AAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAGC GACGACCTGTGCGACACTAATGTTGCTGCAAGTTGCGGCGAGCCT TGGTGCTGAGCTGACGGACAAAGTTGGGAGGAAA | 5702 |
| | GCAACATTAGTGTGCGCA | 5703 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| | TGCGACACTAATGTTGC | 5704 |
| Met Overproduction CGS <i>Mesembryanthemum crystallinum</i> Gly80Asp GGT-GAT | TTCCTCCCAACTTTGTCCGTCAGCTCAGCACCAAGGCTCGCCGCA ACTGCAGCAACATTGATGTGCGCACAGGTCGTGCTGCCTCCTGGT CCAACAACCTCCGATGCCGGCGCCACCTCTTG | 5705 |
| | CAAGAGGTGGCGCCGGCATCGGAGTTGTTGGACCAGGAGGCAG CGACGACCTGTGCGACATCAATGTTGCTGCAGTTGCGGCGAGCC TTGGTGCTGAGCTGACGGACAAAGTTGGGAGGAA | 5706 |
| | CAACATTGATGTGCGCAC | 5707 |
| | GTGCGACATCAATGTTG | 5708 |
| Met Overproduction CGS <i>Zea mays</i> Arg41His CGC-CAC | CCTCTGCTACCATCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGC TTAGCACCAAGGCACACCGCAACTGCAGCAACATCGGCGTCGCG CAGATCGTCGCCGCCGCGTGGTCCGACTGCCC | 5709 |
| | GGGCAGTCGGACCACGCGGCGGCGACGATCTGCGCGACGCCGA TGTTGCTGCAGTTGCGGTGTGCTTGGTGCTAAGCTGGCGGACA AAGTTTGGCGGAAAGCGGAGGATGGTAGCAGAGG | 5710 |
| | CAAGGCACACCGCAACT | 5711 |
| | AGTTGCGGTGTGCTTGTG | 5712 |
| Met Overproduction CGS <i>Zea mays</i> Ser45Asn AGC-AAC | TCCTCCGCTTTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGG CACGCCGCAACTGCAACAACATCGGCGTCGCGCAGATCGTCGCC GCCGCGTGGTCCGACTGCCCCGCCGCTCGCCC | 5713 |
| | GGGCGAGCGGCGGGGCGAGTCGGACCACGCGGCGGCGACGATCT GCGCGACGCCGATGTTGTGTCAGTTGCGGCGTGCTTGGTGCTA AGCTGGCGGACAAAGTTTGGCGGAAAGCGGAGGA | 5714 |
| | CAACTGCAACAACATCG | 5715 |
| | CGATGTTGTGTCAGTTG | 5716 |
| Met Overproduction CGS <i>Zea mays</i> Gly48Ser GGC-AGC | TTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGC AACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCCGCCGCGTG GTCCGACTGCCCCGCCGCTCGCCCCCACTTAG | 5717 |
| | CTAAGTGGGGGCGAGCGGCGGGGCGAGTCGGACCACGCGGCGG CGACGATCTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGTGCC TTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAAA | 5718 |
| | GCAACATCAGCGTCGCG | 5719 |
| | CGCGACGCTGATGTTGC | 5720 |
| Met Overproduction CGS <i>Zea mays</i> Gly48Asp GGC-GAC | TTCCGCCAAACTTTGTCCGCCAGCTTAGCACCAAGGCACGCCGCA ACTGCAGCAACATCAGCGTCGCGCAGATCGTCGCCGCCGCGTG TCCGACTGCCCCGCCGCTCGCCCCCACTTAG | 5721 |
| | CCTAAGTGGGGGCGAGCGGCGGGGCGAGTCGGACCACGCGGCG GCGACGATCTGCGCGACGCTGATGTTGCTGCAGTTGCGGCGTG CTTGGTGCTAAGCTGGCGGACAAAGTTTGGCGGAA | 5722 |
| | CAACATCAGCGTCGCGC | 5723 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | GCGCGACG <u>I</u> CGATGTTG | 5724 |
| Met Overproduction TS <i>Arabidopsis thaliana</i> Leu205Arg CTT-CGT | GTATGAATGATCTGTGGGTGAAACACTGTGGGATTAGTCATACAG GAAGTTTCAAGGATC <u>G</u> TGGAATGACTGTTTTGGTTAGTCAAGTTAA TCGTCTGAGAAAGATGAAACGACCTGTGGT | 5725 |
| | ACCACAGGTCGTTTCATCTTTCTCAGACGATTAACCTTGACTAACCA AAACAGTCATTCCA <u>C</u> GATCCTTGAACTTCCTGTATGACTAATCCC ACAGTGTTTCACCCACAGATCATTACATAC | 5726 |
| | CAAGGATC <u>G</u> TGGAATGA | 5727 |
| | TCATTCCA <u>C</u> GATCCTTG | 5728 |
| Met Overproduction TS <i>Solanum tuberosum</i> Leu198Arg CTT-CGT | GCATGACTGATTTGTGGGTCAAACACTGTGGGATTAGCCATACTG GTAGTTTTAAGGATC <u>G</u> TGGGATGACTGTTTTGGTGAGTCAAGTTAA TCGCTTGCGGAAAATGCATAAACC GGTTGT | 5729 |
| | ACAACCGGTTTATGCATTTTCCGCAAGCGATTAACCTTGACTCACCA AAACAGTCATCCCA <u>C</u> GATCCTTAAACTACCAGTATGGCTAATCCC ACAGTGTTTGACCCACAAATCAGTCATGC | 5730 |
| | TAAGGATC <u>G</u> TGGGATGA | 5731 |
| | TCATCCCA <u>C</u> GATCCTTA | 5732 |
| Lys Overproduction DHPS <i>Zea mays</i> Ser157Asn AGC-AAC | TCATTGGGCACACAGTGAAGTCTTTGGCTCTAGAATCAAAGTGA TAGGCAACACAGGAA <u>A</u> CAACTCAACCAGAGAAGCCGTCACGCA ACAGAACAGGGATTTGCTGTTGGCATGCATGC | 5733 |
| | GCATGCATGCCAACAGCAAATCCCTGTTCTGTTGCGTGGACGGCT TCTCTGGTTGAGTTG <u>I</u> TTCTGTGTTGCCTATCACTTTGATTCTAG AGCCAAAGCAGTTCACTGTGTGCCCAATGA | 5734 |
| | CACAGGAA <u>A</u> CAACTCAA | 5735 |
| | TTGAGTTG <u>I</u> TTCTGTG | 5736 |
| Lys Overproduction DHPS <i>Zea mays</i> Ala166Val GCA-GAA | GCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACCA GAGAAGCCGTCCACG <u>A</u> AACAGAACAGGGATTTGCTGTTGGCATG CATGCGGCTCTCCACATCAATCCTTACTACGG | 5737 |
| | CCGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGC AATCCCTGTTCTGTT <u>I</u> CGTGGACGGCTTCTCTGGTTGAGTTGCTT CCTGTGTTGCCTATCACTTTGATTCTAGAGC | 5738 |
| | CGTCCACG <u>A</u> AACAGAAC | 5739 |
| | GTTCTGTT <u>I</u> CGTGGACG | 5740 |
| Lys Overproduction DHPS <i>Zea mays</i> Ala166Thr GCA-ACA | GGCTCTAGAATCAAAGTGATAGGCAACACAGGAAGCAACTCAACC AGAGAAGCCGTCCAC <u>A</u> CAACAGAACAGGGATTTGCTGTTGGCAT GCATGCGGCTCTCCACATCAATCCTTACTACG | 5741 |
| | CGTAGTAAGGATTGATGTGGAGAGCCGCATGCATGCCAACAGCA AATCCCTGTTCTGTTG <u>I</u> GTGGACGGCTTCTCTGGTTGAGTTGCTT CTGTGTTGCCTATCACTTTGATTCTAGAGCC | 5742 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| | CCGTCCAC <u>A</u> CAACAGAA | 5743 |
| | TTCTGTTG <u>I</u> GTGGACGG | 5744 |
| Lys Overproduction DHPS <i>Oryza sativa</i> Ser124Asn AGT-AAT | TTATTGGGCATACAGTTAACTGCTTTGGCACTAAAATTAAAGTGGT CGGCAACACAGGAA <u>A</u> TAACTCAACAAGGGAGGCTATTCACGCAAC TGAGCAGGGATTGCTGTAGGTATGCACGC | 5745 |
| | GCGTGCATACCTACAGCGAATCCCTGCTCAGTTGCGTGAATAGCC TCCCTTGTTGAGTTA <u>TT</u> CCTGTGTTGCCGACCACTTTAATTTAGT GCCAAAGCAGTTAACTGTATGCCCAATAA | 5746 |
| | CACAGGAA <u>A</u> TAACTCAA | 5747 |
| | TTGAGTTA <u>TT</u> CCTGTG | 5748 |
| Lys Overproduction DHPS <i>Oryza sativa</i> Ala133Val GCA-GTA | GCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTAACTCAACAA GGGAGGCTATTCACG <u>I</u> AAGTGAAGCAGGGATTGCTGTAGGTATG CACGCGGCTCTCCACATCAATCCTTACTACGG | 5749 |
| | CCGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGC GAATCCCTGCTCAGTT <u>A</u> CGTGAATAGCCTCCCTTGTTGAGTTACTT CCTGTGTTGCCGACCACTTTAATTTTAGTGC | 5750 |
| | TATTCACG <u>I</u> AAGTGAAG | 5751 |
| | GCTCAGTT <u>A</u> CGTGAATA | 5752 |
| Lys Overproduction DHPS <i>Oryza sativa</i> Ala133Thr GCA-ACA | GGCACTAAAATTAAAGTGGTCGGCAACACAGGAAGTAACTCAACA AGGGAGGCTATTCAC <u>A</u> CAACTGAGCAGGGATTGCTGTAGGTAT GCACGCGGCTCTCCACATCAATCCTTACTACG | 5753 |
| | CGTAGTAAGGATTGATGTGGAGAGCCGCGTGCATACCTACAGCG AATCCCTGCTCAGTTG <u>I</u> GTGAATAGCCTCCCTTGTTGAGTTACTTC CTGTGTTGCCGACCACTTTAATTTTAGTGCC | 5754 |
| | CTATTCAC <u>A</u> CAACTGAG | 5755 |
| | CTCAGTTG <u>I</u> GTGAATAG | 5756 |
| Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ser165Asn AGT-AAT | TCATCGGGCATACTGTTAACTGCTTTGGAGCCAACATTAAAGTGAT AGGCAACACGGGAA <u>A</u> TAACTCAACCAGAGAAGCTGTTACGCGA CAGAGCAGGGATTGCTGTTGGCATGCATGC | 5757 |
| | GCATGCATGCCAACAGCAAATCCCTGCTCTGTGCGGTGAACAGCT TCTCTGGTTGAGTTA <u>TT</u> CCCGTGTTGCCTATCACTTAATGTTGG CTCCAAAGCAGTTAACAGTATGCCCGATGA | 5758 |
| | CACGGGAA <u>A</u> TAACTCAA | 5759 |
| | TTGAGTTA <u>TT</u> CCCGTG | 5760 |
| Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ala174Val GCG-GTG | GAGCCAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACCA GAGAAGCTGTTACG <u>I</u> TACAGAGCAGGGATTTGCTGTTGGCATG CATGCAGCTCTTCATGTCAATCCTTACTACGG | 5761 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | CCGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGTCA A CGTGAACAGCTTCTCTGGTTGAGTTACTTC CCGTGTTGCCTATCACTTTAATGTTGGCTC | 5762 |
| | TGTTACAGT I GACAGAGC | 5763 |
| | GCTCTGTCA A CGTGAACA | 5764 |
| Lys Overproduction DHPS 1 <i>Triticum aestivum</i> Ala174Thr GCG-ACG | GGAGCCAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACC AGAGAAGCTGTTACAC A CGACAGAGCAGGGATTTGCTGTTGGCAT GCATGCAGCTCTTCATGTCAATCCTTACTACG | 5765 |
| | CGTAGTAAGGATTGACATGAAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGTCTG T GTGAACAGCTTCTCTGGTTGAGTTACTTCC CGTGTTGCCTATCACTTTAATGTTGGCTCC | 5766 |
| | CTGTTACAC A CGACAGAG | 5767 |
| | CTCTGTCTG T GTGAACAG | 5768 |
| Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ser154Asn AGT-AAT | TCATCGGGCACACTGTTAACTGCTTTGGAACAACTAAAGTGAT AGGCAACACGGGAA A TAACCTCACTAGAGAAGCGATTACAGCTTC AGAGCAGGGATTTGCTGTTGGCATGCATGC | 5769 |
| | GCATGCATGCCAACAGCAAATCCCTGCTCTGAAGCGTGAATCGCT TCTCTAGTTGAGTTA I TTCCCGTGTTGCCTATCACTTTAATGTTAGT TCCAAAGCAGTTAACAGTGTGCCCGATGA | 5770 |
| | CACGGGAA A TAACCTCAA | 5771 |
| | TTGAGTTA I TTCCCGTG | 5772 |
| Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ala163Val GCT-GTT | GAACTAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACTA GAGAAGCGATTACAG T TTACAGAGCAGGGATTTGCTGTTGGCATGC ATGCAGCTCTCCATGTCAATCCTTACTATGG | 5773 |
| | CCATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGAA A CGTGAATCGCTTCTCTAGTTGAGTTACTTC CCGTGTTGCCTATCACTTTAATGTTAGTTC | 5774 |
| | GATTCAG T TTACAGAGC | 5775 |
| | GCTCTGAA A CGTGAATC | 5776 |
| Lys Overproduction DHPS 2 <i>Triticum aestivum</i> Ala163Thr GCT-ACT | GGAATAACATTAAAGTGATAGGCAACACGGGAAGTAACTCAACT AGAGAAGCGATTACAC A CTTCAGAGCAGGGATTTGCTGTTGGCATG CATGCAGCTCTCCATGTCAATCCTTACTATG | 5777 |
| | CATAGTAAGGATTGACATGGAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGAAG T GTGAATCGCTTCTCTAGTTGAGTTACTTCC CGTGTTGCCTATCACTTTAATGTTAGTTCC | 5778 |
| | CGATTACAC A CTTCAGAG | 5779 |
| | CTCTGAAG T GTGAATCG | 5780 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ser154Asn AGT-AAT | CTCATTGGGCATACTGTGAACTGCTTTGGCTCTAGAATTAAGTGA TAGGCAACACAGGAAATAACTCAACCAGAGAAGCTGTTACGCAA CAGAGCAGGGATTTGCTGTTGGCATGCATG | 5781 |
| | CATGCATGCCAACAGCAAATCCCTGCTCTGTTGCGTGAACAGCTT CTCTGGTTGAGTTATTTCTGTGTTGCCTATCACTTTAATTCTAGA GCCAAAGCAGTTCACAGTATGCCAATGAG | 5782 |
| | CACAGGAAATAACTCAA | 5783 |
| | TTGAGTTATTTCTGTG | 5784 |
| Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ala163Val GCA-GTA | GCTCTAGAATTAAGTGATAGGCAACACAGGAAGTAACTCAACCA GAGAAGCTGTTACGTAACAGAGCAGGGATTTGCTGTTGGCATGC ATGCAGCTCTCCACATCAATCCTTACTATGG | 5785 |
| | CCATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCA AATCCCTGCTCTGTTACGTGAACAGCTTCTCTGGTTGAGTTACTTC CTGTGTTGCCTATCACTTTAATTCTAGAGC | 5786 |
| | TGTTACGTAACAGAGC | 5787 |
| | GCTCTGTTACGTGAACA | 5788 |
| Lys Overproduction DHPS <i>Coix lacryma-jobi</i> Ala163Thr GCA-ACA | GGCTCTAGAATTAAGTGATAGGCAACACAGGAAGTAACTCAACC AGAGAAGCTGTTACACAACAGAGCAGGGATTTGCTGTTGGCATG CATGCAGCTCTCCACATCAATCCTTACTATG | 5789 |
| | CATAGTAAGGATTGATGTGGAGAGCTGCATGCATGCCAACAGCAA ATCCCTGCTCTGTTGTGTGAACAGCTTCTCTGGTTGAGTTACTTCC TGTGTTGCCTATCACTTTAATTCTAGAGCC | 5790 |
| | CTGTTACACAACAGAG | 5791 |
| | CTCTGTTGTGTGAACAG | 5792 |
| Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ser136Asn AGC-AAC | TCATTGGTCACACAGTCAATTGTTTTGGAGGGTCCATCAAAGTCAT CGGGAACACTGGAAACAACCTCCACAAGGGAAGCAATCCATGCAA CTGAACAGGGATTTGCTGTAGGTATGCATGC | 5793 |
| | GCATGCATACCTACAGCAAATCCCTGTTGAGTTGCATGGATTGCTT CCCTTGTGGAGTTGTTCCAGTGTTCCCGATGACTTTGATGGACC CTCCAAAACAATTGACTGTGTGACCAATGA | 5794 |
| | CACTGGAAACAACCTCCA | 5795 |
| | TGGAGTTGTTCCAGTG | 5796 |
| Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ala145Val GCA-GTA | GAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCACAA GGGAAGCAATCCATGTAACCTGAACAGGGATTTGCTGTAGGTATGC ATGCAGCTCTTACATTAATCCCTACTATGG | 5797 |
| | CCATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCA AATCCCTGTTGAGTTACATGGATTGCTTCCCTTGTGGAGTTGCTTC CAGTGTTCCCGATGACTTTGATGGACCCTC | 5798 |
| | AATCCATGTAACCTGAAC | 5799 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | GTTCAGTTACATGGATT | 5800 |
| Lys Overproduction DHPS <i>Nicotiana tabacum</i> Ala145Thr GCA-ACA | GGAGGGTCCATCAAAGTCATCGGGAACACTGGAAGCAACTCCAC AAGGGAAGCAATCCATACAACTGAACAGGGATTGCTGTAGGTAT GCATGCAGCTCTTCACATTAATCCCTACTATG | 5801 |
| | CATAGTAGGGATTAATGTGAAGAGCTGCATGCATACCTACAGCAA ATCCCTGTTTCAGTTGATGGATTGCTTCCCTTGTGGAGTTGCTTCC AGTGTTCCTCGATGACTTTGATGGACCCTCC | 5802 |
| | CAATCCATCAACTGAA | 5803 |
| | TTCAGTTGATGGATTG | 5804 |
| Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ser142Asn AGC-AAC | TTATAGGCCATACCGTTAACTGTTTTGGCGGAAGCATCAAAGTCAT TGGAAACACTGGAAACAATTCGACTAGAGAAGCAATCCACGCGAC TGAACAAGGATTCGCGGTTGGAATGCATGC | 5805 |
| | GCATGCATTCCAACCGCGAATCCTTGTTTCAGTCGCGTGGATTGCT TCTCTAGTCGAATTGTTCCAGTGTTTCCAATGACTTTGATGCTTC CGCCAAAACAGTTAACGGTATGGCCTATAA | 5806 |
| | CACTGGAAACAATTCGA | 5807 |
| | TCGAATTGTTCCAGTG | 5808 |
| Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ala151Val GCG-GTG | GCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACTA GAGAAGCAATCCACGTGACTGAACAAGGATTCGCGGTTGGAATG CATGCTGCTCTTCATATAAACCCCTTACTATGG | 5809 |
| | CCATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCG AATCCTTGTTTCAGTCAGTGGATTGCTTCTCTAGTCGAATTGCTTC CAGTGTTCATGACTTTGATGCTTCCGC | 5810 |
| | AATCCACGTGACTGAAC | 5811 |
| | GTTCAGTCACTGGATT | 5812 |
| Lys Overproduction DHPS <i>Arabidopsis thaliana</i> Ala151Thr GCG-ACG | GGCGGAAGCATCAAAGTCATTGGAAACACTGGAAGCAATTCGACT AGAGAAGCAATCCACACGACTGAACAAGGATTCGCGGTTGGAAT GCATGCTGCTCTTCATATAAACCCCTTACTATG | 5813 |
| | CATAGTAAGGGTTTATATGAAGAGCAGCATGCATTCCAACCGCGA ATCCTTGTTTCAGTCGTGTGGATTGCTTCTCTAGTCGAATTGCTTCC AGTGTTCATGACTTTGATGCTTCCGCC | 5814 |
| | CAATCCACACGACTGAA | 5815 |
| | TTCAGTCGTGTGGATTG | 5816 |
| Lys Overproduction DHPS <i>Glycine max</i> Ser103Asn AGC-AAC | TTATTGCTCATACAGTCAACTGTTTTGGTGGGAAAATTAAGGTTAT TGGAAATACTGGAAACAACCTCCACCAGGGAAGCAATTCATGCCAC TGAGCAGGGTTTTGCTGTTGGAATGCATGC | 5817 |
| | GCATGCATTCCAACAGCAAAACCCTGCTCAGTGGCATGAATTGCT TCCCTGGTGGAGTTGTTCCAGTATTTCCAATAACCTTAATTTCC CACCAAAACAGTTGACTGTATGAGCAATAA | 5818 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | TACTGGAA <u>A</u> CAACTCCA | 5819 |
| | TGGAGTTG <u>I</u> TTCCAGTA | 5820 |
| Lys Overproduction DHPS <i>Glycine max</i> Ala112Val GCC-GTC | GTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACCA GGGAAGCAATTCATG <u>T</u> CACTGAGCAGGGTTTTGCTGTTGGAATGC ATGCTGCCCTTCACATAAACCCCTTACTATGG | 5821 |
| | CCATAGTAAGGGTTTATGTGAAGGGCAGCATGCATTCCAACAGCA AAACCCTGCTCAGTG <u>A</u> CATGAATTGCTTCCCTGGTGGAGTTGCTT CCAGTATTTCCAATAACCTTAATTTTCCCAC | 5822 |
| | AATTCATG <u>I</u> CACTGAGC | 5823 |
| | GCTCAGTG <u>A</u> CATGAATT | 5824 |
| Lys Overproduction DHPS <i>Glycine max</i> Ala112Thr GCC-ACC | GGTGGGAAAATTAAGGTTATTGGAAATACTGGAAGCAACTCCACC AGGGAAGCAATTCAT <u>A</u> CCACTGAGCAGGGTTTTGCTGTTGGAATG CATGCTGCCCTTCACATAAACCCCTTACTATG | 5825 |
| | CATAGTAAGGGTTTATGTGAAGGGCAGCATGCATTCCAACAGCAA AACCCTGCTCAGTGGT <u>A</u> TGAATTGCTTCCCTGGTGGAGTTGCTTC CAGTATTTCCAATAACCTTAATTTTCCCACC | 5826 |
| | CAATTCAT <u>A</u> CCACTGAG | 5827 |
| | CTCAGTGGT <u>T</u> ATGAATTG | 5828 |
| Trp Overproduction AS <i>Arabidopsis thaliana</i> Asp341Asn GAC-AAC | CTTGCAGGAGACATATTTTCAAGTCGTGCTGAGTCAACGTTTTGAG CGGCGAACATTTGCA <u>A</u> ACCCCTTTGAAGTTTATAGAGCACTAAGA GTTGTGAATCCAAGTCCGTATATGGGTTATT | 5829 |
| | AATAACCCATATACGGACTTGATTCACAACTCTTAGTGCTCTATA AACTTCAAAGGGGT <u>I</u> TGCAAATGTTGCGCGCTCAAACGTTGACT CAGCACGATCTGAAATATGTCTCCTGCAAG | 5830 |
| | CATTTGCA <u>A</u> ACCCCTTT | 5831 |
| | AAAGGGGT <u>T</u> TGCAAATG | 5832 |
| Trp Overproduction AS <i>Nicotiana tabacum</i> Asp326Asn GAC-AAC | GCTGCAGGAGACATATTTCAAATCGTTTTAAGTCAACGCTTTGAGA GAAGAACATTTGCT <u>A</u> ACCCATTTGAAGGTACAGAGCATTAAAGAAT TGTGAATCCAAGCCCATATATGACTTACA | 5833 |
| | TGTAAGTCATATATGGGCTTGATTCACAATTCTTAATGCTCTGTA CACTTCAAATGGGT <u>I</u> AGCAAATGTTCTTCTCTCAAAGCGTTGACTT AAAACGATTTGAAATATGTCTCCTGCAGC | 5834 |
| | CATTTGCT <u>A</u> ACCCATTT | 5835 |
| | AAATGGGT <u>I</u> AGCAAATG | 5836 |
| Trp Overproduction AS <i>Oryza sativa</i> Asp323Asn GAC-AAC | CTAGCTGGTGACATTTTTCAAGTAGTCTTAAGCCAGCGTTTTGAGA GGCGTACATTTGCT <u>A</u> ACCCCTTTGAGGTGTACCGTGCAATTGCGTA TTGTCAATCCTAGTCCTTATATGGCCTATC | 5837 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | GATAGGCCATATAAGGACTAGGATTGACAATACGCAATGCACGGT ACACCTCAAAGGGGT <u>T</u> AGCAAATGTACGCCTCTCAAACGCTGGC TTAAGACTACTTGAAAAATGTCACCAGCTAG | 5838 |
| | CATTGCT <u>A</u> ACCCCTTT | 5839 |
| | AAAGGGGT <u>T</u> AGCAAATG | 5840 |
| Trp Overproduction AS <i>Ruta graveolens</i> Asp354Asn GAC-AAC | CTTGCTGGTGACATATTCCAGATCGTACTAAGTCAGCGTTTTGAAA GGCGAACGTTTCGCA <u>A</u> ACCCATTTGAAATCTATAGATCACTGAGGA TTGTTAATCCAAGCCCATATATGACTTATT | 5841 |
| | AATAAGTCATATATGGGCTTGGATTAAACAATCCTCAGTGATCTATA GATTTCAAATGGGT <u>T</u> TGCGAACGTTTCGCCTTTCAAACGCTGACTT AGTACGATCTGGAATATGTCACCAGCAAG | 5842 |
| | CGTTGCA <u>A</u> ACCCATTT | 5843 |
| | AAATGGGT <u>T</u> TGCGAACG | 5844 |
| Trp Overproduction AS <i>Catharanthus roseus</i> Asp354Asn GAT-AAT | CTGGCTGGGGACATATTCCAGCTTGTCTAAGTCAGCGTTTTGAA CGGCGAACATTTGCA <u>A</u> ATCCATTTGAAGTCTACCGAGCATTGAGA ATTGTCAACCCAAGTCCATATATGACTTATT | 5845 |
| | AATAAGTCATATATGGACTTGGGTTGACAATTCTCAATGCTCGGTA GACTTCAAATGGAT <u>T</u> TGCAAATGTTGCGCGTTCAAACGCTGACTT AGGACAAGCTGGAATATGTCCCCAGCCAG | 5846 |
| | CATTGCA <u>A</u> ATCCATTT | 5847 |
| | AAATGGAT <u>T</u> TGCAAATG | 5848 |

Example 31

Production of modified starch in plants

[259] A principal aim of biotechnology is the improvement of crop plants for food value, agriculture, and to produce a range of plant-derived raw materials. Along with oils, fats and proteins, polysaccharides constitute the main raw materials derived from plants, and apart from cellulose, the storage polymer starch is the most important polysaccharide raw material. Starch is derived from a range of plants, but maize is the most important cultivated plant for the production of starch.

[260] The polysaccharide starch is a polymer made up of glucose molecules. However, starch is not a homogeneous raw material and is, in fact, a highly complex mixture of various types of molecules which differ from each other, for example, in their degree of polymerization and in the degree of branching of the glucose chains. For example, amylose-starch is a basically non-branched polymer made up of α -1,4-glycosidically branched glucose molecules, and amylopectin-starch is a complex mixture of variously branched glucose chains. The branching results from additional α -1,6-glycosidic linkages. In plants from which starch is typically isolated, for example maize or potato, the starch is approximately 25% amylose-starch and 75% amylopectin-starch.

[261] In maize, various mutants in starch metabolism are known, for example *waxy*, *sugary*, *shrunk* and *opaque-2*. In addition to producing a modified starch, these mutations greatly improve grain quality in maize, and thus expand the use of maize not only as the food but also for the important industrial materials in food chemistry. It would therefore be advantageous to be able readily to obtain mutants in these genes in particular maize genotypes as well as other plants. Such plants can be obtained, for example, using traditional breeding methods and through specific genetic modification by means of recombinant DNA techniques.

[262] The attached tables disclose exemplary oligonucleotide base sequences which can be used to generate site-specific mutations in genes involved in starch metabolism.

Table 38
Genome-Altering Oligos Conferring Increased Starch

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Ala99Lys GCA-AAA | GAAC TTGAGACTGAGAAAAGGGATCCAAGGACAGTTGCTTCCATT ATTCTTGGAGGTGGA AA AGGAACTCGACTCTTTCCTCTCACAAAA CGCCGCGCCAAGCCTGCCGTTCTATCGGGG | 5849 |
| | CCCCGATAGGAACGGCAGGCTTGGCGCGGCGTTTTGTGAGAGGA AAGAGTCGAGTTCCTTTCCACCTCCAAGAATAATGGAAGCAACT GTCCTTGGATCCCTTTCTCAGTCTCAAGTTC | 5850 |
| | GAGGTGGA AA AGGAACT | 5851 |
| | AGTTCCTTTCCACCTC | 5852 |
| Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Pro127Leu CCA-CTA | CAAAACGCGCGCCAAGCCTGCCGTTCTATCGGGGGAGCCTAT AGGTTGATAGATGTACTAATGAGCAATTGTATTAACAGCGGAATCA ACAAAGTCTACATACTCACACAATATAACTC | 5853 |
| | GAGTTATATTGTGTGAGTATGTAGACTTTGTTGATTCCGCTGTAA TACAATTGCTCATTAGTACATCTATCAACCTATAGGCTCCCCCGAT AGGAACGGCAGGCTTGGCGCGGCGTTTTG | 5854 |
| | AGATGTACTAATGAGCA | 5855 |
| | TGCTCATTAGTACATCT | 5856 |
| Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAT | TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGC TTACAACCTCCAAT AAT CCTTGGCTTTGGAGATGGCTATGTTGAGGTT CTTGCGGCCACTCAAACGCCAGGAGAATC | 5857 |
| | GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCA TCTCCAAAGCCAAG ATT ATTGGAGTTGTAAGCACGGGCTAAATGC CTGTTCAATGATGCTGAGTTATATTGTGTGA | 5858 |
| | CTCCAAT AAT CCTTGGCT | 5859 |
| | AGCCAAG ATT ATTGGAG | 5860 |
| Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly162Asn GGA-AAC | TCACACAATATAACTCAGCATCATTGAACAGGCATTTAGCCCGTGC TTACAACCTCCAAT AAC CCTTGGCTTTGGAGATGGCTATGTTGAGGTT CTTGCGGCCACTCAAACGCCAGGAGAATC | 5861 |
| | GATTCTCCTGGCGTTTGAGTGGCCGCAAGAACCTCAACATAGCCA TCTCCAAAGCCAAG GTT ATTGGAGTTGTAAGCACGGGCTAAATGC CTGTTCAATGATGCTGAGTTATATTGTGTGA | 5862 |
| | CTCCAAT AAC CCTTGGCT | 5863 |
| | AGCCAAG GTT ATTGGAG | 5864 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Asn100Lys AAT-AAA | GTTTGAGAGAAGAAAGGTAGACCCGCAAAATGTGGCTGCAATCAT TCTAGGAGGAGGCAAAGGAGCTAAACTCTTCCCTCTTACAATGAG AGCCGCAACACCAGCTGTAAATATTCATCTT | 5865 |
| | AAGATGAATATTTACAGCTGGTGTGCGGCTCTCATTGTAAGAGG GAAGAGTTTAGCTCCTTTGCCTCCTCCTAGAATGATTGCAGCCAC ATTTTGCGGGTCTACCTTTCTTCTCTCAAAC | 5866 |
| | GGAGGCAAAGGAGCTAA | 5867 |
| | TTAGCTCCTTTGCCTCC | 5868 |
| Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Pro128Leu CCG-CTG | CTTGTGTCTTCAAATTATGTTAGGTTCTGTTGGTGGATGCTACAG GCTGATCGATATCCTGATGAGTAACTGTATTAACAGCTGCATCAAC AAGATATTTGTGCTGACACAGTTCAACTC | 5869 |
| | GAGTTGAAGTGTGTCAGCACAAATATCTTGTGATGCAGCTGTTAA TACAGTTACTCATCAGGATATCGATCAGCCTGTAGCATCCACCAA CAGGAACCTAACATAATTTGAAGACACAAG | 5870 |
| | CGATATCCTGATGAGTA | 5871 |
| | TACTCATCAGGATATCG | 5872 |
| Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly163Asn GGC-AAT | TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAAC TTATTTTGGGAATAATATAAACTTTGGAGGTGGTTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC | 5873 |
| | GCTGAGAGTTATTATTGTCATAGTGTGTTGTACCTCTACGAAACCAC CTCCAAAGTTTATATTATTCCCAAAATAAGTTTCGTGCTAAATGTGCG ATTAAGGGAAGCTGAGTTGAACTGTGTCA | 5874 |
| | TGGGAATAATATAAACT | 5875 |
| | AGTTTATATTATTCCCA | 5876 |
| Increased Starch ADPGPP <i>Arabidopsis thaliana</i> Gly163Asn GGC-AAC | TGACACAGTTCAACTCAGCTTCCCTTAATCGACATTTAGCACGAAC TTATTTTGGGAATAACATAAACTTTGGAGGTGGTTTCGTAGAGGTA CAAACACTATGACAATAATAACTCTCAGC | 5877 |
| | GCTGAGAGTTATTATTGTCATAGTGTGTTGTACCTCTACGAAACCAC CTCCAAAGTTTATGTTATTCCCAAAATAAGTTTCGTGCTAAATGTGCG ATTAAGGGAAGCTGAGTTGAACTGTGTCA | 5878 |
| | TGGGAATAACATAAACT | 5879 |
| | AGTTTATGTTATTCCCA | 5880 |
| Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Val94Lys GTT-AAA | TTGAGGAACAACCAACGGCAGATCCAAAAGCTGTTGCCTCTGTCA TTCTAGGTGGTGGTAAAGGAACTCGTCTTTTCTCTTACAAGCA GAAGAGCTAAACCAGCTGTTCTATTGGTGG | 5881 |
| | CCACCAATAGGAACAGCTGGTTTAGCTCTTCTGCTTGTAAGAGGA AAAAGACGAGTTCCCTTACCACCACCTAGAATGACAGAGGCAACA GCTTTTGGATCTGCCGTTGGTTGTTCTCTCAA | 5882 |
| | TGGTGGTAAAGGAACTC | 5883 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | GAGTTCCTTTACCACCA | 5884 |
| Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Pro122Leu CCA-CAA | CAAGCAGAAGAGCTAAACCAGCTGTTCTATTGGTGGTTGTTACC GGCTAATTGATGTACAATGAGTAACTGCATTAACAGTGGCATA GGAAAATTTTCATCTTAACACAGTTCAATTC | 5885 |
| | GAATTGAACTGTGTTAAGATGAAAATTTTCCGTATGCCACTGTTAA TGCAGTTACTCATTGTACATCAATTAGCCGGTAACAACCACCAAT AGGAACAGCTGGTTTAGCTCTTCTGCTTG | 5886 |
| | TGATGTACAATGAGTA | 5887 |
| | TACTCATTGTACATCA | 5888 |
| Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Gly158Asn GGA-AAT | CACAGTTCAATTCCTTTTCCCTCAATCGTCACCTTGCCCGCACGTA TAATTTTGGAAATAATGTGGGTTTTGGAGATGGATTTGTGGAGGTT TTAGCTGCAACCCAGACTCCAGGGGATGC | 5889 |
| | GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCA TCTCCAAAACCCACATTATTTCCAAAATTATACGTGCGGGCAAGGT GACGATTGAGGGAAAAGGAATTGAACTGTG | 5890 |
| | TGGAAATAATGTGGGTT | 5891 |
| | AACCCACATTATTTCCA | 5892 |
| Increased Starch ADPGPP <i>Lycopersicon esculentum</i> Gly158Asn GGA-AAC | CACAGTTCAATTCCTTTTCCCTCAATCGTCACCTTGCCCGCACGTA TAATTTTGGAAATAACGTGGGTTTTGGAGATGGATTTGTGGAGGT TTTAGCTGCAACCCAGACTCCAGGGGATGC | 5893 |
| | GCATCCCCTGGAGTCTGGGTTGCAGCTAAAACCTCCACAAATCCA TCTCCAAAACCCACGTTATTTCCAAAATTATACGTGCGGGCAAGGT GACGATTGAGGGAAAAGGAATTGAACTGTG | 5894 |
| | TGGAAATAACGTGGGTT | 5895 |
| | AACCCACGTTATTTCCA | 5896 |
| Increased Starch ADPGPP <i>Cicer arietinum</i> Ala101Lys GCT-AAA | ACGTAGATTTGGAAAAAGAGACCCAAGTACAGTTGTAGCAATTAT ACTAGGTGGAGGTAAAGGAACTCGTCTCTTCCCTCTCACCAAGCG ACGAGCCAAGCCTGCTGTTCCAATTGGAGG | 5897 |
| | CCTCCAATTGGAACAGCAGGCTTGGCTCGTCTGCTTGGTGAGAGG GAAGAGACGAGTTCTTTACCTCCACCTAGTATAATTGCTACAAC GTACTTGGGTCTCTTTTTTCCAAATCTACGT | 5898 |
| | TGGAGGTAAGGAACTC | 5899 |
| | GAGTTCCTTTACCTCCA | 5900 |
| Increased Starch ADPGPP <i>Cicer arietinum</i> Pro129Leu CCA-CTA | CCAAGCGACGAGCCAAGCCTGCTGTTCCAATTGGAGGTGCTTATA GGCTGATAGATGTACTAATGAGTAACTGCATCAATAGTGGGATCA ACAAAGTATACATTCTCACTCAATTTAATTC | 5901 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | GAATTAAATTGAGTGAGAATGTATACTTTGTTGATCCCACTATTGA TGCAGTTACTCATTAGTACATCTATCAGCCTATAAGCACCTCCAAT TGGAACAGCAGGCTTGGCTCGTCGCTTGG | 5902 |
| | AGATGTACTAATGAGTA | 5903 |
| | TACTCATTAGTACATCT | 5904 |
| Increased Starch ADPGPP <i>Cicer arietinum</i> Gly165Asn GGA-AAT | CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAACTCTGGTACTAATGTCACTTTTGGAGATGGCTATGTTGAGGTT CTTGCAAGCAACTCAAACCTCCAGGGGAGCA | 5905 |
| | TGCTCCCCTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCA TCTCCAAAAGTGACATTAGTACCAGAGTTATAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAATTGAG | 5906 |
| | TGGTACTAATGTCACTT | 5907 |
| | AAGTGACATTAGTACCA | 5908 |
| Increased Starch ADPGPP <i>Cicer arietinum</i> Gly165Asn GGA-AAC | CTCAATTTAATTCAGCCTCACTCAACAGGCATATTGCACGTGCTTA TAACTCTGGTACTAACGTCACTTTTGGAGATGGCTATGTTGAGGTT CTTGCAAGCAACTCAAACCTCCAGGGGAGCA | 5909 |
| | TGCTCCCCTGGAGTTTGAGTTGCTGCAAGAACCTCAACATAGCCA TCTCCAAAAGTGACGTTAGTACCAGAGTTATAAGCACGTGCAATAT GCCTGTTGAGTGAGGCTGAATTAATTGAG | 5910 |
| | TGGTACTAACGTCACTT | 5911 |
| | AAGTGACGTTAGTACCA | 5912 |
| Increased Starch ADPGPP <i>Ipomoea batatas</i> Ala94Lys GCA-AAA | ATATTGGAGAGGCGTCGGGGCAAACCCTAAGAATGTGGCTGCAATC ATACTGCCAGGCGGTAAAGGGACACACCTATTCCCTCTCACC AAT CGAGCTGCAACCCCTGCTGTTCCACTTGGAG | 5913 |
| | CTCCAAGTGGAAACAGCAGGGGTTGCAGCTCGATTGGTGAGAGGG AATAGGTGTGTCCCTTTACCGCCTGGCAGTATGATTGCAGCCACA TTCTTAGGGTTTGCCCGACGCCTCTCCAATAT | 5914 |
| | CAGGCGGTAAAGGGACA | 5915 |
| | TGTCCCTTTACCGCCTG | 5916 |
| Increased Starch ADPGPP <i>Ipomoea batatas</i> Pro122Leu CCA-CTA | CCAATCGAGCTGCAACCCCTGCTGTTCCACTTGGAGGATGCTATA GGTTGATCGACATTCTAATGAGCAACTGCATCAACAGCGGGGTTA ACAAGATCTTTGTGCTGACCCAGTTCAATTC | 5917 |
| | GAATTGAACTGGGTGAGCACAAGATCTTGTTAACCCCGCTGTTG ATGCAGTTGCTCATTAGAATGTGATCAACCTATAGCATCCTCCAA GTGGAACAGCAGGGGTTGCAGCTCGATTGG | 5918 |
| | CGACATTCTAATGAGCA | 5919 |
| | TGCTCATTAGAATGTGCG | 5920 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Increased Starch ADPGPP <i>Ipomoea batatas</i> Gly157Asn GGT-AAT | TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTAC CGTCTTTGGCAAT <u>AAT</u> GTGAGCTTCGGAGATGGATTTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC | 5921 |
| | GTTTCCCTTGTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCA TCTCCGAAGCTCAC <u>ATT</u> ATTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGAACTGGGTCA | 5922 |
| | TGGCAAT <u>AAT</u> GTGAGCT | 5923 |
| | AGCTCAC <u>ATT</u> ATTGCCA | 5924 |
| Increased Starch ADPGPP <i>Ipomoea batatas</i> Gly157Asn GGT-AAC | TGACCCAGTTCAATTCAGCTTCTCTTAACCGTCACATTTCCCGTAC CGTCTTTGGCAAT <u>AAC</u> GTGAGCTTCGGAGATGGATTTGTTGAGGT GCTGGCTGCAACCCAAACACAAGGGGAAAC | 5925 |
| | GTTTCCCTTGTGTTTGGGTTGCAGCCAGCACCTCAACAAATCCA TCTCCGAAGCTCAC <u>GTT</u> ATTGCCAAAGACGGTACGGGAAATGTGA CGGTTAAGAGAAGCTGAATTGAACTGGGTCA | 5926 |
| | TGGCAAT <u>AAC</u> GTGAGCT | 5927 |
| | AGCTCAC <u>GTT</u> ATTGCCA | 5928 |
| Increased Starch ADPGPP <i>Oryza sativa</i> Thr96Lys ACC-AAA | CATTCCGGAGGAACTTTGCGGATCCAAATGAGGTTGCTGCTGTTA TATTGGGTGGTGGCA <u>AA</u> GGGACTCAACTTTTTCTCTCACAAGCA CAAGGGCCACGCCTGCTGTTCTATTGGAGG | 5929 |
| | CCTCCAATAGGAACAGCAGGCGTGGCCCTTGTGCTTGTGAGAGG AAAAAGTTGAGTCCCTTTGCCACCACCCAATATAACAGCAGCAAC CTCATTTGGATCCGCAAAGTTCCTCCGGAATG | 5930 |
| | TGGTGGCA <u>AA</u> GGGACTC | 5931 |
| | GAGTCCCTTTGCCACCA | 5932 |
| Increased Starch ADPGPP <i>Oryza sativa</i> Pro124Leu CCC-CTC | CAAGCACAAGGGCCACGCCTGCTGTTCTATTGGAGGATGCTATA GGCTTATCGATATCC <u>T</u> CATGAGCAACTGTTTCAACAGTGGCATAAA CAAGATATTCATAATGACTCAATTCAACTC | 5933 |
| | GAGTTGAATTGAGTCATTATGAATATCTTGTTTATGCCACTGTTGA AACAGTTGCTCATG <u>A</u> GGATATCGATAAGCCTATAGCATCCTCCAAT AGGAACAGCAGGCGTGGCCCTTGTGCTTG | 5934 |
| | CGATATCC <u>T</u> CATGAGCA | 5935 |
| | TGCTCATG <u>A</u> GGATATCG | 5936 |
| Increased Starch ADPGPP <i>Oryza sativa</i> Gly159Asn GGA-AAT | TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTAC GTACCTTGGTGGT <u>AAT</u> ATCAACTTTACTGATGGTTCTGTTGAGGTA TTAGCCGCTACACAAATGCCTGGGGAGGC | 5937 |
| | GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCA TCAGTAAAGTTGAT <u>ATT</u> ACCACCAAGGTACGTACGATGAATGTGA CGATTAAGAGATGCTGAGTTGAATTGAGTCA | 5938 |
| | TGGTGGT <u>AAT</u> ATCAACT | 5939 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| | AGTTGAT <u>ATT</u> ACCACCA | 5940 |
| Increased Starch ADPGPP <i>Oryza sativa</i> Gly159Asn GGA-AAC | TGACTCAATTCAACTCAGCATCTCTTAATCGTCACATTCATCGTAC GTACCTTGTTGGT <u>AAC</u> ATCAACTTTACTGATGGTTCTGTTGAGGTA TTAGCCGCTACACAAATGCCTGGGGAGGC | 5941 |
| | GCCTCCCCAGGCATTTGTGTAGCGGCTAATACCTCAACAGAACCA TCAGTAAAGTTGAT <u>GTT</u> ACCACCAAGGTACGTACGATGAATGTGA CGATTAAGAGATGCTGAGTTGAATTGAGTCA | 5942 |
| | TGGTGGT <u>AAC</u> ATCAACT | 5943 |
| | AGTTGAT <u>GTT</u> ACCACCA | 5944 |
| Increased Starch ADPGPP <i>Triticum aestivum</i> Thr80Lys ACC-AAA | GTCCTTCAGGAGGATTAAGCGATCCGAACGAGGTTGCGGCCGTC ATACTCGGCGGCGGCA <u>AA</u> GGGACTCAGCTCTTCCCACTCACGAG CACAAGGGCCACACCTGCTGTTCTATTGGAGG | 5945 |
| | CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTCGTGAGTGG GAAGAGCTGAGTCCCT <u>TT</u> GCCGCCGCCGAGTATGACGGCCGCAA CCTCGTTCCGATCGCTTAATCCTCCTGAAGGAC | 5946 |
| | CGGCGGCA <u>AA</u> GGGACTC | 5947 |
| | GAGTCCCT <u>TT</u> GCCGCCG | 5948 |
| Increased Starch ADPGPP <i>Triticum aestivum</i> Pro108Leu CCC-CTC | CGAGCACAAGGGCCACACCTGCTGTTCTATTGGAGGATGTTACA GGCTCATCGACATTCTCATGAGCAACTGCTTCAACAGTGGCATCA ACAAGATATTCGTCATGACCCAGTTCAACTC | 5949 |
| | GAGTTGAAGTGGGTCATGACGAATATCTTGTTGATGCCACTGTTG AAGCAGTTGCTCATG <u>AGA</u> ATGTCGATGAGCCTGTAACATCCTCCA ATAGGAACAGCAGGTGTGGCCCTTGTGCTCG | 5950 |
| | CGACATTCTCATGAGCA | 5951 |
| | TGCTCATG <u>AGA</u> ATGTCTG | 5952 |
| Increased Starch ADPGPP <i>Triticum aestivum</i> Gly143Asn GGA-AAT | TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG <u>AAT</u> ATCAATTTCACTGATGGATCCGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC | 5953 |
| | GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC ATCAGTGAAATTGAT <u>ATT</u> CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACTGGGTCA | 5954 |
| | CGGCGGG <u>AAT</u> ATCAATT | 5955 |
| | AATTGAT <u>ATT</u> CCCGCCG | 5956 |
| Increased Starch ADPGPP <i>Triticum aestivum</i> Gly143Asn GGA-AAC | TGACCCAGTTCAACTCGGCCTCCCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG <u>AAC</u> ATCAATTTCACTGATGGATCCGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC | 5957 |
| | GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACGGATCC ATCAGTGAAATTGAT <u>GTT</u> CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGGGAGGCCGAGTTGAACTGGGTCA | 5958 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | CGGCGGG <u>AAC</u> ATCAATT | 5959 |
| | AATTGAT <u>GTT</u> CCCGCCG | 5960 |
| Increased Starch ADPGPP <i>Oryza sativa</i> Thr95Lys ACT-AAA | CCTCCCGAAAGAATTATGCTGATGCAAGCCACGTTTCTGCTGTCA TTTTGGGTGGAGGCA <u>AA</u> GGAGTTCAACTCTTTCCTCTGACAAGCA CAAGGGCTACCCCCGCTGTTCTGTTGGAGG | 5961 |
| | CCTCCAACAGGAACAGCGGGGGTAGCCCTTGCTTGTGCTGTCAGAGG AAAGAGTTGAACTCCTTGCCTCCACCCAAAATGACAGCAGAAAC GTGGCTTGCATCAGCATAATTCTTTCGGGAGG | 5962 |
| | TGGAGGCA <u>AA</u> GGAGTTC | 5963 |
| | GAACCTCCTTGCCTCCA | 5964 |
| Increased Starch ADPGPP <i>Oryza sativa</i> Pro123Leu CCT-CTT | CAAGCACAAGGGCTACCCCCGCTGTTCTGTTGGAGGATGTTACA GGCTTATTGACATCCTTATGAGCAATTGCTTCAATAGCGGAATAAA TAAATATTTGTGATGACTCAGTTCAATTC | 5965 |
| | GAATTGAAGTGAAGTCAACAAATATTTATTTATTCGGCTATTGAA GCAATTGCTCATA <u>AG</u> GATGTCAATAAGCCTGTAACATCCTCCAACA GGAACAGCGGGGGTAGCCCTTGCTTG | 5966 |
| | TGACATCCTTATGAGCA | 5967 |
| | TGCTCATA <u>AG</u> GATGTCA | 5968 |
| Increased Starch ADPGPP <i>Oryza sativa</i> Gly158Asn GGG-AAT | TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATACA TACCTTGGTGGG <u>AAT</u> ATCAACTTTACTGATGGGTCTGTGCAGGTA TTGGCTGCTACACAAATGCCTGACGAACC | 5969 |
| | GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGAT <u>ATT</u> CCCACCAAGGTATGTATGATGGATATGGC GATTAAGAGAAGCAGAATTGAACTGAGTCA | 5970 |
| | TGGTGGG <u>AAT</u> ATCAACT | 5971 |
| | AGTTGAT <u>ATT</u> CCCACCA | 5972 |
| Increased Starch ADPGPP <i>Oryza sativa</i> Gly158Asn GGG-AAC | TGACTCAGTTCAATTCTGCTTCTCTTAATCGCCATATCCATCATACA TACCTTGGTGGG <u>AAC</u> ATCAACTTTACTGATGGGTCTGTGCAGGTA TTGGCTGCTACACAAATGCCTGACGAACC | 5973 |
| | GGTTCGTCAGGCATTTGTGTAGCAGCCAATACCTGCACAGACCCA TCAGTAAAGTTGAT <u>GTT</u> CCCACCAAGGTATGTATGATGGATATGG CGATTAAGAGAAGCAGAATTGAACTGAGTCA | 5974 |
| | TGGTGGG <u>AAC</u> ATCAACT | 5975 |
| | AGTTGAT <u>GTT</u> CCCACCA | 5976 |
| Increased Starch ADPGPP <i>Triticum aestivum</i> Thr99Lys ACC-AAA | CCTTCGCGAGGAATTACGCCGATCCGAACGAGGTCGCGGCCGTC ATACTCGGCGGTGGCA <u>AA</u> GGGACTCAGCTCTTCCCTCTCACAAG CACAAGGGCCACACCTGCTGTTCTATTGGAGG | 5977 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | CCTCCAATAGGAACAGCAGGTGTGGCCCTTGTGCTTGTGAGAGG GAAGAGCTGAGTCCC <u>TT</u> TGCCACCGCCGAGTATGACGGCCGCGA CCTCGTTCGGATCGGCGTAATTCCTGCGGAAGG | 5978 |
| | CGGTGGCA <u>AA</u> GGGACTC | 5979 |
| | GAGTCCC <u>TT</u> TGCCACCG | 5980 |
| Increased Starch ADPGPP <i>Triticum aestivum</i> Pro127Leu CCC-CTC | CAAGCACAAGGGCCACACCTGCTGTTCTTATTGGAGGATGTTACA GGCTCATCGATATTCTCATGAGCAACTGCTTCAATAGTGGCATCAA CAAGATATTCGTCATGACGCAGTTCAACTC | 5981 |
| | GAGTTGAACTGCGTCATGACGAATATCTTGTTGATGCCACTATTGA AGCAGTTGCTCATG <u>AGA</u> AATATCGATGAGCCTGTAACATCCTCCAA TAGGAACAGCAGGTGTGGCCCTTGTGCTTG | 5982 |
| | CGATATTC <u>T</u> CATGAGCA | 5983 |
| | TGCTCATG <u>AGA</u> AATATCG | 5984 |
| Increased Starch ADPGPP <i>Triticum aestivum</i> Gly162Asn GGA-AAT | TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG <u>AA</u> TATCAATTTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC | 5985 |
| | GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC ATCAGTGAAATTGAT <u>ATT</u> CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA | 5986 |
| | CGGCGGG <u>AA</u> TATCAATT | 5987 |
| | AATTGAT <u>ATT</u> CCCGCCG | 5988 |
| Increased Starch ADPGPP <i>Triticum aestivum</i> Gly162Asn GGA-AAC | TGACGCAGTTCAACTCGGCCTCTCTTAATCGTCACATTCACCGCA CCTACCTCGGCGGG <u>AA</u> CATCAATTTCACTGATGGATCTGTTGAGG TATTGGCCGCGACGCAAATGCCCGGGGAGGC | 5989 |
| | GCCTCCCCGGGCATTTGCGTCGCGGCCAATACCTCAACAGATCC ATCAGTGAAATTGAT <u>GTT</u> CCCGCCGAGGTAGGTGCGGTGAATGTG ACGATTAAGAGAGGCCGAGTTGAACTGCGTCA | 5990 |
| | CGGCGGG <u>AA</u> CATCAATT | 5991 |
| | AATTGAT <u>GTT</u> CCCGCCG | 5992 |
| Increased Starch ADPGPP <i>Zea mays</i> Thr96Lys ACC-AAA | CTTTTCGGAGGAATTATGCTGATCCTAATGAAGTCGCTGCCGTCA TTTTGGGTGGTGGTA <u>AA</u> GGGACTCAGCTTTTCCCTCTCACAAGCA CAAGGGCCACCCCTGCTGTTCTTATTGGAGG | 5993 |
| | CCTCCAATAGGAACAGCAGGGGTGGCCCTTGTGCTTGTGAGAGG GAAAAGCTGAGTCCC <u>TTT</u> TACCACCACCCAAAATGACGGCAGCGAC TTCATTAGGATCAGCATAATTCCTCCGAAAAG | 5994 |
| | TGGTGGTA <u>AA</u> GGGACTC | 5995 |
| | GAGTCCC <u>TTT</u> TACCACCA | 5996 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Increased Starch ADPGPP <i>Zea mays</i> Pro124Leu CCC-CTC | CAAGCACAAGGGGCCACCCCTGCTGTTCTATTGGAGGATGTTACA GGCTTATTGATATCCICATGAGCAACTGTTTCAACAGTGGCATAAA CAAGATATTTGTTATGACTCAGTTCAACTC | 5997 |
| | GAGTTGAACTGAGTCATAACAAATATCTTGTTTATGCCACTGTTGA AACAGTTGCTCATGAGGATATCAATAAGCCTGTAACATCCTCCAAT AGGAACAGCAGGGGTGGCCCTTGTGCTTG | 5998 |
| | TGATATCCICATGAGCA | 5999 |
| | TGCTCATGAGGATATCA | 6000 |
| Increased Starch ADPGPP <i>Zea mays</i> Gly159Asn GGG-AAT | TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTAC CTATCTTGGTGGGAATATCAACTTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCTGGGGAGGC | 6001 |
| | GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCA TCAGTGAAGTTGATATTCCCACCAAGATAGGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAACTGAGTCA | 6002 |
| | TGGTGGGAATATCAACT | 6003 |
| | AGTTGATATTCCCACCA | 6004 |
| Increased Starch ADPGPP <i>Zea mays</i> Gly159Asn GGG-AAC | TGACTCAGTTCAACTCAGCTTCTCTTAACCGTCACATTCATCGTAC CTATCTTGGTGGGAACATCAACTTCACTGATGGATCTGTTGAGGT GCTGGCTGCAACACAAATGCCTGGGGAGGC | 6005 |
| | GCCTCCCCAGGCATTTGTGTTGCAGCCAGCACCTCAACAGATCCA TCAGTGAAGTTGATGTTCCCACCAAGATAGGTACGATGAATGTGA CGGTTAAGAGAAGCTGAGTTGAACTGAGTCA | 6006 |
| | TGGTGGGAACATCAACT | 6007 |
| | AGTTGATGTTCCCACCA | 6008 |
| Increased Starch ADPGPP <i>Solanum tuberosum</i> Ala58Lys GCG-AAG | CTTGAGAGGCAAAAGAAGGGCGATGCAAGGACAGTAGTAGCAAT CATTCTAGGAGGGGGAAGGGGAACCTCGTCTTTTCCCCCTCACCAA ACGTCGTGCTAAGCCTGCCGTTCCAATGGGAG | 6009 |
| | CTCCCATTTGGAACGGCAGGCTTAGCACGACGTTTGGTGAGGGGG AAAAGACGAGTTCCCTTTCCCCCTCCTAGAATGATTGCTACTACTG TCCTTGCATCGCCCTTCTTTTGCCTCTCAAG | 6010 |
| | GAGGGGGAAAGGGGAAC | 6011 |
| | AGTTCCCITCCCCCTC | 6012 |
| Increased Starch ADPGPP <i>Solanum tuberosum</i> Pro86Leu CCA-CTA | CCAAACGTCTGTGCTAAGCCTGCCGTTCCAATGGGAGGAGCATATA GGCTAATTGATGTACTAATGAGCAACTGTATTAACAGTGGCATCAA CAAAGTATACATTCTCACTCAATTCAACTC | 6013 |
| | GAGTTGAATTGAGTGAGAATGTATACTTTGTTGATGCCACTGTTAA TACAGTTGCTCATTAGTACATCAATTAGCCTATATGCTCCTCCCAT TGGAACGGCAGGCTTAGCACGACGTTTGG | 6014 |
| | TGATGTACTAATGAGCA | 6015 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | TGCTCATT <u>AG</u> TACATCA | 6016 |
| Increased Starch ADPGPP <i>Solanum tuberosum</i> Gly122Asn GGG-AAT | CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTTGGCAAT <u>AAT</u> GTACATTTCGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT | 6017 |
| | AATTCACCTGGTGTTTGAGTTGCTGCTAAGACCTCGACATAGCCA CTCTCGAATGTGAC <u>ATT</u> ATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTAAAGTGAGGCTGAGTTGAATTGAG | 6018 |
| | TGGCAAT <u>AAT</u> GTACAT | 6019 |
| | ATGTGAC <u>ATT</u> ATTGCCA | 6020 |
| Increased Starch ADPGPP <i>Solanum tuberosum</i> Gly122Asn GGG-AAC | CTCAATTCAACTCAGCCTCACTTAACAGGCATATAGCTCGTGCTTA CAACTTTGGCAAT <u>AAC</u> GTACATTTCGAGAGTGGCTATGTCGAGGT CTTAGCAGCAACTCAAACACCAGGTGAATT | 6021 |
| | AATTCACCTGGTGTTTGAGTTGCTGCTAAGACCTCGACATAGCCA CTCTCGAATGTGAC <u>GTT</u> ATTGCCAAAGTTGTAAGCACGAGCTATAT GCCTGTAAAGTGAGGCTGAGTTGAATTGAG | 6022 |
| | TGGCAAT <u>AAC</u> GTACAT | 6023 |
| | ATGTGAC <u>GTT</u> ATTGCCA | 6024 |
| Increased Starch ADPGPP <i>Beta vulgaris</i> Ala98Lys GCT-AAA | TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGT <u>AAAG</u> GGACTCGCCTCTTTCCTCTTACTAGCAG GAGAGCTAAGCCAGCAGTGCCAATTGGAGG | 6025 |
| | CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCGAGTCCC <u>TTT</u> ACCACCACCCAGCACAAATTGCAGCCACA TTTTTTGGGTCAGCTTTTGGAGATTCAAATA | 6026 |
| | TGGTGGT <u>AAAG</u> GGACTC | 6027 |
| | GAGTCCC <u>TTT</u> ACCACCA | 6028 |
| Increased Starch ADPGPP <i>Beta vulgaris</i> Ala98Lys GCT-AAC | TATTTGAATCTCCAAAAGCTGACCCAAAAAATGTGGCTGCAATTGT GCTGGGTGGTGGT <u>AAC</u> GGGACTCGCCTCTTTCCTCTTACTAGCAG GAGAGCTAAGCCAGCAGTGCCAATTGGAGG | 6029 |
| | CCTCCAATTGGCACTGCTGGCTTAGCTCTCCTGCTAGTAAGAGGA AAGAGGCGAGTCCC <u>GTT</u> ACCACCACCCAGCACAAATTGCAGCCAC ATTTTTGGGTCAGCTTTTGGAGATTCAAATA | 6030 |
| | TGGTGGT <u>AAC</u> GGGACTC | 6031 |
| | GAGTCCC <u>GTT</u> ACCACCA | 6032 |
| Increased Starch ADPGPP <i>Beta vulgaris</i> Pro126Leu CCT-CTT | CTAGCAGGAGAGCTAAGCCAGCAGTGCCAATTGGAGGGTGTAC AGGCTGATTGATGTGCT <u>T</u> ATGAGCAACTGCATCAACAGTGGCATT AGAAAGATTTTCATTCTTACCCAGTTCAATTC | 6033 |
| | GAATTGAAGTGGGTAAGAATGAAAATCTTTCTAATGCCACTGTTGA TGCAGTTGCTCATA <u>AG</u> CACATCAATCAGCCTGTAACACCCTCCAA TTGGCACTGCTGGCTTAGCTCTCCTGCTAG | 6034 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| | TGATGTGCTTATGAGCA | 6035 |
| | TGCTCATAAGCACATCA | 6036 |
| Increased Starch ADPGPP <i>Beta vulgaris</i> Gly162Asn GGT-AAT | CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTTGGAGATAATGTGAATTTGGGGATGGCTTTGTGGAGGTT TTTGCTGCTACACAAACACCTGGAGAATC | 6037 |
| | GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATTCACATTATCTCCAAAATTATAGGTTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAACTGGG | 6038 |
| | TGGAGATAATGTGAATT | 6039 |
| | AATTCACATTATCTCCA | 6040 |
| Increased Starch ADPGPP <i>Beta vulgaris</i> Gly162Asn GGT-AAC | CCCAGTTCAATTCGTTTTCGCTTAATCGTCATCTTGCTCGAACCTA TAATTTTGGAGATAACGTGAATTTGGGGATGGCTTTGTGGAGGT TTTGCTGCTACACAAACACCTGGAGAATC | 6041 |
| | GATTCTCCAGGTGTTTGTGTAGCAGCAAAAACCTCCACAAAGCCA TCCCCAAAATTCACGTTATCTCCAAAATTATAGGTTTCGAGCAAGAT GACGATTAAGCGAAAACGAATTGAACTGGG | 6042 |
| | TGGAGATAACGTGAATT | 6043 |
| | AATTCACGTTATCTCCA | 6044 |

Table 39
Oligonucleotides to produce plants with waxy starch

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser12Term TCA-TGA | GAATCCAGGTAAACGGGTAGTTCATAATGGCAACTGTGACTGCTT CTTCTAACTTTGTGTGAAGAACTTCACTTTTCAACAATCATGGTGCT TCTTCATGCTCTGATGTCGCTCAGATTAC | 6045 |
| | GTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGTTG AAAAGTGAAGTTCTTACACACAAAGTTAGAAGAAGCAGTCACAGTTG CCATTATGAACTACCCGTTTACCTGGATTG | 6046 |
| | CTTTGTGTGAAGAACTT | 6047 |
| | AAGTTCTTACACACAAAG | 6048 |
| Waxy starch GBSS <i>Arabidopsis thaliana</i> Arg13Term AGA-TGA | ATCCAGGTAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTT CTAACTTTGTGTCACTGAAGTTCCTTTTCAACAATCATGGTGCTTCT TCATGCTCTGATGTCGCTCAGATTACCT | 6049 |
| | AGGTAATCTGAGCGACATCAGAGCATGAAGAAGCACCATGATTGT TGAAAAGTGAAGTTCAATGACACAAAGTTAGAAGAAGCAGTCACAGT TGCCATTATGAACTACCCGTTTACCTGGAT | 6050 |
| | TTGTGTCACTGAAGTTC | 6051 |
| | TGAAGTTCAATGACACAA | 6052 |
| Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser15Term TCA-TGA | TAAACGGGTAGTTCATAATGGCAACTGTGACTGCTTCTTCTAACTT TGTGTCAAGAACTTGACTTTTCAACAATCATGGTGCTTCTTCATGCT CTGATGTCGCTCAGATTACCTTAAAAGG | 6053 |
| | CCTTTTAAGGTAATCTGAGCGACATCAGAGCATGAAGAAGCACCAT GATTGTTGAAAAGTCAAGTTCTTGACACAAAGTTAGAAGAAGCAGT CACAGTTGCCATTATGAACTACCCGTTTA | 6054 |
| | AAGAACTTGACTTTTCA | 6055 |
| | TGAAAAGTCAAGTTCTT | 6056 |
| Waxy starch GBSS <i>Arabidopsis thaliana</i> Ser24Term TCA-TGA | TGACTGCTTCTTCTAACTTTGTGTCAAGAACTTCACTTTTCAACAAT CATGGTGCTTCTTGATGCTCTGATGTCGCTCAGATTACCTTAAAAG GCCAATCCTTGACTCATTGTGGGTTAAG | 6057 |
| | CTTAACCCACAATGAGTCAAGGATTGGCCTTTAAGGTAATCTGAG CGACATCAGAGCATCAAGAAGCACCATGATTGTTGAAAAGTGAAG TTCTTGACACAAAGTTAGAAGAAGCAGTCA | 6058 |
| | TGCTTCTTGATGCTCTG | 6059 |
| | CAGAGCATCAAGAAGCA | 6060 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Waxy starch GBSS <i>Arabidopsis thaliana</i> Cys25Term TGC-TGA | TGCTTCTTCTAACTTTGTGTCAAGAACTTCACTTTTCAACAATCATG GTGCTTCTTCATGATCTGATGTCGCTCAGATTACCTTAAAAGGCCA ATCCTTGACTCATTGTGGGTTAAGGTCA | 6061 |
| | TGACCTTAACCCACAATGAGTCAAGGATTGGCCTTTTAAGGTAATC TGAGCGACATCAGATCATGAAGAAGCACCATGATTGTTGAAAAGT GAAGTTCTTGACACAAAGTTAGAAGAAGCA | 6062 |
| | TCTTCATGATCTGATGT | 6063 |
| | ACATCAGATCATGAAGA | 6064 |
| Waxy starch GBSS <i>Antirrhinum majus</i> Lys24Term AAA-TAA | GTAACAGCTTCACAGTTGGTGTACATGTCCATGGTGGAGCAACG TCTTCACCGGATACTTAAACAACTTGGCCCAGGTTGGCCTCAGG AACCAGCAATTCACTCACAATGGGTTGAGAT | 6065 |
| | ATCTCAACCCATTGTGAGTGAATTGCTGGTTCCTGAGGCCAACCTG GGCCAAGTTTGTTTAAGTATCCGGTGAAGACGTTGCTCCACCATG GACATGTGACACCAACTGTGAAGCTGTTAC | 6066 |
| | CGGATACTTAAACAAAC | 6067 |
| | GTTTGTTTAAGTATCCG | 6068 |
| Waxy starch GBSS <i>Antirrhinum majus</i> Leu27Term TTG-TAG | CACAGTTGGTGTACATGTCCATGGTGGAGCAACGTCTTCACCGG ATACTAAACAACTAGGCCAGGTTGGCCTCAGGAACCAGCAAT TCACTCACAATGGGTTGAGATCAATAAACAT | 6069 |
| | ATGTTTATTGATCTCAACCCATTGTGAGTGAATTGCTGGTTCCTGA GGCCAACCTGGGCCAGTTTGTTTAGTATCCGGTGAAGACGTTG CTCCACCATGGACATGTGACACCAACTGTG | 6070 |
| | AACAACTAGGCCAGG | 6071 |
| | CCTGGGCCAGTTTGT | 6072 |
| Waxy starch GBSS <i>Antirrhinum majus</i> Gln29Term CAG-TAG | TTGGTGTACATGTCCATGGTGGAGCAACGTCTTCACCGGATACT AAAACAACTTGGCCAGGTTGGCCTCAGGAACCAGCAATTCAT CACAATGGGTTGAGATCAATAAACATGGTTG | 6073 |
| | CAACCATGTTTATTGATCTCAACCCATTGTGAGTGAATTGCTGGT CCTGAGGCCAACCTAGGCCAAGTTTGTTTAGTATCCGGTGAAGA CGTTGCTCCACCATGGACATGTGACACCAA | 6074 |
| | ACTTGGCCAGGTTGGC | 6075 |
| | GCCAACCTAGGCCAAGT | 6076 |
| Waxy starch GBSS <i>Antirrhinum majus</i> Gln35Term CAG-TAG | GGTGGAGCAACGTCTTCACCGGATACTAAACAACTTGGCCCAG GTTGGCCTCAGGAACAGCAATTCATCACAATGGGTTGAGATCA ATAAACATGGTTGATAAGCTTCAAATGAGGA | 6077 |
| | TCCTCATTTGAAGCTTATCAACCATGTTTATTGATCTCAACCCATTG TGAGTGAATTGCTAGTTCCTGAGGCCAACCTGGGCCAAGTTTGT TAGTATCCGGTGAAGACGTTGCTCCACC | 6078 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | TCAGGAAC <u>T</u> AGCAATTC | 6079 |
| | GAATTGCT <u>A</u> GTTCTGA | 6080 |
| Waxy starch GBSS <i>Antirrhinum majus</i> Gln36Term CAA-TAA | GGAGCAACGTCCTTCACCGGATACTAAAACAACTTGGCCCAGGTT GGCCTCAGGAACCAG <u>T</u> AATTCACCTCACAATGGGTTGAGATCAATAA ACATGGTTGATAAGCTTCAAATGAGGAACA | 6081 |
| | TGTTCTCATTTGAAGCTTATCAACCATGTTTATTGATCTCAACCCA TTGTGAGTGAATT <u>A</u> CTGGTTCCTGAGGCCAACCTGGGCCAAGTTT GTTTTAGTATCCGGTGAAGACGTTGCTCC | 6082 |
| | GGAACCAG <u>T</u> AATTCACCT | 6083 |
| | AGTGAATT <u>A</u> CTGGTTC | 6084 |
| Waxy starch GBSS <i>Ipomoea batatas</i> Gly20Term GGA-TGA | GTGATGGCGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTG GGGGTGCCACTTCT <u>T</u> GAGAATCAAAGTGGGGTTGGGTCAATTAG CCCTGAGGAGCCAAGCTGTGACTCACAATG | 6085 |
| | CATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCAACC CCACTTTTGATTCTC <u>A</u> AGAAGTGGCACCCCCACAGACATGAGAAA CAAAGTGTGAGGCAGTTATAGTCGCCATCAC | 6086 |
| | CCACTTCT <u>T</u> GAGAATCA | 6087 |
| | TGATTCTC <u>A</u> AGAAGTGG | 6088 |
| Waxy starch GBSS <i>Ipomoea batatas</i> Glu21Term GAA-TAA | ATGGCGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGG GTGCCACTTCTGGAT <u>A</u> AATCAAAGTGGGGTTGGGTCAATTAGCCC TGAGGAGCCAAGCTGTGACTCACAATGGGT | 6089 |
| | ACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGACCCA ACCCCACTTTTGATT <u>A</u> TCCAGAAGTGGCACCCCCACAGACATGAG AAACAAAGTGTGAGGCAGTTATAGTCGCCAT | 6090 |
| | CTTCTGGAT <u>A</u> AATCAAAA | 6091 |
| | TTTTGATT <u>A</u> TCCAGAAG | 6092 |
| Waxy starch GBSS <i>Ipomoea batatas</i> Ser22Term TCA-TGA | CGACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGC CACTTCTGGAGAAT <u>G</u> AAAAGTGGGGTTGGGTCAATTAGCCCTGAG GAGCCAAGCTGTGACTCACAATGGGTTGAG | 6093 |
| | CTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATTGA CCCAACCCCACTTTT <u>C</u> ATTCTCCAGAAGTGGCACCCCCACAGACAT GAGAAACAAAGTGTGAGGCAGTTATAGTCG | 6094 |
| | TGGAGAAT <u>G</u> AAAAGTGG | 6095 |
| | CCACTTTT <u>C</u> ATTCTCCA | 6096 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Waxy starch GBSS <i>Ipomoea batatas</i> Lys23Term AAA-TAA | ACTATAACTGCCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCA CTTCTGGAGAATCATTAAGTGGGGTTGGGTCAATTAGCCCTGAGGA GCCAAGCTGTGACTCACAATGGGTTGAGAC | 6097 |
| | GTCTCAACCCATTGTGAGTCACAGCTTGGCTCCTCAGGGCTAATT GACCCAACCCCACTTATGATTCTCCAGAAGTGGCACCCCCACAGA CATGAGAAACAAAGTGTGAGGCAGTTATAGT | 6098 |
| | GAGAATCATTAAGTGGGG | 6099 |
| | CCCCACTTATGATTCTC | 6100 |
| Waxy starch GBSS <i>Ipomoea batatas</i> Leu26Term TTG-TAG | CCTCACACTTTGTTTCTCATGTCTGTGGGGGTGCCACTTCTGGAGA ATCAAAAGTGGGGTAGGGTCAATTAGCCCTGAGGAGCCAAGCTGT GACTCACAATGGGTTGAGACCTGTGAACAA | 6101 |
| | TTGTTACAGGTCTCAACCCATTGTGAGTCACAGCTTGGCTCCTCA GGGCTAATTGACCCCTACCCCACTTTTGATTCTCCAGAAGTGGCACC CCCACAGACATGAGAAACAAAGTGTGAGG | 6102 |
| | AGTGGGGTAGGGTCAAT | 6103 |
| | ATTGACCCCTACCCCACT | 6104 |
| Waxy starch GBSS <i>Astragalus membranaeus</i> Tyr8Term TAT-TAG | CATCGGCGATTGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACG GTGACGGGGTCTTAGGTGGTGTGAGAAGCGCGTGCTTCAATTCC CAGGGAAGAACAGAAGCCAAAGTGAATTCA | 6105 |
| | TGAATTCACCTTTGGCTTCTGTTCTTCCCTGGGAATTGAAGCACGCG CTTCTCGACACCACCTAAGACCCCGTCACCGTTGCCATTCTGTGA GAGAGCAGTAAGGAGCAACAATCGCCGATG | 6106 |
| | GGGTCTTAGGTGGTGTC | 6107 |
| | GACACCACCTAAGACCC | 6108 |
| Waxy starch GBSS <i>Astragalus membranaeus</i> Ser11Term TCG-TAG | ATTGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACGGTGACGG GGTCTTATGTGGTGTAGAGAAGCGCGTGCTTCAATTCCCAGGGAA GAACAGAAGCCAAAGTGAATTCACCTCAGAA | 6109 |
| | TTCTGAGGTGAATTCACCTTTGGCTTCTGTTCTTCCCTGGGAATTGA AGCACGCGCTTCTCTACACCACATAAGACCCCGTCACCGTTGCCA TTCTGTGAGAGAGCAGTAAGGAGCAACAAT | 6110 |
| | TGTGGTGTAGAGAAGCG | 6111 |
| | CGCTTCTCTACACCACA | 6112 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Waxy starch GBSS <i>Astragalus membranaeus</i> Arg12Term AGA-TGA | TGTTGCTCCTTACTGCTCTCTCACAGAATGGCAACGGTGACGGGG TCTTATGTGGTGTCTGAAGCGCGTGCTTCAATTCCCAGGGAAGA ACAGAAGCCAAAGTGAATTCACCTCAGAAGA | 6113 |
| | TCTTCTGAGGTGAATTCACCTTGGCTTCTGTTCTTCCCTGGGAATT GAAGCACGCGCTTCAACGACACCACATAAGACCCCGTCACCGTTGC CATTCTGTGAGAGAGCAGTAAGGAGCAACA | 6114 |
| | TGGTGTCTGGAAGCGCG | 6115 |
| | CGCGCTTCAACGACACCA | 6116 |
| Waxy starch GBSS <i>Astragalus membranaeus</i> Cys15Term TGC-TGA | ACTGCTCTCTCACAGAATGGCAACGGTGACGGGGTCTTATGTGGT GTCGAGAAGCGCGTGAATTCAATTCCCAGGGAAGAACAGAAGCCAA AGTGAATTCACCTCAGAAGATAAATCTCAAT | 6117 |
| | ATTGAGATTTATCTTCTGAGGTGAATTCACCTTGGCTTCTGTTCTTC CCTGGGAATTGAATCACGCGCTTCTCGACACCACATAAGACCCCG TCACCGTTGCCATTCTGTGAGAGAGCAGT | 6118 |
| | AGCGCGTGAATTCAATTC | 6119 |
| | GAATTGAATCACGCGCT | 6120 |
| Waxy starch GBSS <i>Astragalus membranaeus</i> Gln19Term CAG-TAG | CACAGAATGGCAACGGTGACGGGGTCTTATGTGGTGTGAGAAG CGCGTGCTTCAATTCCTAGGGAAGAACAGAAGCCAAAGTGAATTC ACCTCAGAAGATAAATCTCAATAGCCAAGCAT | 6121 |
| | ATGCTTGGCTATTGAGATTTATCTTCTGAGGTGAATTCACCTTGGCT TCTGTTCTTCCCTAGGAATTGAAGCACGCGCTTCTCGACACCACAT AAGACCCCGTCACCGTTGCCATTCTGTG | 6122 |
| | TCAATTCCTAGGGAAGA | 6123 |
| | TCTTCCCTAGGAATTGA | 6124 |
| Waxy starch GBSS <i>Solanum tuberosum</i> Ser7Term TCA-TGA | TGTAGCTTGGTAGATTCCCCTTTTTGTAGACCACACATCACATGGC AAGCATCACAGCTTGACACCACTTTGTGTCAAGAAGCCAAACTTCA CTAGACACCAAATCAACCTTGTACAGAT | 6125 |
| | ATCTGTGACAAGGTTGATTTGGTGTCTAGTGAAGTTTGGCTTCTTG ACACAAAGTGGTGTCAAGCTGTGATGCTTGCCATGTGATGTGTGG TCTACAAAAGGGGAATCTACCAAGCTACA | 6126 |
| | CACAGCTTGACACCACT | 6127 |
| | AGTGGTGTCAAGCTGTG | 6128 |
| Waxy starch GBSS <i>Solanum tuberosum</i> Ser12Term TCA-TGA | TCCCCTTTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTC ACACCACTTTGTGTGAAGAAGCCAAACTTCACTAGACACCAAATCA ACCTTGTACAGATAGGACTCAGGAACCA | 6129 |
| | TGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAGTG AAGTTTGGCTTCTTCACACAAAGTGGTGTGAAGCTGTGATGCTTGC CATGTGATGTGTGGTCTACAAAAGGGGA | 6130 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | CTTTGTGTGAAGAAGCC | 6131 |
| | GGCTTCTTACACAAAG | 6132 |
| Waxy starch GBSS <i>Solanum tuberosum</i> Arg13Term AGA-TGA | CCCTTTTTGTAGACCACACATCACATGGCAAGCATCACAGCTTCAC ACCACTTTGTGTCAATGAAGCCAACTTCACTAGACACCAAATCAAC CTTGTCACAGATAGGACTCAGGAACCATA | 6133 |
| | TATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGTGTCTAG TGAAGTTTGGCTTCAATGACACAAAGTGGTGTGAAGCTGTGATGCTT GCCATGTGATGTGTGGTCTACAAAAGGG | 6134 |
| | TTGTGTCAATGAAGCCAA | 6135 |
| | TTGGCTTCAATGACACAA | 6136 |
| Waxy starch GBSS <i>Solanum tuberosum</i> Gln15Term CAA-TAA | TTGTAGACCACACATCACATGGCAAGCATCACAGCTTCACACCACT TTGTGTCAAGAAGCTAAACTTCACTAGACACCAAATCAACCTTGTC ACAGATAGGACTCAGGAACCATACTCTGA | 6137 |
| | TCAGAGTATGGTTCCTGAGTCCTATCTGTGACAAGGTTGATTTGGT GTCTAGTGAAGTTTAGCTTCTTGACACAAAGTGGTGTGAAGCTGTG ATGCTTGCCATGTGATGTGTGGTCTACAA | 6138 |
| | CAAGAAGCTAAACTTCA | 6139 |
| | TGAAGTTTAGCTTCTTG | 6140 |
| Waxy starch GBSS <i>Solanum tuberosum</i> Ser17Term TCA-TGA | CCACACATCACATGGCAAGCATCACAGCTTCACACCACTTTGTGTC AAGAAGCCAACTTGACTAGACACCAAATCAACCTTGTCACAGATA GGACTCAGGAACCATACTCTGACTACAA | 6141 |
| | TTGTGAGTCAGAGTATGGTTCCTGAGTCCTATCTGTGACAAGGTTG ATTTGGTGTCTAGTCAAGTTTGGCTTCTTGACACAAAGTGGTGTGA AGCTGTGATGCTTGCCATGTGATGTGTGG | 6142 |
| | CCAACTTGACTAGACA | 6143 |
| | TGTCTAGTCAAGTTTGG | 6144 |
| Waxy starch GBSS <i>Pisum sativum</i> Gly6Term GGA-TGA | GTCGATCACTCTTCTCTCACCGCCGAAACAGATTTTGACACAAAA TGGCAACAATAACGTGATCTTCAATGCCGACGAGAACCGCGTGCT TCAATTACCAAGGAAGATCAGCAGAGTCTA | 6145 |
| | TAGACTCTGCTGATCTTCTTGGTAATTGAAGCACGCGGTTCTCGT CGGCATTGAAGATCACGTTATTGTTGCCATTTTGTGTCAAATCT GTTTCGGCGGTGAGAGAAGAGTGATCGAC | 6146 |
| | CAATAACGTGATCTTCA | 6147 |
| | TGAAGATCACGTTATTG | 6148 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| Waxy starch GBSS <i>Pisum sativum</i> Ser8Term TCA-TGA | ACTCTTCTCTCACCGCCGAAACAGATTTTGACACAAAAATGGCAAC AATAACGGGATCTTGAATGCCGACGAGAACCGCGTGCTTCAATTA CCAAGGAAGATCAGCAGAGTCTAAACTGAA | 6149 |
| | TTCAGTTTACTCTGCTGATCTTCCTTGGTAATTGAAGCACGCGG TTCTCGTCGGCATTCAAGATCCCGTTATTGTTGCCATTTTGTGTCA AAATCTGTTTCGGCGGTGAGAGAAGAGT | 6150 |
| | GGGATCTTGAATGCCGA | 6151 |
| | TCGGCATTCAAGATCCC | 6152 |
| Waxy starch GBSS <i>Pisum sativum</i> Arg12Term AGA-TGA | ACCGCCGAAACAGATTTTGACACAAAAATGGCAACAATAACGGGA TCTTCAATGCCGACGTGAACCGCGTGCTTCAATTACCAAGGAAGA TCAGCAGAGTCTAAACTGAATTTGCCTCAGA | 6153 |
| | TCTGAGGCAAATTCAGTTTACTCTGCTGATCTTCCTTGGTAATT GAAGCACGCGGTTACGTCGGCATTGAAGATCCCGTTATTGTTGC CATTTTGTGTCAAATCTGTTTCGGCGGT | 6154 |
| | TGCCGACGTGAACCGCG | 6155 |
| | CGCGGTTCACGTCGGCA | 6156 |
| Waxy starch GBSS <i>Pisum sativum</i> Cys15Term TGC-TGA | AGATTTTGACACAAAAATGGCAACAATAACGGGATCTTCAATGCCG ACGAGAACCGCGTGATTCAATTACCAAGGAAGATCAGCAGAGTCT AAACTGAATTTGCCTCAGATACACTTCAAT | 6157 |
| | ATTGAAGTGTATCTGAGGCAAATTCAGTTTACTCTGCTGATCTT CCTTGGTAATTGAATCACGCGGTTCTCGTCGGCATTGAAGATCCC GTTATTGTTGCCATTTTGTGTCAAATCT | 6158 |
| | ACCGCGTGATTCAATTA | 6159 |
| | TAATTGAATCACGCGGT | 6160 |
| Waxy starch GBSS <i>Pisum sativum</i> Tyr18Term TAC-TAG | CACAAAAATGGCAACAATAACGGGATCTTCAATGCCGACGAGAAC CGCGTGCTTCAATTAGCAAGGAAGATCAGCAGAGTCTAAACTGAA TTTGCCTCAGATACACTTCAATAACAACCAA | 6161 |
| | TTGGTTGTTATTGAAGTGTATCTGAGGCAAATTCAGTTTACTCT GCTGATCTTCCTTGCTAATTGAAGCACGCGGTTCTCGTCGGCATTG AAGATCCCGTTATTGTTGCCATTTTGTG | 6162 |
| | TTCAATTAGCAAGGAAG | 6163 |
| | CTTCCTTGCTAATTGAA | 6164 |
| Waxy starch GBSS <i>Manihot esculenta</i> Ser14Term TCA-TGA | TCTACACCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATT TCGTTTCCAGGAGCTGACACTTGAGCATCCATGCATTAGAGACTAA GGCTAATAATTTGTCTCACTGGACCCTG | 6165 |
| | CAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTAATGCAT GGATGCTCAAGTGTAGCTCCTGGAAACGAAATGTGCAGCTATTA CAGTTGCCATGGTGCTCTCTCCGGTGTAGA | 6166 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | CAGGAGCTGACACTTGA | 6167 |
| | TCAAGTGTGAGCTCCTG | 6168 |
| Waxy starch GBSS <i>Manihot esculenta</i> Leu16Term TTG-TAG | CCGGAGAGAGCACCATGGCAACTGTAATAGCTGCACATTTGTTTT CCAGGAGCTCACACTAGAGCATCCATGCATTAGAGACTAAGGCTA ATAATTTGTCTCACACTGGACCCTGGACCCA | 6169 |
| | TGGGTCCAGGGTCCAGTGTGAGACAAATTATTAGCCTTAGTCTCTA ATGCATGGATGCTCTAGTGTGAGCTCCTGGAAACGAAATGTGCAG CTATTACAGTTGCCATGGTGCTCTCTCCGG | 6170 |
| | CTCACACTAGAGCATCC | 6171 |
| | GGATGCTCTAGTGTGAG | 6172 |
| Waxy starch GBSS <i>Manihot esculenta</i> Leu21Term TTA-TGA | TGGCAACTGTAATAGCTGCACATTTGTTTTCCAGGAGCTCACACTT GAGCATCCATGCATGAGAGACTAAGGCTAATAATTTGTCTCACACT GGACCCTGGACCCAACTATCACTCCCAA | 6173 |
| | TTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAATTA TTAGCCTTAGTCTCTCATGCATGGATGCTCAAGTGTGAGCTCCTGG AAACGAAATGTGCAGCTATTACAGTTGCCA | 6174 |
| | CCATGCATGAGAGACTA | 6175 |
| | TAGTCTCTCATGCATGG | 6176 |
| Waxy starch GBSS <i>Manihot esculenta</i> Glu22Term GAG-TAG | GCAACTGTAATAGCTGCACATTTGTTTTCCAGGAGCTCACACTTGA GCATCCATGCATTATAGACTAAGGCTAATAATTTGTCTCACACTGG ACCCTGGACCCAACTATCACTCCCAATG | 6177 |
| | CATTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAGACAAAT TATTAGCCTTAGTCTATAATGCATGGATGCTCAAGTGTGAGCTCCT GGAAACGAAATGTGCAGCTATTACAGTTGC | 6178 |
| | ATGCATTATAGACTAAG | 6179 |
| | CTTAGTCTATAATGCAT | 6180 |
| Waxy starch GBSS <i>Manihot esculenta</i> Lys24Term AAG-TAG | GTAATAGCTGCACATTTGTTTTCCAGGAGCTCACACTTGAGCATCC ATGCATTAGAGACTTAGGCTAATAATTTGTCTCACACTGGACCCTG GACCCAACTATCACTCCCAATGGTTTAA | 6181 |
| | TTAAACCATTGGGAGTGATAGTTTGGGTCCAGGGTCCAGTGTGAG ACAAATTATTAGCCTAAGTCTCTAATGCATGGATGCTCAAGTGTGA GCTCCTGGAAACGAAATGTGCAGCTATTAC | 6182 |
| | TAGAGACTTAGGCTAAT | 6183 |
| | ATTAGCCTAAGTCTCTA | 6184 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Waxy starch GBSS <i>Phaseolus vulgaris</i> Ser12Term TCA-TGA | ACAACTCCTCCGTCACCGGTATAAGCATGGCAACGGTATCGATGG CATCGTGCGTGCGGTGAAAAGGCGCGTGGAGTACAGAGACAAAA GTGAAATCTTCGGGTCAGATGAGCCTGAACCG | 6185 |
| | CGGTTCAGGCTCATCTGACCCGAAGATTTCACTTTTGTCTCTGTAC TCCACGCGCCTTTTCACGCCACGCACGATGCCATCGATACCGTTG CCATGCTTATACCGGTGACGGAGGAGTTGT | 6186 |
| | CGTGCGGTGAAAAGGCG | 6187 |
| | CGCCTTTTCACGCCACG | 6188 |
| Waxy starch GBSS <i>Phaseolus vulgaris</i> Trp16Term TGG-TGA | CACCGGTATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGC GTCAAAGGCGCGTGAAAGTACAGAGACAAAAGTGAATCTTCGGG TCAGATGAGCCTGAACCGTCATGAATTGAAA | 6189 |
| | TTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGATTTCACT TTTGTCTCTGTACTTCACGCGCCTTTTGACGCCACGCACGATGCCA TCGATACCGTTGCCATGCTTATACCGGTG | 6190 |
| | GGCGCGTGAAAGTACAGA | 6191 |
| | TCTGTACTTCACGCGCC | 6192 |
| Waxy starch GBSS <i>Phaseolus vulgaris</i> Glu19Term GAG-TAG | ATAAGCATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAA GGCGCGTGGAGTACATAGACAAAAGTGAATCTTCGGGTCAGATG AGCCTGAACCGTCATGAATTGAAATACGATG | 6193 |
| | CATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACCCGAAGA TTTCACTTTTGTCTATGTACTCCACGCGCCTTTTGACGCCACGCAC GATGCCATCGATACCGTTGCCATGCTTAT | 6194 |
| | GGAGTACATAGACAAAA | 6195 |
| | TTTTGTCTATGTACTCC | 6196 |
| Waxy starch GBSS <i>Phaseolus vulgaris</i> Lys21Term AAA-TAA | ATGGCAACGGTATCGATGGCATCGTGCGTGGCGTCAAAGGCGC GTGGAGTACAGAGACATAAGTGAAATCTTCGGGTCAGATGAGCCT GAACCGTCATGAATTGAAATACGATGGGTTGA | 6197 |
| | TCAACCCATCGTATTTCAATTCATGACGGTTCAGGCTCATCTGACC CGAAGATTTCACTTATGTCTCTGTACTCCACGCGCCTTTTGACGCC ACGCACGATGCCATCGATACCGTTGCCAT | 6198 |
| | CAGAGACATAAGTGAAA | 6199 |
| | TTTCACTTATGTCTCTG | 6200 |
| Waxy starch GBSS <i>Phaseolus vulgaris</i> Lys23Term AAA-TAA | ACGGTATCGATGGCATCGTGCGTGGCGTCAAAGGCGCGTGGAG TACAGAGACAAAAGTGTAATCTTCGGGTCAGATGAGCCTGAACCG TCATGAATTGAAATACGATGGGTTGAGATCTC | 6201 |
| | GAGATCTCAACCCATCGTATTTCAATTCATGACGGTTCAGGCTCAT CTGACCCGAAGATTACACTTTTGTCTCTGTACTCCACGCGCCTTTT GACGCCACGCACGATGCCATCGATACCGT | 6202 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | CAAAAGTG <u>I</u> AATCTTCG | 6203 |
| | CGAAGATT <u>A</u> CACTTTTG | 6204 |
| Waxy starch GBSS <i>Triticum aestivum</i> Tyr7Term TAT-TAG | GCGCCTAGCTCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGG GTTCCATTCCCTAATTAGTGTCTTATCAAACAAACAGTGTTGGTTCA CTGAAACTGTCGCCTCACATCCAATTCCAG | 6205 |
| | CTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACTGTT TGTTTGATAAGAACA <u>C</u> TAATTAGGAATGGAACCCATTGGTGCAGCC TCTCAATGACGACCTTTTCGAGCTAGGCGC | 6206 |
| | CCTAATTAGTGTCTTA | 6207 |
| | TAAGAACA <u>C</u> TAATTAGG | 6208 |
| Waxy starch GBSS <i>Triticum aestivum</i> Cys8Term TGT-TGA | CCTAGCTCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTTC CATTCCCTAATTATTGATCTTATCAAACAAACAGTGTTGGTTCACTGA AACTGTCGCCTCACATCCAATTCCAGCAA | 6209 |
| | TTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACCAACACT GTTTGTTTGATAAGATCAATAATTAGGAATGGAACCCATTGGTGCA GCCTCTCAATGACGACCTTTTCGAGCTAGG | 6210 |
| | AATTATTGATCTTATCA | 6211 |
| | TGATAAGATCAATAATT | 6212 |
| Waxy starch GBSS <i>Triticum aestivum</i> Tyr10Term TAT-TAG | TCGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCC TAATTATTGTTCTTAGCAAACAAACAGTGTTGGTTCACTGAACTGT CGCCTCACATCCAATTCCAGCAATCTTGT | 6213 |
| | ACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAACC AACACTGTTTGTTTGCTAAGAACAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTTCGA | 6214 |
| | TGTTCTTAGCAAACAAA | 6215 |
| | TTTGTTTGCTAAGAACA | 6216 |
| Waxy starch GBSS <i>Triticum aestivum</i> Gln11Term CAA-TAA | CGAAAAGGTCGTCATTGAGAGGCTGCACCAATGGGTTCCATTCC AATTATTGTTCTTATTAAACAAACAGTGTTGGTTCACTGAACTGTC GCCTCACATCCAATTCCAGCAATCTTGTA | 6217 |
| | TACAAGATTGCTGGAATTGGATGTGAGGCGACAGTTTCAGTGAAC CAACACTGTTTGTTTAATAAGAACAATAATTAGGAATGGAACCCATT GGTGCAGCCTCTCAATGACGACCTTTTCG | 6218 |
| | GTTCTTATTAAACAAAC | 6219 |
| | GTTTGTTTAATAAGAAC | 6220 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| Waxy starch GBSS <i>Triticum aestivum</i> Ser17Term TCA-TGA | AGGCTGCACCAATGGGTTCCATTCTAATTATTGTTCTTATCAAACA AACAGTGTGGTTGACTGAACTGTCGCCTCACATCCAATTCCAGC AATCTTGTAACAATGAAGTTATGTTCT | 6221 |
| | AGGAACATAACTTCATTGTTACAAGATTGCTGGAATTGGATGTGAG GCGACAGTTTCAGTCAACCAACACTGTTTGTGATAAGAACAATA ATTAGGAATGGAACCCATTGGTGCAGCCT | 6222 |
| | TGTTGGTTGACTGAAAC | 6223 |
| | GTTTCAGTCAACCAACA | 6224 |
| Waxy starch GBSS <i>Triticum aestivum</i> Gln28Term CAG-TAG | CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGCAGGTTTCTAGGGCGTGAGGCCCGGAGCCCGGCG GATGCGGCTCTCGGCATGAGGACCGTCGGAGCTA | 6225 |
| | TAGCTCCGACGGTCTCATGCCGAGAGCCGCATCCGCCGGGCTC CGGGGCCTCACGCCCTAGAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG | 6226 |
| | CAGGTTTCTAGGGCGTG | 6227 |
| | CACGCCCTAGAAACCTG | 6228 |
| Waxy starch GBSS <i>Triticum aestivum</i> Gly46Term GGA-TGA | GGTTTCCAGGGCGTGAGGCCCGGAGCCCGGCGGATGCGGCTCT CGGCATGAGGACCGTCTGAGCTAGCGCCGCCCAACGCAAAGCC GGAAAGCGCACCGCGGGACCCGGCGGTGCCTCT | 6229 |
| | AGAGGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGCGTT GGGGCGGCGCTAGCTCAGACGGTCTCATGCCGAGAGCCGCATC CGCCGGGCTCCGGGGCCTCACGCCCTGAAACC | 6230 |
| | GGACCGTCTGAGCTAGC | 6231 |
| | GCTAGCTCAGACGGTCC | 6232 |
| Waxy starch GBSS <i>Triticum aestivum</i> Gln53Term CAA-TAA | CGGAGCCCGGCGGATGCGGCTCTCGGCATGAGGACCGTCGGAG CTAGCGCCGCCCAACGTAAAGCCGAAAGCGCACCGCGGGACC CGGCGGTGCCTCTCCATGGTGGTGCGCGCCACCG | 6233 |
| | CGGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTACGTTGGGGCGGCGCTAGCTCCGACGG TCCTCATGCCGAGAGCCGCATCCGCCGGGCTCCG | 6234 |
| | CCCCAACGTAAAGCCGG | 6235 |
| | CCGGCTTTACGTTGGGG | 6236 |
| Waxy starch GBSS <i>Triticum aestivum</i> Lys56Term AAA-TAA | GCGGATGCGGCTCTCGGCATGAGGACCGTCGGAGCTAGCGCCGC CCCAACGAAAGCCGGTAAGCGCACCGCGGGACCCGGCGGTGC CTCTCCATGGTGGTGCGCGCCACCGGCAGCGGCG | 6237 |
| | CGCCGCTGCCGGTGCGCGCACCACCATGGAGAGGCACCGCCG GGTCCCGCGGTGCGCTTACCGGCTTTGCGTTGGGGCGGCGCTAG CTCCGACGGTCTCATGCCGAGAGCCGCATCCGC | 6238 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | AAAGCCGGT <u>I</u> AAGCGCAC | 6239 |
| | GTGCGCTT <u>A</u> CCGGCTTT | 6240 |
| Waxy starch GBSS <i>Triticum aestivum</i> Glu85Term GAG-TAG | CTCTCCATGGTGGTGCGCGCCACCGGCAGCGGCGGCATGAACCT CGTGTTCTGTCGGCGCC <u>I</u> AGATGGCGCCCTGGAGCAAGACCGGCG GCCTCGGCGACGTCTCGGGGGCCTCCCCCAG | 6241 |
| | CTGGGGGGAGGCCCCCGAGGACGTGCGCGAGGCGCCGGTCTT GCTCCAGGGCGCCATCT <u>A</u> GGCGCCGACGAACACGAGGTTTCATGC CGCCGCTGCCGGTGCGCGCACCAACCATGGAGAG | 6242 |
| | TCGGCGCC <u>I</u> AGATGGCG | 6243 |
| | CGCCATCT <u>A</u> GGCGCCGA | 6244 |
| Waxy starch GBSS <i>Triticum aestivum</i> Gln8Term CAG-TAG | GTCGTCTCTCGCTGCAGGTAGCCACACCCTGCGCGCGCGATGGC GGCTCTGGTCACGTCTG <u>I</u> AGCTCGCCACCTCCGGCACCGTCCTCG GCATCACCGACAGGTTCCGGCGTGAGGTTTTTC | 6245 |
| | GAAAACCTGCACGCCGGAACCTGTCGGTGATGCCGAGGACGGTG CCGGAGGTGGCGAGCT <u>A</u> CGACGTGACCAGAGCCGCCATCGCGC GCGCAGGGTGTGGCTACCTGCAGCGAGAGACGAC | 6246 |
| | TCACGTCTG <u>I</u> AGCTCGCC | 6247 |
| | GGCGAGCT <u>A</u> CGACGTGA | 6248 |
| Waxy starch GBSS <i>Triticum aestivum</i> Gln28Term CAG-TAG | CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGACAGTTTTT <u>I</u> AGGGTGAGAGCCCCGGAGCCCGGCAG ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA | 6249 |
| | TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACACCCT <u>A</u> AAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG | 6250 |
| | CAGGTTTT <u>I</u> AGGGTG | 6251 |
| | CACACCCT <u>A</u> AAAACCTG | 6252 |
| Waxy starch GBSS <i>Triticum aestivum</i> Lys52Term AAG-TAG | CCCCGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGG AGCGAGCGCCGCCCGT <u>I</u> AGCAACAAAGCCGGAAGCGCACCGCG GGACCCGGCGGTGCCTCTCCATGGTGGTGCGCG | 6253 |
| | CGCGCACCACCATGGAGAGGCACCGCCGGTCCCGCGGTGCGC TTTCCGGCTTTGTTGCT <u>A</u> CGGGGCGGCGCTCGCTCCGGTAGTCCT CATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG | 6254 |
| | CCGCCCCG <u>I</u> AGCAACAA | 6255 |
| | TTGTTGCT <u>A</u> CGGGGCGG | 6256 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| Waxy starch GBSS <i>Triticum aestivum</i> Gln53Term CAA-TAA | CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCGGAAGTAACAAAGCCGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA | 6257 |
| | TGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGGTAGT CCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG | 6258 |
| | CCCCGAAGTAACAAAGC | 6259 |
| | GCTTTGTTACTTCGGGG | 6260 |
| Waxy starch GBSS <i>Triticum aestivum</i> Gln54Term CAA-TAA | AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAG CGCCGCCCGGAAGCAATAAAGCCGAAAGCGCACCGCGGGACCC GGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG | 6261 |
| | CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGGT AGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT | 6262 |
| | CGAAGCAATAAAGCCGG | 6263 |
| | CCGGCTTTATTGCTTCG | 6264 |
| Waxy starch GBSS <i>Triticum durum</i> Gln28Term CAG-TAG | CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTGAGGTTTCTAGGGCGTGAGGCCCGGAACCCGGCG GATGCGGCCCTCGTCATGAGGACTATCGGAGCGA | 6265 |
| | TCGCTCCGATAGTCCTCATGACGAGGGCCGCATCCGCCGGGTTC CGGGGCCCTACGCCCTAGAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG | 6266 |
| | CAGGTTTCTAGGGCGTG | 6267 |
| | CACGCCCTAGAAACCTG | 6268 |
| Waxy starch GBSS <i>Triticum durum</i> Lys52Term AAG-TAG | CCCCGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGG AGCGAGCGCCGCCCGTAGCAAAGCCGAAAGCGCACCGCGGG AGCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA | 6269 |
| | TGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGCTACGGGGCGGCGCTCGCTCCGATAGTCCT CATGACGAGGGCCGCATCCGCCGGGTTCGGGG | 6270 |
| | CCGCCCCGTAGCAAAGC | 6271 |
| | GCTTTGCTACGGGGCGG | 6272 |
| Waxy starch GBSS <i>Triticum durum</i> Gln53Term CAA-TAA | CGGAACCCGGCGGATGCGGCCCTCGTCATGAGGACTATCGGAGC GAGCGCCGCCCGGAAGTAAGCCGAAAGCGCACCGCGGGAGC CGGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG | 6273 |
| | CCGTGGCGCGCACCACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTACTTCGGGGCGGCGCTCGCTCCGATAGT CCTCATGACGAGGGCCGCATCCGCCGGGTTCG | 6274 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | CCCCGAAGTAAAGCCGG | 6275 |
| | CCGGCTTTACTTCGGGG | 6276 |
| Waxy starch GBSS <i>Triticum durum</i> Lys56Term AAA-TAA | GCGGATGCGGCCCTCGTCATGAGGACTATCGGAGCGAGCGCCGC CCCGAAGCAAAGCCGGTAAGCGCACCGCGGGAGCCGGCGGTGC CTCTCCATGGTGGTGC GCGCCACGGGCAGCGGCG | 6277 |
| | CGCCGCTGCCCCTGGCGCGCACCAACCATGGAGAGGCACCGCCG GCTCCCGCGGTGCGCTTACCGGCTTTGCTTCGGGGCGGCGCTCG CTCCGATAGTCCTCATGACGAGGGCCGCATCCGC | 6278 |
| | AAAGCCGGTAAGCGCAC | 6279 |
| | GTGCGCTTACCGGCTTT | 6280 |
| Waxy starch GBSS <i>Triticum durum</i> Cys64Term TGC-TGA | TATCGGAGCGAGCGCCGCCCGAAGCAAAGCCGGAAAGCGCACCC GCGGGAGCCGGCGGTGACTCTCCATGGTGGTGC GCGCCACGGG CAGCGGCGGCATGAACCTCGTGTTCTGTCGGCGCC | 6281 |
| | GGCGCCGACGAACACGAGGTTTCATGCCGCGCTGCCCGTGGCGC GCACCACCATGGAGAGTCACCGCCGGCTCCCGCGGTGCGCTTTC CGGCTTTGCTTCGGGGCGGCGCTCGCTCCGATA | 6282 |
| | CGGCGGTGACTCTCCAT | 6283 |
| | ATGGAGAGTCACCGCCG | 6284 |
| Waxy starch GBSS <i>Triticum turgidum</i> Gln28Term CAG-TAG | CAGCTCGCCACCTCCGGCACCGTCCTCGGCATCACCGACAGGTT CCGGCGTG CAGGTTTTTAGGGTGTGAGGCCCGGAGCCCGGCAG ATGCGCCGCTCGGCATGAGGACTACCGGAGCGA | 6285 |
| | TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACACCCTAAAAACCTGCACGCCGGAACCTGTCGGT GATGCCGAGGACGGTGCCGGAGGTGGCGAGCTG | 6286 |
| | CAGGTTTTTAGGGTGTG | 6287 |
| | CACACCCTAAAAACCTG | 6288 |
| Waxy starch GBSS <i>Triticum turgidum</i> Lys52Term AAG-TAG | CCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGG AGCGAGCGCCGCCCGTAGCAACAAAGCCGGAAAGCGCACCGCG GGACCCGGCGGTGCCTCTCCATGGTGGTGC GCG | 6289 |
| | CGCGCACCAACCATGGAGAGGCACCGCCGGGTCCCGCGGTGCGC TTTCCGGCTTTGTTGCTACGGGGCGGCGCTCGCTCCGGTAGTCCT CATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG | 6290 |
| | CCGCCCCGTAGCAACAA | 6291 |
| | TTGTTGCTACGGGGCGG | 6292 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Waxy starch GBSS <i>Triticum turgidum</i> Gln53Term CAA-TAA | CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAG CGAGCGCCGCCCCGAAGTAACAAAGCCGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCCATGGTGGTGCGCGCCA | 6293 |
| | TGGCGCGCACCAACCATGGAGAGGCACCGCCGGGTCCCGCGGTG CGCTTTCCGGCTTTGTTACTTCGGGGCGGCGCTCGCTCCGGTAGT CCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG | 6294 |
| | CCCCGAAGTAACAAAGC | 6295 |
| | GCTTTGTTACTTCGGGG | 6296 |
| Waxy starch GBSS <i>Triticum turgidum</i> Gln54Term CAA-TAA | AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTACCGGAGCGAG CGCCGCCCCGAAGCAATAAAGCCGAAAGCGCACCGCGGGACCC GGCGGTGCCTCTCCATGGTGGTGCGCGCCACGG | 6297 |
| | CCGTGGCGCGCACCAACCATGGAGAGGCACCGCCGGGTCCCGCG GTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGGT AGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT | 6298 |
| | CGAAGCAATAAAGCCGG | 6299 |
| | CCGGCTTTATTGCTTCG | 6300 |
| Waxy starch GBSS <i>Triticum turgidum</i> Lys57Term AAA-TAA | GATGCGCCGCTCGGCATGAGGACTACCGGAGCGAGCGCCGCCCC GAAGCAACAAAGCCGGTAAGCGCACCGCGGGACCCGGCGGTGC CTCTCCATGGTGGTGCGCGCCACGGGCAGCGCCG | 6301 |
| | CGGCGCTGCCCGTGCGCGCACCAACCATGGAGAGGCACCGCCG GGTCCCGCGGTGCGCTTACCGGCTTTGTTGCTTCGGGGCGGCGC TCGCTCCGGTAGTCCTCATGCCGAGCGGCGCATC | 6302 |
| | AAAGCCGGTAAGCGCAC | 6303 |
| | GTGCGCTTACCGGCTTT | 6304 |
| Waxy starch GBSS <i>Aegilops speltoides</i> Gln28Term CAG-TAG | CAGCTCGCCACCTCCGCCACCGTCCTCGGCATCACCGACAGGTTC CGCCATGCAGGTTTCTAGGGCGTGAGGCCCCGGAGCCCGGCAGA TGCGCCGCTCGGCATGAGGACTGTCGGAGCGA | 6305 |
| | TCGCTCCGACAGTCCTCATGCCGAGCGGCGCATCTGCCGGGCTC CGGGGCCTCACGCCCTAGAAACCTGCATGGCGGAACCTGTGGT GATGCCGAGGACGGTGCGGAGGTGGCGAGCTG | 6306 |
| | CAGGTTTCTAGGGCGTG | 6307 |
| | CACGCCCTAGAAACCTG | 6308 |
| Waxy starch GBSS <i>Aegilops speltoides</i> Gly46Term GGA-TGA | GGTTTCCAGGGCGTGAGGCCCGGAGCCCGGCAGATGCGCCGCT CGGCATGAGGACTGTCTGAGCGAGCGCCGCCCCGAAGCAACAAA GCCGAAAGCGCACCGCGGGACCCGGCGGTGCC | 6309 |
| | GGCACCGCCGGGTCCCGCGGTGCGCTTTCCGGCTTTGTTGCTTC GGGGCGGCGCTCGCTCAGACAGTCCTCATGCCGAGCGGCGCATC TGCCGGGCTCCGGGGCCTCACGCCCTGGAAACC | 6310 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | GGACTGTC <u>I</u> GAGCGAGC | 6311 |
| | GCTCGCTC <u>A</u> GACAGTCC | 6312 |
| Waxy starch GBSS <i>Aegilops speltoides</i> Lys52Term AAG-TAG | CCCCGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGG AGCGAGCGCCGCCCGCTAGCAACAAAGCCGAAAGCGCACCGCG GGACCCGGCGGTGCCTCTCGATGGTGGTGC | 6313 |
| | CGCGCACCACCATCGAGAGGCACCGCCGGTCCCGCGGTGCGCT TTCCGGCTTTGTTGCT <u>A</u> CGGGGCGGCGCTCGCTCCGACAGTCCTC ATGCCGAGCGGCGCATCTGCCGGGCTCCGGGG | 6314 |
| | CCGCCCCG <u>T</u> AGCAACAA | 6315 |
| | TTGTTGCT <u>A</u> CGGGGCGG | 6316 |
| Waxy starch GBSS <i>Aegilops speltoides</i> Gln53Term CAA-TAA | CGGAGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAG CGAGCGCCGCCCGAAGTAAACAAAGCCGAAAGCGCACCGCGG GACCCGGCGGTGCCTCTCGATGGTGGTGC | 6317 |
| | TGGCGCGCACCACCATCGAGAGGCACCGCCGGTCCCGCGGTG CGCTTTCCGGCTTTGTT <u>A</u> CTTCGGGGCGGCGCTCGCTCCGACAGT CCTCATGCCGAGCGGCGCATCTGCCGGGCTCCG | 6318 |
| | CCCCGAAGTAAACAAAGC | 6319 |
| | GCTTTGTT <u>A</u> CTTCGGGG | 6320 |
| Waxy starch GBSS <i>Aegilops speltoides</i> Gln54Term CAA-TAA | AGCCCGGCAGATGCGCCGCTCGGCATGAGGACTGTCGGAGCGAG CGCCGCCCGAAGCAATAAAGCCGAAAGCGCACCGCGGGACCC GGCGGTGCCTCTCGATGGTGGTGC | 6321 |
| | CGGTGGCGCGCACCACCATCGAGAGGCACCGCCGGTCCCGCG GTGCGCTTTCCGGCTTTATTGCTTCGGGGCGGCGCTCGCTCCGAC AGTCCTCATGCCGAGCGGCGCATCTGCCGGGCT | 6322 |
| | CGAAGCAATAAAGCCGG | 6323 |
| | CCGGCTTTATTGCTTCG | 6324 |
| Waxy starch GBSS <i>Oryza glaberrima</i> Gln8Term CAG-TAG | AGTGCAGAGATCTTCCACAGCAACAGCTAGACAACCACCATGTCG GCTCTACCACGTCTAGCTCGCCACCTCGGCCACCGGCTTCGG CATCGCTGACAGGTCGGCGCCGTCGTCGCTGC | 6325 |
| | GCAGCGACGACGGCGCCGACCTGTCAGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTAGGACGTGGTGAGAGCCGACATGGTG GTTGTCTAGCTGTTGCTGTGGAAGATCTTGCACT | 6326 |
| | CCACGTCC <u>T</u> AGCTCGCC | 6327 |
| | GGCGAGCTAGGACGTGG | 6328 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Waxy starch GBSS <i>Oryza glaberrima</i> Ser12Term TCG-TAG | TCCACAGCAACAGCTAGACAACCACCATGTCGGCTCTCACCACGT CCCAGCTCGCCACCTAGGCCACCGGCTTCGGCATCGCTGACAGG TCGGCGCCGTCGTCGCTGCTCCGCCACGGTT | 6329 |
| | AACCCGTGGCGGAGCAGCGACGACGGCGCCGACCTGTCAGCGAT GCCGAAGCCGGTGGCTAGGTGGCGAGCTGGGACGTGGTGAGA GCCGACATGGTGGTTGTCTAGCTGTTGCTGTGGA | 6330 |
| | CGCCACCTAGGCCACCG | 6331 |
| | CGGTGGCCTAGGTGGCG | 6332 |
| Waxy starch GBSS <i>Oryza glaberrima</i> Ser22Term TCG-TAG | CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC GGCATCGCTGACAGGTAGGCGCCGTCGTCGCTGCTCCGCCACGG GTTCCAGGGCCTCAAGCCCCGCAGCCCCGCCGG | 6333 |
| | CCGGCGGGGCTGCGGGGCTTGAGGCCCTGGAACCCGTGGCGGA GCAGCGACGACGGCGCCTACCTGTCAGCGATGCCGAAGCCGGTG GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG | 6334 |
| | TGACAGGTAGGCGCCGT | 6335 |
| | ACGGCGCCTACCTGTCA | 6336 |
| Waxy starch GBSS <i>Oryza glaberrima</i> Ser25Term TCG-TAG | CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCT GACAGGTGCGGCGCCGTAGTCGCTGCTCCGCCACGGGTTCCAGGG CCTCAAGCCCCGCAGCCCCGCCGGCGGCGACGC | 6337 |
| | GCGTCGCCGCGCGGGGCTGCGGGGCTTGAGGCCCTGGAACC CGTGCGGAGCAGCGACTACGGCGCCGACCTGTCAGCGATGCCG AAGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG | 6338 |
| | GGCGCCGTAGTCGCTGC | 6339 |
| | GCAGCGACTACGGCGCC | 6340 |
| Waxy starch GBSS <i>Oryza glaberrima</i> Ser26Term TCG-TAG | CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCTGAC AGGTGCGGCGCCGTCGTAGCTGCTCCGCCACGGGTTCCAGGGCCT CAAGCCCCGCAGCCCCGCCGGCGGCGACGCGAC | 6341 |
| | GTCGCGTCGCCGCGGGGCTGCGGGGCTTGAGGCCCTGGA ACCCGTGGCGGAGCAGCTACGACGGCGCCGACCTGTCAGCGATG CCGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG | 6342 |
| | GCCGTCGTAGCTGCTCC | 6343 |
| | GGAGCAGCTACGACGGC | 6344 |
| Waxy starch GBSS <i>Oryza sativa</i> Gln8Term CAG-TAG | TCCACAGCAAGAGCTAAACAGCCGACCGTGTGCACCACCATGTG GCTCTCACCACGTCTAGCTCGCCACCTCGGCCACCGGCTTCGG CATCGCCGACAGGTGCGCGCCGTCGTCGCTGC | 6345 |
| | GCAGCGACGACGGCGCCGACCTGTGCGCGATGCCGAAGCCGGT GGCCGAGGTGGCGAGCTAGGACGTGGTGAGAGCCGACATGGTG GTGCACACGGTCGGCTGTTAGCTCTTGCTGTGGA | 6346 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| | CCACGTCC <u>T</u> AGCTCGCC | 6347 |
| | GGCGAGCT <u>A</u> GGACGTGG | 6348 |
| Waxy starch GBSS <i>Oryza sativa</i> Ser12Term TCG-TAG | CTAAACAGCCGACCGTGTGCACCACCATGTCTGGCTCTCACCACGT CCCAGCTCGCCACCT <u>A</u> GGCCACCGGCTTCGGCATCGCCGACAGG TCGGCGCCGTCGTCGCTGCTTCGCCACGGGT | 6349 |
| | AACCCGTGGCGAAGCAGCGACGACGGCGCCGACCTGTCTGGCGAT GCCGAAGCCGGTGGCC <u>T</u> AGGTGGCGAGCTGGGACGTGGTGAGA GCCGACATGGTGGTGCACACGGTCGGCTGTTTAG | 6350 |
| | CGCCACCT <u>A</u> GGCCACCG | 6351 |
| | CGGTGGCC <u>T</u> AGGTGGCG | 6352 |
| Waxy starch GBSS <i>Oryza sativa</i> Ser22Term TCG-TAG | CGGCTCTCACCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTC GGCATCGCCGACAGGT <u>A</u> GGCGCCGTCGTCGCTGCTTCGCCACGG GTTCCAGGGCCTCAAGCCCCGTAGCCACAGCCG | 6353 |
| | CCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACCCGTGGCGAA GCAGCGACGACGGCGCC <u>T</u> ACCTGTCTGGCGATGCCGAAGCCGGTG GCCGAGGTGGCGAGCTGGGACGTGGTGAGAGCCG | 6354 |
| | CGACAGGT <u>A</u> GGCGCCGT | 6355 |
| | ACGGCGCC <u>T</u> ACCTGTCTG | 6356 |
| Waxy starch GBSS <i>Oryza sativa</i> Ser25Term TCG-TAG | CCACGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCC GACAGGTCGGCGCCGT <u>A</u> GTCTGCTTCGCCACGGGTTCCAGGG CCTCAAGCCCCGTAGCCACAGCCGGCGGGGACGC | 6357 |
| | GCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAACCC GTGGCGAAGCAGCGAC <u>T</u> ACGGCGCCGACCTGTCTGGCGATGCCGA AGCCGGTGGCCGAGGTGGCGAGCTGGGACGTGG | 6358 |
| | GGCGCCGT <u>A</u> GTCTGCTGC | 6359 |
| | GCAGCGACT <u>T</u> ACGGCGCC | 6360 |
| Waxy starch GBSS <i>Oryza sativa</i> Ser26Term TCG-TAG | CGTCCCAGCTCGCCACCTCGGCCACCGGCTTCGGCATCGCCGAC AGGTCTGGCGCCGTCGT <u>A</u> GCTGCTTCGCCACGGGTTCCAGGGCCT CAAGCCCCGTAGCCACAGCCGGCGGGGACGCATC | 6361 |
| | GATGCGTCCCCGCCGGCTGGGCTACGGGGCTTGAGGCCCTGGAA CCCGTGGCGAAGCAGCT <u>T</u> ACGACGGCGCCGACCTGTCTGGCGATGC CGAAGCCGGTGGCCGAGGTGGCGAGCTGGGACG | 6362 |
| | GCCGTCGT <u>A</u> GCTGCTTC | 6363 |
| | GAAGCAGCT <u>T</u> ACGACGGC | 6364 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| Waxy starch GBSS <i>Hordeum vulgare</i> Gln8Term CAG-TAG | GTCTCTCACTGCAGGTAGCCACACCCTGTGCGCGGCGCCATGGC GGCTCTGGCCACGTCC <u>T</u> AGCTCGCCACCTCCGGCACCCTCCTCG GCGTCACCGACAGATTCCGGCGTCCAGGTTTTTC | 6365 |
| | GAAAACCTGGACGCCGGAATCTGTGCGGTGACGCCGAGGACGGTG CCGGAGGTGGCGAGCT <u>A</u> GGACGTGGCCAGAGCCGCCATGGCGC CGCGCACAGGGTGTGGCTACCTGCAGTGAGAGAC | 6366 |
| | CCACGTCC <u>T</u> AGCTCGCC | 6367 |
| | GGCGAGCT <u>A</u> GGACGTGG | 6368 |
| Waxy starch GBSS <i>Hordeum vulgare</i> Arg21Term AGA-TGA | ATGGCGGCTCTGGCCACGTCCCAGCTCGCCACCTCCGGCACCGT CCTCGGCGTCACCGAC <u>T</u> GATTCCGGCGTCCAGGTTTTTCAGGGCCT CAGGCCCCGGAACCCGGCGGATGCGGCGCTTG | 6369 |
| | CAAGCGCCGCATCCGCCGGGTTCCGGGGCCTGAGGCCCTGAAAA CCTGGACGCCGGAATC <u>A</u> GTGCGGTGACGCCGAGGACGGTGCCGG AGGTGGCGAGCTGGGACGTGGCCAGAGCCGCCAT | 6370 |
| | TCACCGAC <u>T</u> GATTCCGG | 6371 |
| | CCGGAATC <u>A</u> GTGCGGTGA | 6372 |
| Waxy starch GBSS <i>Hordeum vulgare</i> Gln28Term CAG-TAG | CAGCTCGCCACCTCCGGCACCGTCCTCGGCGTCACCGACAGATT CCGGCGTCCAGGTTTTT <u>T</u> AGGGCCTCAGGCCCCGGAACCCGGCGG ATGCGGCGCTTGGTATGAGGACTATCGGAGCAA | 6373 |
| | TTGCTCCGATAGTCCTCATACCAAGCGCCGCATCCGCCGGGTTCC GGGGCCTGAGGCCCT <u>A</u> AAAACTGGACGCCGGAATCTGTGCGTG ACGCCGAGGACGGTGCCGGAGGTGGCGAGCTG | 6374 |
| | CAGGTTTT <u>T</u> AGGGCCTC | 6375 |
| | GAGGCCCT <u>A</u> AAAACTG | 6376 |
| Waxy starch GBSS <i>Hordeum vulgare</i> Gly46Term GGA-TGA | GGTTTTCAGGGCCTCAGGCCCCGGAACCCGGCGGATGCGGCGCT TGGTATGAGGACTATC <u>T</u> GAGCAAGCGCCGCCCGAAGCAAAGCC GGAAAGCGCACCGCGGGAGCCGGCGGTGCCTCT | 6377 |
| | AGAGGCACCGCCGGCTCCCGCGGTGCGCTTTCCGGCTTTGCTTC GGGGCGGCGCTTGCTC <u>A</u> GATAGTCCTCATACCAAGCGCCGCATC CGCCGGGTTCCGGGGCCTGAGGCCCTGAAAACC | 6378 |
| | GGAATATC <u>T</u> GAGCAAGC | 6379 |
| | GCTTGCTC <u>A</u> GATAGTCC | 6380 |
| Waxy starch GBSS <i>Hordeum vulgare</i> Lys52Term AAG-TAG | CCCCGGAACCCGGCGGATGCGGCGCTTGGTATGAGGACTATCGG AGCAAGCGCCGCCCG <u>T</u> AGCAAAGCCGGAAGCGCACCGCGGG AGCCGGCGGTGCCTCTCCGTGGTGGTGAGCGCCA | 6381 |
| | TGGCGCTCACCACCACGAGAGGCACCGCCGGCTCCCGCGGTGC GCTTTCCGGCTTTGCT <u>A</u> CGGGGCGGCGCTTGCTCCGATAGTCCTC ATACCAAGCGCCGCATCCGCCGGGTTCCGGGG | 6382 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| | CCGCCCCG <u>T</u> AGCAAAGC | 6383 |
| | GCTTTGCT <u>A</u> CGGGGCGG | 6384 |
| Waxy starch GBSS <i>Zea mays</i> Gln8Term CAG-TAG | ACGTCTTTTCTCTCTCTCTCTACGCAGTGGATTAATCGGCATGGCGGCTCTGGCCACGTCG <u>T</u> AGCTCGTCGCAACGCGCGCCGGCCTGGGC GTCCCGGACGCGTCCACGTTCCGCCGCGGCG | 6385 |
| | CGCCGCGGCGGAACGTGGACGCGTCCGGGACGCCCAGGCCGGC GCGCGTTGCGACGAGCT <u>A</u> CGACGTGGCCAGAGCCGCCATGCCGA TTAATCCACTGCGTAGGAGAGAGAGAAAAGACGT | 6386 |
| | CCACGTCG <u>T</u> AGCTCGTC | 6387 |
| | GACGAGCT <u>A</u> CGACGTGG | 6388 |
| | | |
| Waxy starch GBSS <i>Zea mays</i> Gln30Term CAG-TAG | GTCGCAACGCGCGCCGGCCTGGGCGTCCCGGACGCGTCCACGTT CCGCCGCGGCGCCGCG <u>T</u> AGGGCCTGAGGGGGGGCCCGGGCGTCTG GCGGCGGCGGACACGCTCAGCATGCGGACCAGCG | 6389 |
| | CGCTGGTCCGCATGCTGAGCGTGTCCGCCGCCGCGACGCCCGG GCCCCCCTCAGGCCCT <u>A</u> CGCGGCGCCGCGGCGGAACGTGGACG CGTCCGGGACGCCCAGGCCGGCGCGCGTTGCGAC | 6390 |
| | GCGCCGCG <u>T</u> AGGGCCTG | 6391 |
| | CAGGCCCT <u>A</u> CGCGGCGC | 6392 |
| | | |
| Waxy starch GBSS <i>Zea mays</i> Ser38Term TCG-TAG | TCCCGGACGCGTCCACGTTCCGCCGCGGCGCCGCGCAGGGCCT GAGGGGGGGCCCGGGCGT <u>A</u> GGCGGCGGCGGACACGCTCAGCATG CGGACCAGCGCGCGCGCGGCCAGGCACCAGCA | 6393 |
| | TGCTGGTGCCTGGGCGCCGCGCGCGCGCTGGTCCGCATGCTGAG CGTGTCCGCCCGCCGCT <u>T</u> ACGCCCCGGGCCCCCTCAGGCCCTGCG CGGCGCCGCGGCGGAACGTGGACGCGTCCGGGA | 6394 |
| | CCGGGCGT <u>A</u> GGCGGCGG | 6395 |
| | CCGCCGCC <u>T</u> ACGCCCGG | 6396 |
| | | |
| Waxy starch GBSS <i>Zea mays</i> Ser57Term CAG-TAG | GCGTCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGC GCGCGGCGCCAGGCAGT <u>A</u> GCAGCAGGCGCGCCGCGGGGGCAG GTTCCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCA | 6397 |
| | TGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCCCCC GCGGCGCGCCTGCTGCT <u>A</u> GTGCCTGGGCGCCGCGCGCGCTG GTCCGCATGCTGAGCGTGTCCGCCGCCGCGGACGC | 6398 |
| | CCAGGCACT <u>A</u> GACAGCAG | 6399 |
| | CTGCTGCT <u>A</u> GTGCCTGG | 6400 |
| | | |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Waxy starch GBSS <i>Zea mays</i> Gln58Term CAG-TAG | TCGGCGGCGGCGGACACGCTCAGCATGCGGACCAGCGCGCGCG CGGCGCCAGGCACCAGTAGCAGGCGCGCCGCGGGGGCAGGTT CCCGTCGCTCGTCGTGTGCGCCAGCGCCGGCATGA | 6401 |
| | TCATGCCGGCGCTGGCGCACACGACGAGCGACGGGAACCTGCCC CCGCGGCGCGCCTGCTACTGGTGCCTGGGCGCCGCGCGCGCGC TGGTCCGCATGCTGAGCGTGTCCGCCGCCGCCGA | 6402 |
| | GGCACCAGTAGCAGGCG | 6403 |
| | CGCCTGCTACTGGTGCC | 6404 |

Example 32

Altering fatty acid content of plants

[263] Improved means to manipulate fatty acid compositions, from biosynthetic or natural plant sources, are needed. For example, oils containing reduced saturated fatty acids are desired for dietary reasons and oils containing increased saturated fatty acids are also needed as alternatives to current sources of highly saturated oil products, such as tropical oils or chemically hydrogenated oils. It would therefore be advantageous to influence directly the production and composition of fatty acids in crop plants.

[264] Higher plants synthesize fatty acids, primarily palmitic, stearic and oleic acids, in the plastids (i.e., chloroplasts, proplastids, or other related organelles) as part of the Fatty Acid Synthase (FAS) complex. Fatty acid synthesis is the result of the three enzymatic activities: acyl-ACP elongase, acyl-ACP desaturase and acyl-ACP thioesterases specific for each of palmitoyl-, stearyl- and oleoyl-ACP.

[265] A variety of enzymes have been identified that influence the relative levels of saturated vs. unsaturated fatty acids in plants. For example, the enzymes stearyl-acyl carrier protein (stearyl-ACP) desaturase, oleoyl desaturase and linoleate desaturase produce unsaturated fatty acids from saturated precursors. Similarly, relative enzymatic activities of the various acyl-ACP thioesterases influences the relative acyl-chain composition of the resultant fatty acids. Consequently a reduction or an increase of the activity of these enzymes can alter the properties of oils produced in a plant. In fact, specific targeting of particular enzymatic activities can results in altered levels of particular fatty acids.

[266] The attached tables disclose exemplary oligonucleotides base sequences which can be used to generate site-specific mutations in plant genes encoding proteins involved in fatty acid biosynthesis.

Table 40
Oligonucleotides to produce plants with reduced palmitate

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|------------|
| Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser8Term TCG-TAG | TTTGGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGC CACCTCTGCTACGTAGTCATTCTTTCTGTACCATCTTCTTCACTTG ATCCTAATGGAAAAGGCAATAAGATTGG | 6405 |
| | CCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATGGTA CAGGAAAGAATGACTACGTAGCAGAGGTGGCCACCATGACGAGG AGATGAAGCGTTCAAAGACACTGCCACCAA | 6406 |
| | TGCTACGTAGTCATTCT | 6407 |
| | AGAATGACTACGTAGCA | 6408 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser9Term TCA-TGA | GGTGGCAGTGTCTTTGAACGCTTCATCTCCTCGTCATGGTGGCCA CCTCTGCTACGTGCTGATTCTTTCTGTACCATCTTCTTCACTTGAT CCTAATGGAAAAGGCAATAAGATTGGGTC | 6409 |
| | GACCCAATCTTATTGCCTTTTCCATTAGGATCAAGTGAAGAAGATG GTACAGGAAAGAATCACGACGTAGCAGAGGTGGCCACCATGACG AGGAGATGAAGCGTTCAAAGACACTGCCACC | 6410 |
| | TACGTGCTGATTCTTTC | 6411 |
| | GAAAGAATCACGACGTA | 6412 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Ser17Term TCA-TGA | ATCTCCTCGTCATGGTGGCCACCTCTGCTACGTCGTCATTCTTTCC TGTACCATCTTCTTGACTTGATCCTAATGGAAAAGGCAATAAGATT GGGTCTACGAATCTTGCTGGACTCAATTC | 6413 |
| | GAATTGAGTCCAGCAAGATTCGTAGACCCAATCTTATTGCCTTTTC CATTAGGATCAAGTCAAGAAGATGGTACAGGAAAGAATGACGACG TAGCAGAGGTGGCCACCATGACGAGGAGAT | 6414 |
| | ATCTTCTTGACTTGATC | 6415 |
| | GATCAAGTCAAGAAGAT | 6416 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Arabidopsis thaliana</i> Gly22Term GGA-TGA | GTGGCCACCTCTGCTACGTCGTCATTCTTTCTGTACCATCTTCTT CACTTGATCCTAATTGAAAAGGCAATAAGATTGGGTCTACGAATCT TGCTGGACTCAATTCTGCACCTAACTCTG | 6417 |
| | CAGAGTTAGGTGCAGAATTGAGTCCAGCAAGATTCGTAGACCCAA TCTTATTGCCTTTTCAATTAGGATCAAGTGAAGAAGATGGTACAGG AAAGAATGACGACGTAGCAGAGGTGGCCAC | 6418 |
| | ATCCTAATTGAAAAGGC | 6419 |
| | GCCTTTTCAATTAGGAT | 6420 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Ser8Term TCA-TGA | GCTTGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGC TACTGCCGCCACGTGATCATTCTTTCCGTTGACTTCCCCTTCTGGG GATGCCAAATCGGGCAATCCCGGAAAAGG | 6421 |
| | CCTTTTCCGGGATTGCCCGATTGGCATCCCCAGAAGGGGAAGTC AACGGAAAGAATGATCACGTGGCGGCAGTAGCAACCATTGTGGCC ACAATTAACCAATCAGATCACAAATTCAAGC | 6422 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | CGCCACGT <u>G</u> ATCATTCT | 6423 |
| | AGAATGAT <u>C</u> ACGTGGCG | 6424 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Ser9Term TCA-TGA | TGAATTTGTGATCTGATTGGTTAATTGTGGCCACAATGGTTGCTAC TGCCGCCACGTCAT <u>G</u> ATTCTTTCCGTTGACTTCCCCTTCTGGGGAT GCCAAATCGGGCAATCCCGGAAAAGGGTC | 6425 |
| | GACCCTTTTCCGGGATTGCCCGATTGGCATCCCCAGAAGGGGAA GTCAACGGAAAGAAT <u>C</u> ATGACGTGGCGGCAGTAGCAACCATTGTG GCCACAATTAACCAATCAGATCACAATTCA | 6426 |
| | CACGTCAT <u>G</u> ATTCTTTC | 6427 |
| | GAAAGAAT <u>C</u> ATGACGTG | 6428 |
| | | |
| Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Leu13Term TTG-TAG | CTGATTGGTTAATTGTGGCCACAATGGTTGCTACTGCCGCCACGT CATCATTCTTTCCGT <u>A</u> GACTTCCCCTTCTGGGGATGCCAAATCGGG CAATCCCGGAAAAGGGTCGGTGAGTTTTGG | 6429 |
| | CCAAACTCACCGACCCTTTTCCGGGATTGCCCGATTGGCATCC CCAGAAGGGGAAGT <u>C</u> TACGGAAAGAATGATGACGTGGCGGCAGT AGCAACCATTGTGGCCACAATTAACCAATCAG | 6430 |
| | CTTTCCGT <u>A</u> GACTTCCC | 6431 |
| | GGGAAGT <u>C</u> TACGGAAAG | 6432 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Garcinia mangostana</i> Lys21Term AAA-TAA | ATGGTTGCTACTGCCGCCACGTCATCATTCTTTCCGTTGACTTCCC CTTCTGGGGATGCC <u>T</u> AATCGGGCAATCCCGGAAAAGGGTCGGTG AGTTTTGGGTCAATGAAGTCGAAATCCGCGG | 6433 |
| | CCGCGGATTTGACTTCATTGACCCAAAACCTCACCGACCCTTTTCC GGGATTGCCCGATT <u>A</u> GGCATCCCCAGAAGGGGAAGTCAACGGAA AGAATGATGACGTGGCGGCAGTAGCAACCAT | 6434 |
| | GGGATGCC <u>T</u> AATCGGGC | 6435 |
| | GCCCGATT <u>A</u> GGCATCCC | 6436 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser8Term TCG-TAG | GGGATTTGAGCACGAAATTGAAGTTGTTTTTAAAAACCATGGTTGC TACTGCTGTGACAT <u>A</u> GGCGTTTTTCCCAGTCACTTCTTACCTGAC TCCTCTGACTCGAAAAACAAGAAGCTCGG | 6437 |
| | CCGAGCTTCTTGTTTTTCGAGTCAGAGGAGTCAGGTGAAGAAGTG ACTGGGAAAAACGCC <u>T</u> ATGTACAGCAGTAGCAACCATGGTTTTTA AAAACAACCTTCAATTTCTGTGCTGAAATCCC | 6438 |
| | TGTGACAT <u>A</u> GGCGTTTT | 6439 |
| | AAAACGCC <u>T</u> ATGTCACA | 6440 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser16Term TCA-TGA | TGTTTTTAAAAACCATGGTTGCTACTGCTGTGACATCGGCGTTTTT CCCAGTCACTTCTTGACCTGACTCCTCTGACTCGAAAAACAAGAAG CTCGGAAGCATCAAGTCGAAGCCATCGGT | 6441 |
| | ACCGATGGCTTCGACTTGATGCTTCCGAGCTTCTTGTTTTTCGAGT CAGAGGAGTCAGGTCAAGAAGTGACTGGGAAAAACGCCGATGTCA CAGCAGTAGCAACCATGGTTTTTAAAAACA | 6442 |
| | CACTTCTTGACCTGACT | 6443 |
| | AGTCAGGTCAAGAAGTG | 6444 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Ser22Term TCG-TAG | TTGCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACC TGACTCCTCTGACTAGAAAAACAAGAAGCTCGGAAGCATCAAGTC GAAGCCATCGGTTTCTTCTGGAAGTTTGCA | 6445 |
| | TGCAAACTTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCCG AGCTTCTTGTTTTTCTAGTCAGAGGAGTCAGGTGAAGAAGTGACTG GGAAAAACGCCGATGTCACAGCAGTAGCAA | 6446 |
| | CTCTGACTAGAAAAACA | 6447 |
| | TGTTTTTCTAGTCAGAG | 6448 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Gossypium hirsutum</i> Lys23Term AAA-TAA | GCTACTGCTGTGACATCGGCGTTTTTCCCAGTCACTTCTTCACCTG ACTCCTCTGACTCGTAAAAACAAGAAGCTCGGAAGCATCAAGTCGA AGCCATCGGTTTCTTCTGGAAGTTTGCAAG | 6449 |
| | CTTGCAAACTTCCAGAAGAAACCGATGGCTTCGACTTGATGCTTCC GAGCTTCTTGTTTTACGAGTCAGAGGAGTCAGGTGAAGAAGTGAC TGGGAAAAACGCCGATGTCACAGCAGTAGC | 6450 |
| | CTGACTCGTAAAAACAAG | 6451 |
| | CTTGTTTTACGAGTCAG | 6452 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Ser14Term TCG-TAG | CTCCCGCTCGTTGAAAGACAATGGTGGCTACCGCTGCAAGCTCTG CATTCTTCCCCGTGTAGTCCCCGGTCACCTCCTCTAGACCAGGAA AGCCCGGAAATGGGTCATCGAGCTTCAGCCC | 6453 |
| | GGGCTGAAGCTCGATGACCCATTTCGGGGCTTTCCTGGTCTAGAG GAGGTGACCGGGGACTACACGGGGAAGAATGCAGAGCTTGCAGC GGTAGCCACCATTGTCTTTCAACGAGCGGGAG | 6454 |
| | CCCCGTGTAGTCCCCGG | 6455 |
| | CCGGGGACTACACGGGG | 6456 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Arg21Term AGA-TGA | ATGGTGGCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCC CCGGTCACCTCCTCTTGACCAGGAAAGCCCGGAAATGGGTGTCG AGCTTCAGCCCCATCAAGCCCAAATTTGTCTG | 6457 |
| | CGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACCCATTTT CGGGCTTTCCTGGTCAAGAGGAGGTGACCGGGGACGACACGGG GAAGAATGCAGAGCTTGCAGCGGTAGCCACCAT | 6458 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|------------|
| | CCTCCTCTIGACCAGGA | 6459 |
| | TCCTGGTCAAGAGGAGG | 6460 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Gly23Term GGA-TGA | GCTACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTC ACCTCCTCTAGACCAIGAAAGCCCGGAAATGGGTCATCGAGCTTC AGCCCCATCAAGCCCAAATTTGTCGCCAATG | 6461 |
| | CATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATGACC CATTTCCGGGCTTTCAATGGTCTAGAGGAGGTGACCGGGGACGAC ACGGGGAAGAATGCAGAGCTTGCAGCGGTAGC | 6462 |
| | CTAGACCATGAAAGCCC | 6463 |
| | GGGCTTTCATGGTCTAG | 6464 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys24Term AAG-TAG | ACCGCTGCAAGCTCTGCATTCTTCCCCGTGTCGTCCCCGGTCACC TCCTCTAGACCAGGATAGCCCGGAAATGGGTCATCGAGCTTCAGC CCCATCAAGCCCAAATTTGTCGCCAATGGCG | 6465 |
| | CGCCATTGGCGACAAATTTGGGCTTGATGGGGCTGAAGCTCGATG ACCCATTTCCGGGCTATCCTGGTCTAGAGGAGGTGACCGGGGAC GACACGGGGAAGAATGCAGAGCTTGCAGCGGT | 6466 |
| | GACCAGGATAGCCCGGA | 6467 |
| | TCCGGGCTATCCTGGTC | 6468 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Gly23Term GGA-TGA | GCCACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGAC ACCTCCTCTAGGCCGTGAAAGCTCGGAAATGGGTCATCGAGCTTG AGCCCCCTCAAGCCCAAATTTGTCGCCAATG | 6469 |
| | CATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGATGACC CATTTCCGAGCTTTACCGGCCTAGAGGAGGTGTCCGGGGACGGC AGGGGGAAGAATGCAGAACTTGCAGCGGTGGC | 6470 |
| | CTAGGCCGTGAAAGCTC | 6471 |
| | GAGCTTTCACGGCCTAG | 6472 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Lys24Term AAG-TAG | ACCGCTGCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACC TCCTCTAGGCCGGGATAGCTCGGAAATGGGTCATCGAGCTTGAGC CCCCTCAAGCCCAAATTTGTCGCCAATGCCG | 6473 |
| | CGGCATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGCTCGAT GACCCATTTCCGAGCTATCCCGGCCTAGAGGAGGTGTCCGGGGA CGGCAGGGGGAAGAATGCAGAACTTGCAGCGGT | 6474 |
| | GGCCGGGATAGCTCGGA | 6475 |
| | TCCGAGCTATCCCGGCC | 6476 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|------------|
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Gly26Term GGA-TGA | GCAAGTTCTGCATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCT AGGCCGGGAAAGCTCTGAAATGGGTCATCGAGCTTGAGCCCCCT CAAGCCCAAATTTGTCGCCAATGCCGGGTGA | 6477 |
| | TCAACCCGGCATTGGCGACAAATTTGGGCTTGAGGGGGCTCAAGC TCGATGACCCATTTCAAGAGCTTTCCCGGCCTAGAGGAGGTGTCCG GGGACGGCAGGGGGAAGAATGCAGAACTTGC | 6478 |
| | GAAAGCTCTGAAATGGG | 6479 |
| | CCCATTTCAGAGCTTTC | 6480 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea lanceolata</i> Ser29Term TCA-TGA | CATTCTTCCCCCTGCCGTCCCCGGACACCTCCTCTAGGCCGGGAA AGCTCGGAAATGGGTGATCGAGCTTGAGCCCCCTCAAGCCCAAAT TTGTCGCCAATGCCGGGTGAAGGTTAAGGC | 6481 |
| | GCCTTAACCTTCAACCCGGCATTGGCGACAAATTTGGGCTTGAGG GGGCTCAAGCTCGATCACCCATTTCCGAGCTTTCCCGGCCTAGAG GAGGTGTCCGGGGACGGCAGGGGGAAGAATG | 6482 |
| | AAATGGGTGATCGAGCT | 6483 |
| | AGCTCGATCACCCATTT | 6484 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Ser9Term TCG-TAG | CGTTTAAGTGGATCGGACATTTAAGTGTTTTAATCATGGTAGCTAT GAGTGCTACTGCGTAGCTGTTTCCGGTTTCTTCCCCAAAACCTCAC TCTGGAGCCAAGACATCTGATAAGCTTGG | 6485 |
| | CCAAGCTTATCAGATGTCTTGGCTCCAGAGTGAGGTTTTGGGGAA GAAACCGGAAACAGCTACGCAGTAGCACTCATAGCTACCATGATT AAAACACTTAAATGTCCGATCCACTTAAACG | 6486 |
| | TACTGCGTAGCTGTTTC | 6487 |
| | GAAACAGCTACGCAGTA | 6488 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Lys17Term AAA-TAA | AGTGTTTTAATCATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTC CGGTTTCTTCCCCATAACCTCACTCTGGAGCCAAGACATCTGATAA GCTTGGAGGTGAACCAGGTAGTGTTGCTG | 6489 |
| | CAGCAACACTACCTGGTTACCTCCAAGCTTATCAGATGTCTTGGC TCCAGAGTGAGGTTATGGGGAAGAAACCGGAAACAGCGACGCAG TAGCACTCATAGCTACCATGATTAACACT | 6490 |
| | CTTCCCCATAACCTCAC | 6491 |
| | GTGAGGTTATGGGGAAG | 6492 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Gly21Term GGA-TGA | ATGGTAGCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCC CAAAACCTCACTCTGAGCCAAGACATCTGATAAGCTTGAGGGTG AACCAGGTAGTGTTGCTGTGCGCGGAATCA | 6493 |
| | TGATTCCGCGCACAGCAACACTACCTGGTTACCTCCAAGCTTATC AGATGTCTTGGCTCAAGAGTGAGGTTTTGGGGAAGAAACCGGAAA CAGCGACGCAGTAGCACTCATAGCTACCAT | 6494 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | CTCACTCT <u>I</u> GAGCCAAG | 6495 |
| | CTTGGCTC <u>A</u> AGAGTGAG | 6496 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Helianthus annuus</i> Lys23Term AAG-TAG | GCTATGAGTGCTACTGCGTCGCTGTTTCCGGTTTCTTCCCCAAAAC CTCACTCTGGAGCCT <u>I</u> AGACATCTGATAAGCTTGGAGGTGAACCAG GTAGTGTTGCTGTGCGCGGAATCAAGACAA | 6497 |
| | TTGTCTTGATTCCGCGCACAGCAACACTACCTGGTTTACCTCCAAG CTTATCAGATGTCT <u>A</u> GGCTCCAGAGTGAGGTTTTGGGGAAGAAAC CGGAAACAGCGACGCAGTAGCACTCATAGC | 6498 |
| | CTGGAGCCT <u>I</u> AGACATCT | 6499 |
| | AGATGTCT <u>A</u> GGCTCCAG | 6500 |
| | | |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Lys21Term AAA-TAA | ATGGTGGCTGCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCC CCAGGAGCCTCCCCT <u>I</u> AACCTGGGAAGTTAGGCAACTGGTCATCG AGTTTGAGCCCTTCCCTGAAGCCCAAGTCAA | 6501 |
| | TTGACTTGGGCTTCAAGGAAGGGCTCAAACCTCGATGACCAGTTGC CTAACTTCCCAGGTT <u>A</u> AGGGGAGGCTCCTGGGGATGGAACAGGG AAGCATGCAGAACTTGCTGCAGCAGCCACCAT | 6502 |
| | CCTCCCCT <u>I</u> AACCTGGG | 6503 |
| | CCCAGGTT <u>A</u> AGGGGAGG | 6504 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Lys24Term AAG-TAG | GCTGCAGCAAGTTCTGCATGCTTCCCTGTTCCATCCCCAGGAGCC TCCCCTAAACCTGGG <u>I</u> AGTTAGGCAACTGGTCATCGAGTTTGAGC CCTTCCTTGAAGCCCAAGTCAATCCCCAATG | 6505 |
| | CATTGGGGATTGACTTGGGCTTCAAGGAAGGGCTCAAACCTCGATG ACCAGTTGCCTAACT <u>A</u> CCAGGTTTAGGGGAGGCTCCTGGGGATG GAACAGGGAAGCATGCAGAACTTGCTGCAGC | 6506 |
| | AACCTGGG <u>I</u> AGTTAGGC | 6507 |
| | GCCTAACT <u>A</u> CCAGGTT | 6508 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Trp28Term TGG-TGA | TGCATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAAACCTGG GAAGTTAGGCAACTG <u>A</u> TCATCGAGTTTGAGCCCTTCCCTGAAGCC CAAGTCAATCCCCAATGGCGGATTTCAAGTT | 6509 |
| | AACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAAGG GCTCAAACCTCGATGAT <u>C</u> AGTTGCCTAACTTCCCAGGTTTAGGGGA GGCTCCTGGGGATGGAACAGGGAAGCATGCA | 6510 |
| | GGCAACTG <u>A</u> TCATCGAG | 6511 |
| | CTCGATGAT <u>C</u> AGTTGCC | 6512 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea palustris</i> Ser29Term TCA-TGA | CATGCTTCCCTGTTCCATCCCCAGGAGCCTCCCCTAAACCTGGGA AGTTAGGCAACTGGT G ATCGAGTTTGAGCCCTTCCTTGAAGCCCA AGTCAATCCCCAATGGCGGATTT C AGGTAA | 6513 |
| | TTAACCTGAAATCCGCCATTGGGGATTGACTTGGGCTTCAAGGAA GGGCTCAA A CTCGAT C ACCAGTTGCCTAACTTCCCAGGTTTAGGG GAGGCTCCTGGGGATGGAACAGGGAAGCATG | 6514 |
| | CAACTGGT G ATCGAGTT | 6515 |
| | AACTCGAT C ACCAGTTG | 6516 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys21Term AAA-TAA | ATGGTGGCTGCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACC CCGGGAATCTCCCCT T AACCCGGGAAGTTCGGTAATGGTGGCTTT CAGGTAAAGGCAAACGCCAATGCCCATCCTA | 6517 |
| | TAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGCCACCATTAC CGAACTTCCCGGGTT A AGGGGAGATTCCCGGGGTTGGAACGGAG AAGAATGCAGAACTTGCTGCGGCAGCCACCAT | 6518 |
| | TCTCCCCT T AACCCGGG | 6519 |
| | CCCGGGTT A AGGGGAGA | 6520 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys24Term AAG-TAG | GCCGCAGCAAGTTCTGCATTCTTCTCCGTTCCAACCCCGGGAATC TCCCCTAAACCCGGG T AGTTCCGGTAATGGTGGCTTTCAGGTAAAG GCAAACGCCAATGCCCATCCTAGTCTAAAGT | 6521 |
| | ACTTTAGACTAGGATGGGCATTGGCGTTTGCCTTAACCTGAAAGC CACCATTACCGAACT A CCCGGGTTTAGGGGAGATTCCCGGGGTTG GAACGGAGAAGAATGCAGAACTTGCTGCGGC | 6522 |
| | AACCCGGG T AGTTCCGGT | 6523 |
| | ACCGAACT A CCCGGGTT | 6524 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Gln31Term CAG-TAG | TTCTCCGTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTC GGTAATGGTGGCTTT T AGGTTAAGGCAAACGCCAATGCCCATCCT AGTCTAAAGTCTGGCAGCCTCGAGACTGAAG | 6525 |
| | CTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGGCATTGG CGTTTGCCTTAACCT A AAAGCCACCATTACCGAACTTCCCGGGTTT AGGGGAGATTCCCGGGGTTGGAACGGAGAA | 6526 |
| | GTGGCTTT T AGGTTAAG | 6527 |
| | CTTAACCT A AAAGCCAC | 6528 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Cuphea hookeriana</i> Lys33Term AAG-TAG | GTTCCAACCCCGGGAATCTCCCCTAAACCCGGGAAGTTCGGTAAT GGTGGCTTTCAGGTT T AGGCAAACGCCAATGCCCATCCTAGTCTA AAGTCTGGCAGCCTCGAGACTGAAGATGACA | 6529 |
| | TGTCATCTTCAGTCTCGAGGCTGCCAGACTTTAGACTAGGATGGG CATTGGCGTTTGCCT A AACCTGAAAGCCACCATTACCGAACTTCCC GGGTTTAGGGGAGATTCCCGGGGTTGGAAC | 6530 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|------------|
| | TTCAGGTT <u>T</u> AGGCAAAC | 6531 |
| | GTTTGCCT <u>A</u> AACCTGAA | 6532 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Gln21Term CAA-TAA | ATGTTGAAGCTCTCGTGTAATGCGACTGATAAGTTACAGACCCTCTCTCGCATTCTCAT <u>T</u> AACCGGATCCGGCACACCGGAGAACCGTCTCCTCCGTGTCGTGCTCTCATCTGAGGAAAC | 6533 |
| | GTTTCCTCAGATGAGAGCACGACACGGAGGAGACGGTTCTCCGGTGTGCCGGATCCGGTT <u>A</u> ATGAGAATGCGAGAAGAGGGTCTGTAACCTATCAGTCGCATTACACGAGAGCTTCAACAT | 6534 |
| | ATTCTCAT <u>T</u> AACCGGAT | 6535 |
| | ATCCGGTT <u>A</u> ATGAGAAT | 6536 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Arg28Term AGA-TGA | GCGACTGATAAGTTACAGACCCTCTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGTGAACCGTCTCCTCCGTGTCGTGCTCTCATCTGAGGAAACCGGTTCTCGATCCTTTGCGAG | 6537 |
| | CTCGCAAAGGATCGAGAACCGGTTTCCTCAGATGAGAGCACGACACGGAGGAGACGGTTC <u>A</u> CCGGTGTGCCGGATCCGGTTGATGAGAA | 6538 |
| | TGCGAGAAGAGGGTCTGTAACCTATCAGTCGC | 6539 |
| | CACACCGGTGAACCGTC | 6540 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Ser24Term TCG-TAG | GACGGTTC <u>A</u> CCGGTGTG | 6541 |
| | CCCTCTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAA | 6542 |
| | CCGTCTCCTCCGTGT <u>A</u> GTGCTCTCATCTGAGGAAACCGGTTCTCGATCCTTTGCGAGCGATCGTATCTGCTGATCA | 6543 |
| | TGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGGTTTCCTCAGATGAGAGCACT <u>T</u> ACACGGAGGAGACGGTTCTCCGGTGTGCCGGATCCGGTTGATGAGAATGCGAGAAGAGGG | 6544 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Brassica rapa</i> Cys25Term TGC-TGA | CTCCGTGT <u>A</u> GTGCTCTC | 6545 |
| | GAGAGCACT <u>T</u> ACACGGAG | 6546 |
| | CTTCTCGCATTCTCATCAACCGGATCCGGCACACCGGAGAACCGTCTCCTCCGTGTCGTG <u>A</u> TCTCATCTGAGGAAACCGGTTCTCGATCC | 6547 |
| | TTTGCGAGCGATCGTATCTGCTGATCAAGGATCCTTGATCAGCAGATACGATCGCTCGCAAAGGATCGAGAACCGGTTTCCTCAGATGAGAT <u>C</u> ACGACACGGAGGAGACGGTTCTCCGGTG | 6548 |
| | TGCCGGATCCGGTTGATGAGAATGCGAGAAG | |
| | GTGTCGTG <u>A</u> TCTCATCT | |
| | AGATGAGAT <u>C</u> ACGACAC | |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Leu2Term TTG-TAG | ATTCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAAGG GCATCAAAAATGTAGAAGCTTTCGTGTAATGTGACTAACAACCTTAC ACACCTTCTCCTTCTTCTCCGATTCTCCTC | 6549 |
| | GAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCACA TTACACGAAAGCTTCTACATTTTTGATGCCCTTTTTTTTTTATGGTTC CTGAGGTTTTGGTTTATAGAAGAAGAAT | 6550 |
| | AAAAATGTAGAAGCTTT | 6551 |
| | AAAGCTTCTACATTTTT | 6552 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Lys3Term AAG-TAG | TCTTCTTCTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAAGGG CATCAAAAATGTTGTAGCTTTCGTGTAATGTGACTAACAACCTTACAC ACCTTCTCCTTCTTCTCCGATTCTCTCC | 6553 |
| | GGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTTGTTAGTCA CATTACACGAAAGCTACAACATTTTTGATGCCCTTTTTTTTTATGG TTCCTGAGGTTTTGGTTTATAGAAGAAGA | 6554 |
| | AAATGTTGTAGCTTTTCG | 6555 |
| | CGAAAGCTACAACATTT | 6556 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Ser5Term TCG-TAG | CTATAAACCAAAACCTCAGGAACCATAAAAAAAAAAAGGGCATCAAA AATGTTGAAGCTTTAGTGTAAATGTGACTAACAACCTTACACACCTTCT CCTTCTTCTCCGATTCTCTCCCTTTTCAT | 6557 |
| | ATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTAAGTT GTTAGTCACATTACACTAAAGCTTCAACATTTTTGATGCCCTTTTTT TTTTATGGTTCCTGAGGTTTTGGTTTATAG | 6558 |
| | GAAGCTTTAGTGTAAATG | 6559 |
| | CATTACACTAAAGCTTC | 6560 |
| Reduced palmitate Acyl-ACP-thioesterase <i>Brassica napus</i> Cys6Term TGT-TGA | AAACCAAAACCTCAGGAACCATAAAAAAAAAAAGGGCATCAAAAATG TTGAAGCTTTCGTGAAATGTGACTAACAACCTTACACACCTTCTCCTT CTTCTCCGATTCTCTCCCTTTTCATCCCG | 6561 |
| | CGGGATGAAAAGGGAGGAATCGGAGAAGAAGGAGAAGGTGTGTA AGTTGTTAGTCACATTACGAAAGCTTCAACATTTTTGATGCCCTT TTTTTTTTATGGTTCCTGAGGTTTTGGTTT | 6562 |
| | CTTTCGTGAAATGTGAC | 6563 |
| | GTCACATTACGAAAG | 6564 |

Table 41
Oligonucleotides to produce plants with increased stearate

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Lys4Term AAG-TAG | GGGAGAGCTCTAGCTCTGTAGAAAAGAAGGATTCATTCATCATATC CAGAAATGGCTCTATAGTTTAAACCCTTTGGTGGCATCTCAGCCTTA CAAATTCCTTCCTCGACTCGTCCGCCAA | 6565 |
| | TTGGCGGACGAGTCGAGGAAGGGAATTTGTAAGGCTGAGATGCC ACCAAAGGGTTAAACTATAGAGCCATTCTGGATATGATGAATGAA TCCTTCTTTTCTACAGAGCTAGAGCTCTCCC | 6566 |
| | TGGCTCTATAGTTTAAAC | 6567 |
| | GTAAACTATAGAGCCA | 6568 |
| Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Leu8Term TTG-TAG | CTCTGTAGAAAAGAAGGATTCATTCATCATATCCAGAAATGGCTCT AAAGTTTAAACCCTTAGGTGGCATCTCAGCCTTACAAATTCCTTCC TCGACTCGTCCGCCAACTCCTTCTTTCAG | 6569 |
| | CTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAAGGGAATTTGTA AGGCTGAGATGCCACCTAAGGGTTAACTTTAGAGCCATTTCTGG ATATGATGAATGAATCCTTCTTTTCTACAGAG | 6570 |
| | TAACCCTTAGGTGGCAT | 6571 |
| | ATGCCACCTAAGGGTTA | 6572 |
| Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Gln12Term CAG-TAG | AGAAGGATTCATTCATCATATCCAGAAATGGCTCTAAAGTTTAAACC CTTTGGTGGCATCTTAGCCTTACAAATTCCCTTCCTCGACTCGTCC GCCAACTCCTTCTTTCAGATCTCCCAAGT | 6573 |
| | ACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAGTCGAGGAA GGGAATTTGTAAGGCTAAGATGCCACCAAAGGGTTAACTTTAGA GCCATTTCTGGATATGATGAATGAATCCTTCT | 6574 |
| | TGGCATCTTAGCCTTAC | 6575 |
| | GTAAGGCTAAGATGCCA | 6576 |
| Increased stearate stearoyl-ACP desaturase <i>Arabidopsis thaliana</i> Phe14Term TAC-TAG | TCATTCATCATATCCAGAAATGGCTCTAAAGTTTAAACCCTTTGGTG GCATCTCAGCCTTAGAAATTCCCTTCCTCGACTCGTCCGCCAACTC CTTCTTTCAGATCTCCCAAGTTCCTCTGC | 6577 |
| | GCAGAGGAACTTGGGAGATCTGAAAGAAGGAGTTGGCGGACGAG TCGAGGAAGGGAATTTCTAAGGCTGAGATGCCACCAAAGGGTTAA ACTTTAGAGCCATTTCTGGATATGATGAATGA | 6578 |
| | CAGCCTTAGAAATTTCC | 6579 |
| | GGGAATTTCTAAGGCTG | 6580 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Leu3Term TTG-TAG | GAGAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAA AAAGAAAATGGCATAGAAGCTTAACCCTTTGGCATCTCAGCCTTAC AAACTCCCTTCCTCGGCTCGTCCGCCAAT | 6581 |
| | ATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAAGGCTGAGATGC CAAAGGGTTAAGCTTCTATGCCATTTTCTTTTTTTTGATACGAGGTT TGATGTTCTTTCAGACACGAGCGAGCTCTC | 6582 |
| | AATGGCATAGAAGCTTA | 6583 |
| | TAAGCTTCTATGCCATT | 6584 |
| Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Lys4Term AAG-TAG | GAGCTCGCTCGTGTCTGAAAGAACATCAAACCTCGTATCAAAAA AGAAAATGGCATTGTAGCTTAACCCTTTGGCATCTCAGCCTTACAA ACTCCCTTCCTCGGCTCGTCCGCCAATCT | 6585 |
| | AGATTGGCGGACGAGCCGAGGAAGGGAGTTTGTAAAGGCTGAGAT GCCAAAGGGTTAAGCTACAATGCCATTTTCTTTTTTTTGATACGAG GTTTGATGTTCTTTCAGACACGAGCGAGCTC | 6586 |
| | TGGCATTGTAGCTTAAC | 6587 |
| | GTTAAGCTACAATGCCA | 6588 |
| Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Leu8Term TTG-TAG | TCTGAAAGAACATCAAACCTCGTATCAAAAAAAGAAAATGGCATT GAAGCTTAACCCTTAGGCATCTCAGCCTTACAACTCCCTTCCTCG GCTCGTCCGCCAATCTCTACTCTCAGATC | 6589 |
| | GATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAAGGGAGTTT GTAAGGCTGAGATGCCTAAGGGTTAAGCTTCAATGCCATTTTCTTT TTTTTGATACGAGGTTTGATGTTCTTTCAGA | 6590 |
| | TAACCCTTAGGCATCTC | 6591 |
| | GAGATGCCTAAGGGTTA | 6592 |
| Increased stearate stearoyl-ACP desaturase <i>Brassica napus</i> Gln11Term CAG-TAG | AACATCAAACCTCGTATCAAAAAAAGAAAATGGCATTGAAGCTTA ACCCTTTGGCATCTTAGCCTTACAACTCCCTTCCTCGGCTCGTCC GCCAATCTCTACTCTCAGATCTCCCAAGT | 6593 |
| | ACTTGGGAGATCTGAGAGTAGAGATTGGCGGACGAGCCGAGGAA GGGAGTTTGTAAAGGCTAAGATGCCAAAGGGTTAAGCTTCAATGCC ATTTTCTTTTTTTTGATACGAGGTTTGATGTT | 6594 |
| | TGGCATCTTAGCCTTAC | 6595 |
| | GTAAGGCTAAGATGCCA | 6596 |
| Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Gln27Term CAA-TAA | AACCAAAAGAAAAAGGTAAGAAAAAAACAATGGCTCTCAAGCTCA ATCCTTTCCTTCTTAAACCCAAAAGTTACCTTCTTTCGCTCTTCCA CCAATGGCCAGTACCAGATCTCCTAAGT | 6597 |
| | ACTTAGGAGATCTGGTACTGGCCATTGGTGGAAGAGCGAAAGAAG GTAACTTTTGGGTTTAAAGAAAGGAAAGGATTGAGCTTGAGAGCCAT TGTTTTTTTCTTACCTTTTTCTTTTGTT | 6598 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | TCCTTTCTTAAACCCAA | 6599 |
| | TTGGGTTTAAAGAAAGGA | 6600 |
| Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Gln29Term CAA-TAA | AAGAAAAAGGTAAGAAAAAAACAATGGCTCTCAAGCTCAATCCTT TCCTTTCTCAAACCTTAAAGTTACCTTCTTTGCTCTTCCACCAATG GCCAGTACCAGATCTCCTAAGTTCTACA | 6601 |
| | TGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAAGAGCGA AAGAAGGTAACTTTTAGGTTTGAGAAAGGAAAGGATTGAGCTTGA GAGCCATTGTTTTTTTCTTACCTTTTTCTT | 6602 |
| | CTCAAACCTTAAAGTTA | 6603 |
| | TAACTTTTAAAGTTGAG | 6604 |
| Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Lys30Term AAG-TAG | AAAAAGGTAAGAAAAAAACAATGGCTCTCAAGCTCAATCCTTTCC TTTCTCAAACCCAAAGTTACCTTCTTTGCTCTTCCACCAATGGCC AGTACCAGATCTCCTAAGTTCTACATGG | 6605 |
| | CCATGTAGAACTTAGGAGATCTGGTACTGGCCATTGGTGGAAAGAG CGAAAGAAGGTAACCTATTGGGTTTGAGAAAGGAAAGGATTGAGCT TGAGAGCCATTGTTTTTTTCTTACCTTTTT | 6606 |
| | AAACCCAAAGTTACCT | 6607 |
| | AGGTAACCTATTGGGTTT | 6608 |
| Increased stearate stearoyl-ACP desaturase <i>Ricinus communis</i> Lys46Term AAG-TAG | TCTCAAACCCAAAAGTTACCTTCTTTGCTCTTCCACCAATGGCCA GTACCAGATCTCCTTAGTTCTACATGGCCTCTACCCTCAAGTCTGG TTCTAAGGAAGTTGAGAATCTCAAGAAGC | 6609 |
| | GCTTCTTGAGATTCTCAACTTCCTTAGAACCAGACTTGAGGGTAGA GGCCATGTAGAACTAAGGAGATCTGGTACTGGCCATTGGTGGAAAG AGCGAAAGAAGGTAACCTTTGGGTTTGAGA | 6610 |
| | GATCTCCTTAGTTCTAC | 6611 |
| | GTAGAACTAAGGAGATC | 6612 |
| Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Gln11Term CAA-TAA | TCTTCTGATTCATTTAATCTTTACTCATCAATGGCTCTGAGACTGAA CCCTATCCCCACCTTAAACCTTCTCCCTCCCCCAAATGGCCAGTCTC AGATCTCCCAGGTTCCGCATGGCCTCTA | 6613 |
| | TAGAGGCCATGCGGAACCTGGGAGATCTGAGACTGGCCATTTGG GGGAGGGAGAAGGTTTAAAGTGGGGATAGGGTTCACTCTCAGAGC CATTGATGAGTAAAGATTAAATGAATCAGAAGA | 6614 |
| | TCCCCACCTTAAACCTTC | 6615 |
| | GAAGGTTTAAAGTGGGGA | 6616 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Gln17Term CAA-TAA | CTTTACTCATCAATGGCTCTGAGACTGAACCCTATCCCCACCCAAA CCTTCTCCCTCCCCTAAATGGCCAGTCTCAGATCTCCCAGGTTCC GCATGGCCTCTACCCTCCGCTCCGGTTCCA | 6617 |
| | TGGAACCGGAGCGGAGGGTAGAGGCCATGCGGAACCTGGGAGAT CTGAGACTGGCCATTTAGGGGAGGGAGAAGGTTTGGGTGGGGAT AGGGTTCAGTCTCAGAGCCATTGATGAGTAAAG | 6618 |
| | CCCTCCCCTAAATGGCC | 6619 |
| | GGCCATTTAGGGGAGGG | 6620 |
| Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Arg22Term AGA-TGA | GCTCTGAGACTGAACCCTATCCCCACCCAAACCTTCTCCCTCCCC CAAATGGCCAGTCTCTGATCTCCCAGGTTCCGCATGGCCTCTACC CTCCGCTCCGGTTCCAAAGAGGTTGAAAATA | 6621 |
| | TATTTTCAACCTCTTTGGAACCGGAGCGGAGGGTAGAGGCCATGC GGAACCTGGGAGATCAGAGACTGGCCATTTGGGGGAGGGAGAAG GTTTGGGTGGGGATAGGGTTCAGTCTCAGAGC | 6622 |
| | CCAGTCTCTGATCTCCC | 6623 |
| | GGGAGATCAGAGACTGG | 6624 |
| Increased stearate stearoyl-ACP desaturase <i>Glycine max</i> Lys37Term AAA-TAA | CAAATGGCCAGTCTCAGATCTCCCAGGTTCCGCATGGCCTCTACC CTCCGCTCCGGTTCCTAAGAGGTTGAAAATATTAAGAAGCCATTCA CTCCTCCCAGAGAAGTGCATGTTCAAGTAA | 6625 |
| | TTACTTGAACATGCACTTCTCTGGGAGGAGTGAATGGCTTCTTAAT ATTTTCAACCTCTTAGGAACCGGAGCGGAGGGTAGAGGCCATGCG GAACCTGGGAGATCTGAGACTGGCCATTTG | 6626 |
| | CCGGTTCCTAAGAGGTT | 6627 |
| | AACCTCTTAGGAACCGG | 6628 |
| Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Gln11Term CAA-TAA | CAACAAGCACACACAAGAACAACATCAACAATGGCGATTTCGCATC AATACGGCGACGTTTTAATCAGACCTGTACCGTTTCATTCGCGTTTC CTCAACCGAAACCTCTCAGATCTCCCAAAT | 6629 |
| | ATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAATGAAC GGTACAGGTCTGATTAAAACGTCGCCGATTGATGCGAATCGCCA TTGTTGATGTTGTTCTTGTGTGTGCTTGTTG | 6630 |
| | CGACGTTTAAATCAGAC | 6631 |
| | GTCTGATTAAAACGTCG | 6632 |
| Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Ser12Term TCA-TGA | AAGCACACACAAGAACAACATCAACAATGGCGATTTCGCATCAATAC GGCGACGTTTCAATGAGACCTGTACCGTTTCATTCGCGTTTCTCAA CCGAAACCTCTCAGATCTCCCAAATTCGC | 6633 |
| | GCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGGAAACGCGAAT GAACGGTACAGGTCTCATTGAAACGTCGCCGATTGATGCGAATC GCCATTGTTGATGTTGTTCTTGTGTGTGCTT | 6634 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|------------|
| | GTTTCAAT <u>G</u> AGACCTGT | 6635 |
| | ACAGGTCT <u>C</u> ATTGAAAC | 6636 |
| Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Tyr15Term TAC-TAG | AAGAACAACATCAACAATGGCGATTTCGCATCAATACGGCGACGTTT CAATCAGACCTGTAG <u>G</u> CGTTTCATTTCGCGTTTCCTCAACCGAAACCTC TCAGATCTCCCAAATTCGCCATGGCTTCC | 6637 |
| | GGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGTTGAGG AAACGCGAATGAACG <u>C</u> TACAGGTCTGATTGAAACGTCGCCGTATT GATGCGAATCGCCATTGTTGATGTTGTTCTT | 6638 |
| | GACCTGTAG <u>G</u> CGTTCATT | 6639 |
| | AATGAACG <u>C</u> TACAGGTC | 6640 |
| Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Ser17Term TCA-TGA | CAACATCAACAATGGCGATTTCGCATCAATACGGCGACGTTTCAATC AGACCTGTACCGTT <u>G</u> ATTTCGCGTTTCCTCAACCGAAACCTCTCAGA TCTCCCAAATTCGCCATGGCTTCCACCAT | 6641 |
| | ATGGTGGAAGCCATGGCGAATTTGGGAGATCTGAGAGGTTTCGGT TGAGGAAACGCGAAT <u>C</u> AACGGTACAGGTCTGATTGAAACGTCGCC GTATTGATGCGAATCGCCATTGTTGATGTTG | 6642 |
| | GTACCGTT <u>G</u> ATTTCGCGT | 6643 |
| | ACGCGAAT <u>C</u> AACGGTAC | 6644 |
| Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Arg4Term CGA-TGA | ACACACAACACACACTCAATCACACACACATCATCATCTTCTTCATC AACGATGGCGCTTT <u>I</u> GAATGAGTCCGGTGACGCTTCAACGGGAGAT ATATCCTTCATACACTTTTCATCAATCGA | 6645 |
| | TCGATTGATGAAAAGTGTATGAAGGATATATCTCCCGTTGAAGCGT CACCGGACTCATT <u>C</u> AAGCGCCATCGTTGATGAAGAAGATGATGA TGTGTGTGTGATTGAGTGTGTGTTGTGTGT | 6646 |
| | TGGCGCTTT <u>I</u> GAATGAGT | 6647 |
| | ACTCATT <u>C</u> AAGCGCCA | 6648 |
| Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Gln11Term CAA-TAA | ACACACACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGA GTCCGGTGACGCTTT <u>I</u> AACGGGAGATATATCCTTCATACACTTTTCA TCAATCGAAAAATCTCAGATCTCCTAAAT | 6649 |
| | ATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTATGAAGG ATATATCTCCCGTT <u>A</u> AAGCGTCACCGGACTCATTGAAGCGCCATC GTTGATGAAGAAGATGATGATGTGTGTGT | 6650 |
| | TGACGCTTT <u>I</u> AACGGGAG | 6651 |
| | CTCCCGTT <u>A</u> AAGCGTCA | 6652 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|------------|
| Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Glu13Term GAG-TAG | ACATCATCATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGG TGACGCTTCAACGGTAGATATATCCTTCATACACTTTTCATCAATCG AAAAATCTCAGATCTCCTAAATTCGCGA | 6653 |
| | TCGCGAATTTAGGAGATCTGAGATTTTTCGATTGATGAAAAGTGTA TGAAGGATATATCTACCGTTGAAGCGTCACCGGACTCATTCTGAAG CGCCATCGTTGATGAAGAAGATGATGATGT | 6654 |
| | TTCAACGGTAGATATAT | 6655 |
| | ATATATCTACCGTTGAA | 6656 |
| Increased stearate stearoyl-ACP desaturase <i>Helianthus annuus</i> Tyr15Term TAT-TAG | ATCTTCTTCATCAACGATGGCGCTTCGAATGAGTCCGGTGACGCTT CAACGGGAGATATAGCCTTCATACACTTTTCATCAATCGAAAAATC TCAGATCTCCTAAATTCGCGATGGCTTCC | 6657 |
| | GGAAGCCATCGCGAATTTAGGAGATCTGAGATTTTTCGATTGATGA AAAGTGTATGAAGGCTATATCTCCCGTTGAAGCGTCACCGGACTC ATTCGAAGCGCCATCGTTGATGAAGAAGAT | 6658 |
| | GAGATATAGCCTTCATA | 6659 |
| | TATGAAGGCTATATCTC | 6660 |
| Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Lys4Term AAG-TAG | AACTCAGCCAGCTTGCCCCAAACAACAGCGCAGAAAAACCTTCA ACAACAATGGCTCTCTAGCTCAACCCAGTCACCACCTTCCCTTCAA CACGCTCCCTCAACAATTCTCCTCCAGAT | 6661 |
| | ATCTGGAGGAGAAGTTGTTGAGGGAGCGTGTTGAAGGGAAGGTG GTGACTGGGTTGAGCTAGAGAGCCATTGTTGTTGAAGGTTTTCT GCGCTGTTGTTTGGGGCAAGCTGGCTGAGTT | 6662 |
| | TGGCTCTCTAGCTCAAC | 6663 |
| | GTTGAGCTAGAGAGCCA | 6664 |
| Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Ser13Term TCA-TGA | GCGCAGAAAAACCTTCAACAACAATGGCTCTCAAGCTCAACCCAG TCACCACCTTCCCTTGAAACACGCTCCCTCAACAATTCTCCTCCAG ATCTCCTCGCACCTTTCTCATGGCTGCTTC | 6665 |
| | GAAGCAGCCATGAGAAAGGTGCGAGGAGATCTGGAGGAGAAGTT GTTGAGGGAGCGTGTTCAAGGGAAGGTGGTGACTGGGTTGAGCT TGAGAGCCATTGTTGTTGAAGGTTTTCTGCGC | 6666 |
| | CTTCCCTTGAAACACGCT | 6667 |
| | AGCGTGTTCAAGGGAAG | 6668 |
| Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Arg23Term AGA-TGA | CTCAAGCTCAACCCAGTCACCACCTTCCCTTCAACACGCTCCCTCA ACAATTCTCCTCTGATCTCCTCGCACCTTTCTCATGGCTGCTTC CACTTTCAATTCCACCTCCACCAAGTAAG | 6669 |
| | CTTACTTGGTGGAGGTGGAATTGAAAGTGGAAGCAGCCATGAGAA AGGTGCGAGGAGATCAAGGAGGAGAAGTTGTTGAGGGAGCGTGTT GAAGGGAAGGTGGTGACTGGGTTGAGCTTGAG | 6670 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | TCTCCTCC <u>I</u> GATCTCCT | 6671 |
| | AGGAGATC <u>A</u> GGAGGAGA | 6672 |
| Increased stearate stearoyl-ACP desaturase <i>Linum usitatissimum</i> Lys41Term AAG-TAG | TCCTCCAGATCTCCTCGCACCTTTCTCATGGCTGCTTCCACTTTCA ATTCCACCTCCACCT <u>I</u> AGTAAGCATCTCCTCCTCCTCGGAATCTCCG CCGATTTCTTTTAAGCGATTGATCGTAGA | 6673 |
| | TCTACGATCAATCGCTTAAAGAAATCGGCGGAGATTCCGAGGAG GAGGAGATGCTTACT <u>A</u> GGTGGAGGTGGAATTGAAAGTGAAGCA GCCATGAGAAAGGTGCGAGGAGATCTGGAGGA | 6674 |
| | CCTCCACCT <u>I</u> AGTAAGCA | 6675 |
| | TGCTTACT <u>A</u> GGTGGAGG | 6676 |
| Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Arg21Term AGA-TGA | ATGGCACTGAAACTTTGCTTTCCACCCACAAGATGCCTTCCTTCC CCGATGCTCGTATC <u>I</u> GATCTCACAGGGTTTTTCATGGCTTCAACTAT TCATTCTCCTTCTATGGAGGTTCGAAAAG | 6677 |
| | CTTTTCCGACCTCCATAGAAGGAGAATGAATAGTTGAAGCCATGAA AACCCTGTGAGATC <u>A</u> GATACGAGCATCGGGGAAGGAAGGCATCTT GTGGGGTGGAAGCAAAGTTTCAGTGCCAT | 6678 |
| | CTCGTATC <u>I</u> GATCTCAC | 6679 |
| | GTGAGATC <u>A</u> GATACGAG | 6680 |
| Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Ser29Term TCA-TGA | CCCACAAGATGCCTTCCTTCCCGATGCTCGTATCAGATCTCACAG GGTTTTCATGGCTT <u>G</u> AACTATTCAATTCTCCTTCTATGGAGGTTCGGA AAAGTTAAAAAGCCTTTCACGCCTCCACG | 6681 |
| | CGTGGAGGCGTGAAAGGCTTTTAACTTTTCCGACCTCCATAGAA GGAGAATGAATAGTT <u>C</u> AAGCCATGAAAACCCTGTGAGATCTGATAC GAGCATCGGGGAAGGAAGGCATCTTGTGGG | 6682 |
| | CATGGCTT <u>G</u> AACTATTC | 6683 |
| | GAATAGTT <u>C</u> AAGCCATG | 6684 |
| Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Glu37Term GAG-TAG | GATGCTCGTATCAGATCTCACAGGGTTTTTCATGGCTTCAACTATTC ATTCTCCTTCTATG <u>I</u> AGGTTCGAAAAGTTAAAAAGCCTTTCACGCC TCCACGAGAGGTACATGTTCAAGTAACCC | 6685 |
| | GGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAGGCTTTT TAACTTTTCCGACCT <u>A</u> CATAGAAGGAGAATGAATAGTTGAAGCCAT GAAAACCCTGTGAGATCTGATACGAGCATC | 6686 |
| | CTTCTATG <u>I</u> AGGTTCGGA | 6687 |
| | TCCGACCT <u>A</u> CATAGAAG | 6688 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Increased stearate stearoyl-ACP desaturase <i>Olea europaea</i> Gly39Term GGA-TGA | CGTATCAGATCTCACAGGGTTTTTCATGGCTTCAACTATTCATTCTC CTTCTATGGAGGTCIGAAAAGTTAAAAAGCCTTTCACGCCTCCACG AGAGGTACATGTTCAAGTAACCCATTCT | 6689 |
| | AGGAATGGGTTACTTGAACATGTACCTCTCGTGGAGGCGTGAAAG GCTTTTTAACTTTTCAAGACCTCCATAGAAGGAGAATGAATAGTTGA AGCCATGAAAACCCTGTGAGATCTGATACG | 6690 |
| | TGGAGGTCIGAAAAGTT | 6691 |
| | AACTTTTCAAGACCTCCA | 6692 |
| Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Lys4Term AAA-TAA | TTCTCGTTTTTGTCGTCCCCTCTGCTCTCTCTCTATCAGGCACG GAGAAATGGCACTGTAACTCAGTCCAGTCATGTTTCAATCTCAGAA GCTTCCATTTCTTGCCCTCCTATCCGCCTT | 6693 |
| | AAGGCGGATAGGAGGCAAGAAATGGAAGCTTCTGAGATTGAAACA TGAAGGACTGAGTTAAGTGCCTTTCTCCGTGCCTGATAGAGA GAGAGAGCAGAGGGGACGACAAAACGAGAA | 6694 |
| | TGGCACTGTAACTCAGT | 6695 |
| | ACTGAGTTAAGTGCCA | 6696 |
| Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Gln11Term CAA-TAA | CTGCTCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCA GTCCAGTCATGTTTAAATCTCAGAAGCTTCCATTTCTTGCCCTCCTAT CCGCCTTCCAATCTCAGATCTCCGAGGG | 6697 |
| | CCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAAGAAAT GGAAGCTTCTGAGATTAAACATGACTGGACTGAGTTTCAGTGCC ATTTCTCCGTGCCTGATAGAGAGAGAGAGCAG | 6698 |
| | TCATGTTTAAATCTCAG | 6699 |
| | CTGAGATTAAACATGA | 6700 |
| Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Gln13Term CAG-TAG | TCTCTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCA GTCATGTTTCAATCTTAGAAGCTTCCATTTCTTGCCCTCCTATCCGCC TTCCAATCTCAGATCTCCGAGGGTTTTCA | 6701 |
| | TGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAGGCAA GAAATGGAAGCTTCTAAGATTGAAACATGACTGGACTGAGTTTCAG TGCCATTTCTCCGTGCCTGATAGAGAGAGA | 6702 |
| | TTCAATCTTAGAAGCTT | 6703 |
| | AAGCTTCTAAGATTGAA | 6704 |
| Increased stearate stearoyl-ACP desaturase <i>Persea americana</i> Lys14Term AAG-TAG | CTCTCTATCAGGCACGGAGAAATGGCACTGAAACTCAGTCCAGTC ATGTTTCAATCTCAGTAGCTTCCATTTCTTGCCCTCCTATCCGCCTTC CAATCTCAGATCTCCGAGGGTTTTCATGG | 6705 |
| | CCATGAAAACCCTCGGAGATCTGAGATTGGAAGGCGGATAGGAG GCAAGAAATGGAAGCTACTGAGATTGAAACATGACTGGACTGAGT TTCAGTGCCATTTCTCCGTGCCTGATAGAGAG | 6706 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| | AATCTCAG <u>I</u> AGCTTCCA | 6707 |
| | TGGAAGCT <u>A</u> CTGAGATT | 6708 |
| Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Tyr12Term TAC-TAG | CCCCGAGATCTCGCTGCCGCTGCTCATGGCGTTCGCGGCGTCCC ACACCGCATCGCCGTA <u>G</u> TCCTGCGGCGGCGTGGCGCAGAGGAG GAGCAATGGGATGTCTGAAGATGGTGGCCATGGCC | 6709 |
| | GGCCATGGCCACCATCTTCGACATCCCATTGCTCCTCCTCTGCGC CACGCCGCCGAGGAC <u>T</u> ACGGCGATGCGGTGTGGGACGCCGCG AACGCCATGAGCAGCGGCAGCGAGATCTCGGGG | 6710 |
| | TCGCCGTA <u>G</u> TCCTGCGG | 6711 |
| | CCGCAGGA <u>C</u> TACGGCGA | 6712 |
| | | |
| Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Gln19Term CAG-TAG | CTGCTCATGGCGTTCGCGGCGTCCCACACCGCATCGCCGTA <u>C</u> CTCC TGCGGCGGCGTGGCGT <u>I</u> AGAGGAGGAGCAATGGGATGTCTGAAGAT GGTGGCCATGGCCTCCACCATCAACAGGGTCA | 6713 |
| | TGACCCTGTTGATGGTGGAGGCCATGGCCACCATCTTCGACATCC CATTGCTCCTCCTCT <u>A</u> CGCCACGCCGCCGAGGAGTACGGCGAT GCGGTGTGGGACGCCGGAACGCCATGAGCAG | 6714 |
| | GCGTGGCGT <u>I</u> AGAGGAGG | 6715 |
| | CCTCCTCT <u>A</u> CGCCACGC | 6716 |
| | | |
| Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Ser26Term TCG-TAG | CCCACACCGCATCGCCGTA <u>C</u> CTGCGGCGGCGTGGCGCAGAGG AGGAGCAATGGGATGT <u>A</u> GAAGATGGTGGCCATGGCCTCCACCAT CAACAGGGTCAAGACTGCTAAGAAGCCCTACAC | 6717 |
| | GTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGGCC ATGGCCACCATCTTCT <u>I</u> ACATCCCATTGCTCCTCCTCTGCGCCACGC CGCCGCAGGAGTACGGCGATGCGGTGTGGG | 6718 |
| | TGGGATGT <u>A</u> GAAGATGG | 6719 |
| | CCATCTTCT <u>I</u> ACATCCCA | 6720 |
| | | |
| Increased stearate stearoyl-ACP desaturase <i>Oryza sativa</i> Lys27Term AAG-TAG | CACACCGCATCGCCGTA <u>C</u> CTGCGGCGGCGTGGCGCAGAGGAG GAGCAATGGGATGTCTG <u>I</u> AGATGGTGGCCATGGCCTCCACCATCAA CAGGGTCAAGACTGCTAAGAAGCCCTACACTC | 6721 |
| | GAGTGTAGGGCTTCTTAGCAGTCTTGACCCTGTTGATGGTGGAGG CCATGGCCACCATCT <u>A</u> CGACATCCCATTGCTCCTCCTCTGCGCCA CGCCGCCGAGGAGTACGGCGATGCGGTGTG | 6722 |
| | GGATGTCTG <u>I</u> AGATGGTG | 6723 |
| | CACCATCT <u>A</u> CGACATCC | 6724 |
| | | |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Leu3Term TTG-TAG | TTCTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGA GAGAAGCAATGGCGTGAAGCTTCACCACACGGCCTTCAATCCTT CCATGGCGGTTACCTCTTCGGGACTTCCTCG | 6725 |
| | CGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAGGC CGTGTGGTGAAGCTTACGCCATTGCTTCTCTCTCCTAAGTGCTT CTGTTGGTAACCGCTCAACCTAGAGAGAGAA | 6726 |
| | AATGGCGTGAAGCTTC | 6727 |
| | GAAGCTTCTACGCCATT | 6728 |
| Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Lys4Term AAG-TAG | CTCTCTCTAGGTTGAGCGGTTACCAACAGAAGCACTTAGGAGAGA GAAGCAATGGCGTTGTAGCTTCACCACACGGCCTTCAATCCTTCC ATGGCGGTTACCTCTTCGGGACTTCCTCGAT | 6729 |
| | ATCGAGGAAGTCCCGAAGAGGTAACCGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCTACAACGCCATTGCTTCTCTCTCCTAAGTG CTTCTGTTGGTAACCGCTCAACCTAGAGAGAG | 6730 |
| | TGGCGTTGTAGCTTCAC | 6731 |
| | GTGAAGCTACAACGCCA | 6732 |
| Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Ser19Term TCG-TAG | AAGCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCAT GGCGGTTACCTCTTAGGGACTTCCTCGATCGTATCACCTCAGATCT CACCGCGTTTTTCATGGCTTCTTCTACAAT | 6733 |
| | ATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGATAC GATCGAGGAAGTCCCTAAGAGGTAACCGCCATGGAAGGATTGAAG GCCGTGTGGTGAAGCTTCAACGCCATTGCTT | 6734 |
| | TACCTCTTAGGGACTTC | 6735 |
| | GAAGTCCCTAAGAGGTA | 6736 |
| Increased stearate stearoyl-ACP desaturase <i>Simmondsia chinensis</i> Gly20Term GGA-TGA | GCAATGGCGTTGAAGCTTCACCACACGGCCTTCAATCCTTCCATG GCGGTTACCTCTTCGTGACTTCCTCGATCGTATCACCTCAGATCTC ACCGCGTTTTTCATGGCTTCTTCTACAATTG | 6737 |
| | CAATTGTAGAAGAAGCCATGAAAACGCGGTGAGATCTGAGGTGAT ACGATCGAGGAAGTCAAGAAGAGGTAACCGCCATGGAAGGATTG AAGGCCGTGTGGTGAAGCTTCAACGCCATTGC | 6738 |
| | CCTCTTCGTGACTTCCT | 6739 |
| | AGGAAGTCAAGAAGAGG | 6740 |
| Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Ser21Term TCA-TGA | TGGCTCTGAATCTCAACCCCGTTTCCACACCATTTAGTGTCGTG ATTGCCGTCTTTCTGACCTCGTCAAACGCCTTCTCGCAGATCTCCC AAATTCTTCATGGCTTCCACTCTCAGCAG | 6741 |
| | CTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATCTGCGAGAA GGCGTTTGACGAGGTGAGAAAGACGGCAATCGACGACACTGAAAT GGTGTGGAACGGGGTTGAGATTCAGAGCCA | 6742 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| | GTCTTTCTGACCTCGTC | 6743 |
| | GACGAGGTGAGAAAGAC | 6744 |
| Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Gln24Term CAA-TAA | AATCTCAACCCCGTTTCCACACCATTTCAGTGTCGTCGATTGCCGT CTTTCTCACCTCGTTAAACGCCTTCTCGCAGATCTCCCAAATTCTT CATGGCTTCCACTCTCAGCAGCTCTTCTC | 6745 |
| | GAGAAGAGCTGCTGAGAGTGGAAGCCATGAAGAATTTGGGAGATC TGCGAGAAGGCGTTTAAACGAGGTGAGAAAGACGGCAATCGACGA CACTGAAATGGTGTGGAACGGGGTTGAGATT | 6746 |
| | CACCTCGTTAAACGCCT | 6747 |
| | AGGCGTTTAAACGAGGTG | 6748 |
| Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Arg29Term AGA-TGA | TCCACACCATTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGTC AAACGCCTTCTCGCTGATCTCCCAAATTCTTCATGGCTTCCACTCT CAGCAGCTCTTCTCCTAAGGAAGCGGAAA | 6749 |
| | TTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGGAAGCCATGA AGAATTTGGGAGATCAGCGAGAAGGCGTTTGACGAGGTGAGAAA GACGGCAATCGACGACACTGAAATGGTGTGGA | 6750 |
| | CTTCTCGCTGATCTCCC | 6751 |
| | GGGAGATCAGCGAGAAG | 6752 |
| Increased stearate stearoyl-ACP desaturase <i>Spinacia oleracea</i> Lys32Term AAA-TAA | TTTCAGTGTCGTCGATTGCCGTCTTTCTCACCTCGTCAAACGCCTT CTCGCAGATCTCCCTAATTCTTCATGGCTTCCACTCTCAGCAGCTC TTCTCCTAAGGAAGCGGAAAGCCTGAAGA | 6753 |
| | TCTTCAGGCTTTCCGCTTCCTTAGGAGAAGAGCTGCTGAGAGTGG AAGCCATGAAGAATTAGGGAGATCTGCGAGAAGGCGTTTGACGAG GTGAGAAAGACGGCAATCGACGACACTGAAA | 6754 |
| | GATCTCCCIAATTCTTC | 6755 |
| | GAAGAATTAGGGAGATC | 6756 |
| Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Leu10Term TTA-TGA | AAATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATAT CAATGGGGTGTCGTGAAAATCTCACAAAATGTTACCATTTCTTGT TCTTCAGCCAGATCTGAGCGAGTTTTTCAT | 6757 |
| | ATGAAACTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTAAC ATTTTGTGAGATTTTACGACACCCCATTTGATATTCAGTGCCATTGT TGATGCTCTGTTTTTCACCTCGACTATTT | 6758 |
| | GGTGTCGTGAAAATCTC | 6759 |
| | GAGATTTTACGACACC | 6760 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|------------|
| Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Lys11Term AAA-TAA | ATAGTCGAGGTGAAAAACAGAGCATCAACAATGGCACTGAATATCA ATGGGGTGTCTGTTATAATCTCACAAAATGTTACCATTTCCTTGTTCT TCAGCCAGATCTGAGCGAGTTTTCATGG | 6761 |
| | CCATGAAAACCTCGCTCAGATCTGGCTGAAGAACAAGGAAATGGTA ACATTTTGTGAGATTATAACGACACCCCATTTGATATTCAGTGCCATT GTTGATGCTCTGTTTTTCACCTCGACTAT | 6762 |
| | TGTCGTTATAATCTCAC | 6763 |
| | GTGAGATTATAACGACA | 6764 |
| Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Lys14Term AAA-TAA | GTGAAAAACAGAGCATCAACAATGGCACTGAATATCAATGGGGTG TCGTTAAAATCTCACTAAATGTTACCATTTCCTTGTTCTTCAGCCAG ATCTGAGCGAGTTTTCATGGCTTCAACCA | 6765 |
| | TGTTGAAGCCATGAAAACCTCGCTCAGATCTGGCTGAAGAACAAG GAAATGGTAACATTTAGTGAGATTTTAACGACACCCCATTTGATATT CAGTGCCATTGTTGATGCTCTGTTTTTCAC | 6766 |
| | AATCTCACTAAATGTTA | 6767 |
| | TAACATTTAGTGAGATT | 6768 |
| Increased stearate stearoyl-ACP desaturase <i>Solanum tuberosum</i> Leu16Term TTA-TGA | ACAGAGCATCAACAATGGCACTGAATATCAATGGGGTGTCTGTTAAA ATCTCACAAAATGTGACCATTTCCTTGTTCTTCAGCCAGATCTGAG CGAGTTTTTCATGGCTTCAACCATTTCATCG | 6769 |
| | CGATGAATGGTTGAAGCCATGAAAACCTCGCTCAGATCTGGCTGAA GAACAAGGAAATGGTCACATTTTGTGAGATTTTAACGACACCCCAT TGATATTCAGTGCCATTGTTGATGCTCTGT | 6770 |
| | CAAAATGTGACCATTTC | 6771 |
| | GAAATGGTCACATTTTG | 6772 |
| Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser21Term TCA-TGA | TGGCTCTGAGGCTGAACCCTAACCCCTCACAGAAGCTCTTTCTCTC TCCTTCTTCATCATGATCTTCTTCTTCTTCATCGTTCTCGCTTCCTC AAATGGCTAGCCTCAGATCTCCAAGGT | 6773 |
| | AACCTTGAGATCTGAGGCTAGCCATTTGAGGAAGCGAGAACGAT GAAGAAGAAGAAGATCATGATGAAGAAGGAGAGAGAAAGAGCTTC TGTGAAGGGTTAGGGTTCAGCCTCAGAGCCA | 6774 |
| | TTCATCATGATCTTCTT | 6775 |
| | AAGAAGATCATGATGAA | 6776 |
| Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser26Term TCA-TGA | ACCCTAACCCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCA TCTTCTTCTTCTTGATCGTTCTCGCTTCCTCAAATGGCTAGCCTCA GATCTCCAAGGTTCCGCATGGCCTCCAC | 6777 |
| | GTGGAGGCCATGCGGAACCTTGAGATCTGAGGCTAGCCATTTGA GGAAGCGAGAACGATCAAGAAGAAGAAGATGATGATGAAGAAGGA GAGAGAAAGAGCTTCTGTGAAGGGTTAGGGT | 6778 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| | TTCTTCTT <u>G</u> ATCGTTCT | 6779 |
| | AGAACGAT <u>C</u> AAGAAGAA | 6780 |
| Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser27Term TCG-TAG | CTAACCCTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCT TCTTCTTCTTCAT <u>A</u> GTTCTCGCTTCCTCAAATGGCTAGCCTCAGAT CTCCAAGGTTCCGCATGGCCTCCACCCT | 6781 |
| | AGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCTAGCCAT TTGAGGAAGCGAGAAC <u>T</u> ATGAAGAAGAAGAAGATGATGATGAAGA AGGAGAGAGAAAGAGCTTCTGTGAAGGGTTAG | 6782 |
| | TTCTTCAT <u>A</u> GTTCTCGC | 6783 |
| | GCGAGAAC <u>T</u> ATGAAGAA | 6784 |
| Increased stearate stearoyl-ACP desaturase <i>Arachis hypogaea</i> Ser29Term TCG-TAG | CTTCACAGAAGCTCTTTCTCTCTCCTTCTTCATCATCATCTTCTTCT TCTTCATCGTTCT <u>A</u> GCTTCCTCAAATGGCTAGCCTCAGATCTCCAA GGTCCGCATGGCCTCCACCCTCCGCAC | 6785 |
| | GTGCGGAGGGTGGAGGCCATGCGGAACCTTGGAGATCTGAGGCT AGCCATTTGAGGAAGCT <u>T</u> AGAACGATGAAGAAGAAGAAGATGATGA TGAAGAAGGAGAGAGAAAGAGCTTCTGTGAAG | 6786 |
| | ATCGTTCT <u>A</u> GCTTCCTC | 6787 |
| | GAGGAAGCT <u>T</u> AGAACGAT | 6788 |
| Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Leu3Term TTG-TAG | AAAGTTAAAGCCGTCCAAAACCCAAACCAGGAAAGGCAAACGAA AAGAAAAATGGCTT <u>A</u> GAATTTTAATGCCATCGCCTCGAAATCTCA GAAGCTCCCTTGCTTTGCTCTTCCACCAA | 6789 |
| | TTTGGTGAAGAGCAAAGCAAGGGAGCTTCTGAGATTTGAGGGCG ATGGCATTAAATTCT <u>A</u> AGCCATTTTTCTTTTCGTTTGCCTTTCCT GGTTTGGGTTTTGGACGGCTTTTAACTTT | 6790 |
| | AATGGCTT <u>A</u> GAATTTTA | 6791 |
| | TAAAATTCT <u>A</u> AGCCATT | 6792 |
| Increased stearate stearoyl-ACP desaturase <i>Gossypium hirsutum</i> Ser1-Term TCG-TAG | CCCAAACCAGGAAAGGCAAACGAAAAGAAAAATGGCTTTGAATTT TAATGCCATCGCCT <u>A</u> GAAATCTCAGAAGCTCCCTTGCTTTGCTCTT CCACCAAAGGCCACCCTTAGATCTCCAA | 6793 |
| | TTGGGAGATCTAAGGGTGGCCTTTGGTGAAGAGCAAAGCAAGG GAGCTTCTGAGATTTCT <u>T</u> AGGCGATGGCATTAAATTCAAAGCCATT TTTTCTTTTCGTTTGCCTTTCCTGGTTTGGG | 6794 |
| | CATCGCCT <u>A</u> GAAATCTC | 6795 |
| | GAGATTTCT <u>T</u> AGGCGATG | 6796 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Increased stearate stearyl-ACP desaturase <i>Gossypium hirsutum</i> Lys11Term AAA-TAA | CAAACCAGGAAAGGCCAAACGAAAAGAAAAAATGGCTTTGAATTTTA ATGCCATCGCCTCGTAATCTCAGAAGCTCCCTTGCTTTGCTCTTCC ACCAAAGGCCACCCTTAGATCTCCCAAGT | 6797 |
| | ACTTGGGAGATCTAAGGGTGGCCTTTGGTGGAGAGCAAAGCAAG GGAGCTTCTGAGATTACGAGGCGATGGCATTAAAATTCAAAGCCA TTTTTCTTTTCGTTTGCCTTTCCTGGTTTG | 6798 |
| | TCGCCTCGTAATCTCAG | 6799 |
| | CTGAGATTACGAGGCGA | 6800 |
| Increased stearate stearyl-ACP desaturase <i>Gossypium hirsutum</i> Gln13Term CAG-TAG | AGGAAAGGCCAAACGAAAAGAAAAAATGGCTTTGAATTTTAATGCCA TCGCCTCGAAATCTTAGAAGCTCCCTTGCTTTGCTCTTCCACCAAA GGCCACCCTTAGATCTCCCAAGTTTTCCA | 6801 |
| | TGGAAAACCTGGGAGATCTAAGGGTGGCCTTTGGTGGAGAGCAA AGCAAGGGAGCTTCTAAGATTTTCGAGGCGATGGCATTAAAATTCA AAGCCATTTTTCTTTTCGTTTGCCTTTCCT | 6802 |
| | CGAAATCTTAGAAGCTC | 6803 |
| | GAGCTTCTAAGATTTTCG | 6804 |

Table 42
Oligonucleotides to produce plants with reduced linolenic acid

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Ser4Term TCG-TAG | AATAGAACGACAGAGACTTTTTCTCTTTCTTCTTGGGAAGAGGC TCCAATGGCGAGCTAGGTTTTATCAGAATGTGGTTTTAGACCTCTC CCCAGATTCTACCCTAAACACACAACCTC | 6805 |
| | GAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTAAACCA CATTCTGATAAAACCTAGCTCGCCATTGGAGCCTCTTCCCAAGAAG AAAAGAGGAAAAAGTCTCTGTCTGTTCTATT | 6806 |
| | GGCGAGCTTGGTTTTAT | 6807 |
| | ATAAAACCAGCTCGCC | 6808 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Leu6Term TTA-TGA | ACGACAGAGACTTTTTCTCTTTCTTCTTGGGAAGAGGCTCCAAT GGCGAGCTCGGTTTGATCAGAATGTGGTTTTAGACCTCTCCCCAG ATTCTACCCTAAACACACAACCTCTTTTGC | 6809 |
| | GCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGTCTA AAACCACATTCTGATCAAACCGAGCTCGCCATTGGAGCCTCTTCCC AAGAAGAAAAGAGGAAAAAGTCTCTGTCTGT | 6810 |
| | CTCGGTTTGATCAGAAT | 6811 |
| | ATTCTGATCAAACCGAG | 6812 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Ser7Term TCA-TGA | ACAGAGACTTTTTCTCTTTCTTCTTGGGAAGAGGCTCCAATGGC GAGCTCGGTTTTATGAGAATGTGGTTTTAGACCTCTCCCCAGATTCT TACCCTAAACACACAACCTCTTTTGCCTC | 6813 |
| | GAGGCCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAGGT CTAAAACCACATTCTCATAAAACCGAGCTCGCCATTGGAGCCTCTT CCCAAGAAGAAAAGAGGAAAAAGTCTCTGT | 6814 |
| | GGTTTTATGAGAATGTG | 6815 |
| | CACATTCTCATAAAACC | 6816 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Arabidopsis thaliana</i> Glu8Term GAA-TAA | AGAGACTTTTTCTCTTTCTTCTTGGGAAGAGGCTCCAATGGCGA GCTCGGTTTTATCATTAATGTGGTTTTAGACCTCTCCCCAGATTCTA CCCTAAACACACAACCTCTTTTGCCTCTA | 6817 |
| | TAGAGGCCAAAAGAGGTTGTGTGTTTAGGGTAGAATCTGGGGAGAG GTCTAAAACCACATTATGATAAAACCGAGCTCGCCATTGGAGCCTC TTCCAAGAAGAAAAGAGGAAAAAGTCTCT | 6818 |
| | TTTTATCATTAATGTGGT | 6819 |
| | ACCACATTATGATAAAA | 6820 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Leu4Term TTG-TAG | TCATCATCTTCTTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTC TAGCAATGGCGAACTAGGTCTTATCCGAATGTGGCATAAGACCTC TCCCCAGAATCTACACCACACCCAGATCCAC | 6821 |
| | GTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTTATGCCA CATTCGGATAAGACCTAGTTCGCCATTGCTAGAGCTCTTTTGCTCT CTCTCTCTCCCCAGAAGAAGAAGATGATGA | 6822 |
| | GGCGAACTAGGTCTTAT | 6823 |
| | ATAAGACCTAGTTCGCC | 6824 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Leu6Term TTA-TGA | TCTTCTTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAA TGCGGAACCTGGTCTGATCCGAATGTGGCATAAGACCTCTCCCCA GAATCTACACCACACCCAGATCCACTTTCT | 6825 |
| | AGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGAGGTCTT ATGCCACATTTCGGATCAGACCAAGTTCGCCATTGCTAGAGCTCTTT TGCTCTCTCTCTCTCCCCAGAAGAAGAAGA | 6826 |
| | CTTGGTCTGATCCGAAT | 6827 |
| | ATTCGGATCAGACCAAG | 6828 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Glu8Term GAA-TAA | TTCTTCTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCG AACTTGGTCTTATCCTAATGTGGCATAAGACCTCTCCCCAGAATCT ACACCACACCCAGATCCACTTTCTCTCCA | 6829 |
| | TGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGGGGAGA GGTCTTATGCCACATTAGGATAAGACCAAGTTCGCCATTGCTAGA GCTCTTTTGCTCTCTCTCTCTCCCCAGAAGAA | 6830 |
| | TCTTATCCTAATGTGGC | 6831 |
| | GCCACATTAGGATAAGA | 6832 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica juncea</i> Cys9Term TGT-TGA | CTGGGGAGAGAGAGAGAGCAAAAGAGCTCTAGCAATGGCGAACT TGGTCTTATCCGAATGAGGCATAAGACCTCTCCCCAGAATCTACAC CACACCCAGATCCACTTTCTCTCCAACACC | 6833 |
| | GGTGTGGAGAGGAAAGTGGATCTGGGTGTGGTGTAGATTCTGG GGAGAGGTCTTATGCCCTCATTTCGGATAAGACCAAGTTCGCCATTG CTAGAGCTCTTTTGCTCTCTCTCTCTCCCCAG | 6834 |
| | TCCGAATGAGGCATAAG | 6835 |
| | CTTATGCCCTCATTTCGGA | 6836 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Trp5Term TGG-TGA | ATAACAGAATTGCTGAATTCTTGCATTTTAGCTTCTGGGTTTTCAA TGGCTGCTGGTTGAGTATTATCAGAATGTGGTTTAAGGCCTCTCCC AAGAATCTACTCACGACCCAGAATTGGT | 6837 |
| | ACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTTAAACC ACATTCTGATAATACTCAACCAGCAGCCATTGAAAACCCAGAAGCT AAAAATGCAAGAATTCAGCAATTCTGTTAT | 6838 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| | GCTGGTTGAGTATTATC | 6839 |
| | GATAATACTCAACCAGC | 6840 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Leu7Term TTA-TGA | AGAATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCT GCTGGTTGGGTATGATCAGAATGTGGTTTAAGGCCTCTCCCAAGA ATCTACTCACGACCCAGAATTGGTTTTAC | 6841 |
| | GTAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGCCTT AAACCACATTCTGATCATAACCAACCAGCAGCCATTGAAAACCCAG AAGCTAAAAATGCAAGAATTCAGCAATTCT | 6842 |
| | TTGGGTATGATCAGAAT | 6843 |
| | ATTCTGATCATAACCAA | 6844 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Ser8Term TCA-TGA | ATTGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCT GGTTGGGTATTATGAGAATGTGGTTTAAGGCCTCTCCCAAGAATCT ACTCACGACCCAGAATTGGTTTTACATC | 6845 |
| | GATGTAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAGGC CTTAAACCACATTCTCATAATACCAACCAGCAGCCATTGAAAACC CAGAAGCTAAAAATGCAAGAATTCAGCAAT | 6846 |
| | GGTATTATGAGAATGTG | 6847 |
| | CACATTCTCATAATACC | 6848 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Ricinus communis</i> Glu9Term GAA-TAA | TGCTGAATTCTTGCATTTTTAGCTTCTGGGTTTTCAATGGCTGCTG GTTGGGTATTATCATTAATGTGGTTTAAGGCCTCTCCCAAGAATCTA CTCACGACCCAGAATTGGTTTTACATCGA | 6849 |
| | TCGATGTAAACCAATTCTGGGTCGTGAGTAGATTCTTGGGAGAG GCCTTAAACCACATTATGATAATACCAACCAGCAGCCATTGAAAA CCCAGAAGCTAAAAATGCAAGAATTCAGCA | 6850 |
| | TATTATCATTAATGTGGT | 6851 |
| | ACCACATTATGATAATA | 6852 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Arg22Term AGA-TGA | GCAAGTTGGGTTTTATCAGAATGTGGTCTTAGACCACTCCCAAGAA TCTACCCTAAGCCCTGAAGTGGGGCAGCCACTTCTGCCTCCTCTC ACATTAAGTTGAGAATTCACGTACAGATC | 6853 |
| | GATCTGTACGTGAAATTCTCAACTTAATGTGAGAGGAGGCAGAAAGT GGCTGCCCCAGTTCAAGGGCTTAGGGTAGATTCTTGGGAGTGGTCT AAGACCACATTCTGATAAAACCAACTTGC | 6854 |
| | CTAAGCCCIGAAGTGGG | 6855 |
| | CCCAGTTCAGGGCTTAG | 6856 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|---------------|
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Lys34Term AAG-TAG | CTCCCAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCT GCCTCCTCTCACATTAGTTGAGAATTTACGTACAGATCTGAGTG GTTCTGCAATTTCTTTGTCTAATACTAATA | 6857 |
| | TATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGTACG TGAAATTCTCAACTAATGTGAGAGGAGGCAGAAGTGGCTGCCCC AGTTCTGGGCTTAGGGTAGATTCTTGGGAG | 6858 |
| | CTCACATTAGTTGAGA | 6859 |
| | TCTCAACTAATGTGAG | 6860 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Leu35Term TTG-TAG | CAAGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCT CCTCTCACATTAAGTAGAGAATTTACGTACAGATCTGAGTGGTTC TGCAATTTCTTTGTCTAATACTAATAAAGA | 6861 |
| | TCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCTGT ACGTGAAATTCTCTACTTAATGTGAGAGGAGGCAGAAGTGGCTGC CCCAGTTCTGGGCTTAGGGTAGATTCTTG | 6862 |
| | CATTAAGTAGAGAATTT | 6863 |
| | AAATTCTCTACTTAATG | 6864 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Nicotiana tabacum</i> Arg36Term AGA-TGA | AGAATCTACCCTAAGCCCAGAACTGGGGCAGCCACTTCTGCCTCC TCTCACATTAAGTTGTGAATTTACGTACAGATCTGAGTGGTCTG CAATTTCTTTGTCTAATACTAATAAAGAGA | 6865 |
| | TCTCTTTATTAGTATTAGACAAAGAAATTGCAGAACCACTCAGATCT GTACGTGAAATTCACAACTTAATGTGAGAGGAGGCAGAAGTGGCT GCCCCAGTTCTGGGCTTAGGGTAGATTCT | 6866 |
| | TTAAGTTGTGAATTTCA | 6867 |
| | TGAAATTCACAACTTAA | 6868 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Arg22Term AGA-TGA | GCGAGTTGGGTTTTATCAGAATGTGGTCTGAGGCCACTCCCGAGG GTCTATCCTAAGCCATGAAGTGGCCACCCTTTGTTGAATTCCAATC CCACAAAGCTGAGATTTTCAAGAACAGATC | 6869 |
| | GATCTGTTCTTGAAAATCTCAGCTTTGTGGGATTGGAATTCAACAA AGGGTGGCCAGTTCTATGGCTTAGGATAGACCCTCGGGAGTGGCC TCAGACCACATTCTGATAAAACCCAACCTCGC | 6870 |
| | CTAAGCCATGAAGTGGC | 6871 |
| | GCCAGTTCATGGCTTAG | 6872 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu27Term TTG-TAG | CAGAATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAA GAAGTGGCCACCCTTAGTTGAATTCCAATCCCACAAAGCTGAGATT TTCAAGAACAGATCTTGGAATGGTTCTTC | 6873 |
| | GAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTTTGTGG GATTGGAATTCAACTAAGGGTGGCCAGTTCTTGGCTTAGGATAGA CCCTCGGGAGTGGCCTCAGACCACATTCTG | 6874 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|---|------------|
| | CCACCCCTT <u>A</u> GTTGAATT | 6875 |
| | AATTCAACT <u>A</u> AAGGGTGG | 6876 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Leu28Term TTG-TAG | AATGTGGTCTGAGGCCACTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCTTTGT <u>A</u> GAATTCCAATCCCACAAAGCTGAGATTTTCAAGAACAGATCTTGAAATGGTTCTTCATT | 6877 |
| | AATGAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCTTTGTGGGATTGGAATTC <u>T</u> ACAAAGGGTGGCCAGTTCTTGGCTTAGGATAGACCCTCGGGAGTGGCCTCAGACCACATT | 6878 |
| | CCCTTTGT <u>A</u> GAATTCCA | 6879 |
| | TGGAATTC <u>T</u> ACAAAGGG | 6880 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Sesamum indicum</i> Lys34Term AAG-TAG | CTCCCGAGGGTCTATCCTAAGCCAAGAACTGGCCACCCTTTGTTGAATTCCAATCCCACAT <u>A</u> AGCTGAGATTTTCAAGAACAGATCTTGGAATGGTTCTTCATTCTGTTTGTGCGAGTGGGA | 6881 |
| | TCCCACTCGACAAACAGAATGAAGAACCATTTCCAAGATCTGTTCTTGAAAATCTCAGCT <u>A</u> TGTGGGATTGGAATTCAACAAAGGGTGGCCAGTTCTTGGCTTAGGATAGACCCTCGGGAG | 6882 |
| | ATCCCACAT <u>A</u> AGCTGAGA | 6883 |
| | TCTCAGCT <u>A</u> TGTGGGAT | 6884 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Tyr3Term TAC-TAG | CATCAGAGCGGCGATACCTAAGCATTGCTGGGTAAAGAATCCATGGAAGTCTATGAGTTA <u>G</u> GTCGTCAGAGAGCTAGCCATCGTGTTTCGCCTAGCTGCTGGAGCTGCTTACCTCAACAAT | 6885 |
| | ATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACACGATGGCTAGCTCTCTGACGAC <u>C</u> TAAGCTCATAGACTTCCATGGATTCTTAACCCAGCAATGCTTAGGTATCGCCGCTCTGATG | 6886 |
| | ATGAGTTA <u>G</u> GTCGTCAG | 6887 |
| | CTGACGAC <u>C</u> TAAGCTCAT | 6888 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Arg6Term AGA-TGA | GCGGCGATACCTAAGCATTGCTGGGTAAAGAATCCATGGAAGTCTATGAGTTACGTCGTC <u>I</u> GAGAGCTAGCCATCGTGTTTCGCACTAGCTGCTGGAGCTGCTTACCTCAACAATTGGCTTG | 6889 |
| | CAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGAACACGATGGCTAGCTCTC <u>A</u> GACGACGTAAGCTCATAGACTTCCATGGATTCTTAACCCAGCAATGCTTAGGTATCGCCGC | 6890 |
| | ACGTCGTC <u>I</u> GAGAGCTA | 6891 |
| | TAGCTCTC <u>A</u> GACGACGT | 6892 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
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| Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Glu7Term GAG-TAG | GCGATACCTAAGCATTGCTGGGTAAAGAATCCATGGAAGTCTATGA GTTACGTCGTCAGATAGCTAGCCATCGTGTTTCGCACTAGCTGCTG GAGCTGCTTACCTCAACAATTGGCTTGTTT | 6893 |
| | AAACAAGCCAATTGTTGAGGTAAGCAGCTCCAGCAGCTAGTGCGA ACACGATGGCTAGCTATCTGACGACGTAACCTCATAGACTTCCATG GATTCTTAACCCAGCAATGCTTAGGTATCGC | 6894 |
| | TCGTCAGATAGCTAGCC | 6895 |
| | GGCTAGCTATCTGACGA | 6896 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Brassica napus</i> Gly17Term GGA-TGA | CCATGGAAGTCTATGAGTTACGTCGTCAGAGAGCTAGCCATCGTG TTCGCACTAGCTGCTTGAGCTGCTTACCTCAACAATTGGCTTGTTT GGCCTCTCTATTGGATTGCTCAAGGAACCA | 6897 |
| | TGTTTCCTTGAGCAATCCAATAGAGAGGCCAAACAAGCCAATTGTT GAGGTAAGCAGCTCAAGCAGCTAGTGCGAACACGATGGCTAGCT CTCTGACGACGTAACCTCATAGACTTCCATGG | 6898 |
| | TAGCTGCTTGAGCTGCT | 6899 |
| | AGCAGCTCAAGCAGCTA | 6900 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Arg22Term AGA-TGA | GCAAGTTGGGTCTATCAGAATGTGGTCTTAGACCACTACCAAGAA TATACCCAAAGCCCTGAATAGGGTCTTCTTCCGTTTGCGCCACCAA TTTAAATCTGAGAAGAATTTACCTTCAC | 6901 |
| | GTGAAGGTGAAATCTTCTCAGATTTAAATTGGTGGCGCAAACGGA AGAAGACCCTATTCAGGGCTTTGGGTATATTCTTGGTAGTGGTCTA AGACCACATTCTGATAGAACCCAACTTGC | 6902 |
| | CAAAGCCCTGAATAGGG | 6903 |
| | CCCTATTCAGGGCTTTG | 6904 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Cys29Term TGC-TGA | TGGTCTTAGACCACTACCAAGAATATACCCAAAGCCCAGAATAGG GTCTTCTTCCGTTTGAGCCACCAATTTAAATCTGAGAAGAATTTCA CCTTCACCTATACGAACAGATCGGAATTGT | 6905 |
| | ACAATTCCGATCTGTTCTGATAGGTGAAGGTGAAATCTTCTCAGA TTTAAATTGGTGGCTCAAACGGAAGAAGACCCTATTCTGGGCTTTG GGTATATTCTTGGTAGTGGTCTAAGACCA | 6906 |
| | TCCGTTTGAGCCACCAA | 6907 |
| | TTGGTGGCTCAAACGGA | 6908 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Leu33Term TTA-TGA | CACTACCAAGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGT TTGCGCCACCAATTGAATCTGAGAAGAATTTACCTTCACCTATA CGAACAGATCGGAATTGTTGGGCATTGAG | 6909 |
| | CTCAATGCCCAACAATTCCGATCTGTTCTGATAGGTGAAGGTGAAA TTCTTCTCAGATTTCAATTGGTGGCGCAAACGGAAGAAGACCCTAT TCTGGGCTTTGGGTATATTCTTGGTAGTG | 6910 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| | CACCAATTGAAATCTGA | 6911 |
| | TCAGATTTCAATTGGTG | 6912 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Solanum tuberosum</i> Arg36Term AGA-TGA | AGAATATACCCAAAGCCCAGAATAGGGTCTTCTTCCGTTTGCGCCA CCAATTTAAATCTGTGAAGAATTTACCTTCACCTATACGAACAGAT CGGAATTGTTGGGCATTGAGGGTAAGTG | 6913 |
| | CACCTACCCTCAATGCCCAACAATTCCGATCTGTTCGTATAGGTGA AGGTGAAATTCTTCAAGATTTAAATTGGTGGCGCAAACGGAAGAA GACCCTATTCTGGGCTTTGGGTATATTCT | 6914 |
| | TAAATCTGTGAAGAATT | 6915 |
| | AATTCTTCAAGATTTA | 6916 |
| | | |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Trp4Term TGG-TGA | CTCTTTATTATCCTCCTCTTCTTTGTTTTTTTGAGTTCTGAGTCACC TATGGCAAGTTGAGTGATTTTCAAGATGTGGGCTAAGGCCACTTCC AAGAATCTATGCCAGGCCCAAGAGTGA | 6917 |
| | TCCACTTCTGGGCCTGGCATAGATTCTTGAAGTGGCCTTAGCCC ACATTCTGAAATCACTCAACTTGCCATAGGTGACTCAGAACTCAA AAAAACAAAGAAGAGGAGGATAATAAAGAG | 6918 |
| | GCAAGTTGAGTGATTTT | 6919 |
| | GAAATCACTCAACTTGC | 6920 |
| | | |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Ser7Term TCA-TGA | TATCCTCCTCTTCTTTGTTTTTTTGAGTTCTGAGTCACCTATGGCA AGTTGGGTGATTTGAGAATGTGGGCTAAGGCCACTTCCAAGAATC TATGCCAGGCCCAAGAGTGGAGCTTCATG | 6921 |
| | CATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGAAGTGGC CTTAGCCACATTCTCAATCACCAACTTGCCATAGGTGACTCAG AACTCAAAAAAAAAACAAAGAAGAGGAGGATA | 6922 |
| | GGTGATTTGAGAATGTG | 6923 |
| | CACATTCTCAATCACC | 6924 |
| | | |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Glu8Term GAA-TAA | TCCTCCTCTTCTTTGTTTTTTTGAGTTCTGAGTCACCTATGGCAAG TTGGGTGATTTCAATATGTGGGCTAAGGCCACTTCCAAGAATCTAT GCCAGGCCCAAGAGTGGAGCTTCATGTT | 6925 |
| | AACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGAAGTG GCCTTAGCCACATTATGAAATCACCAACTTGCCATAGGTGACTC AGAAGTCAAAAAAAAAACAAAGAAGAGGAGGA | 6926 |
| | TGATTTCAATATGTGGG | 6927 |
| | CCCACATTATGAAATCA | 6928 |
| | | |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|---------------|
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Petroselinum crispum</i> Cys9Term TGT-TGA | CTCTTCTTTGTTTTTTTTGAGTTCTGAGTCACCTATGGCAAGTTGGG TGATTTCAAGATGAGGGCTAAGGCCACTTCCAAGAATCTATGCCA GGCCCAGAAGTGGAGCTTCATGTTTCAAC | 6929 |
| | GTTGAAACATGAAGCTCCACTTCTGGGCCTGGCATAGATTCTTGG AAGTGGCCTTAGCCCTCATTCTGAAATCACCCAACCTGCCATAGGT GACTCAGAACTCAAAAAAACAAAGAAGAG | 6930 |
| | TCAGAATGAGGGCTAAG | 6931 |
| | CTTAGCCCCCATTCTGA | 6932 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Lys21Term AAA-TAA | ATGAAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTA ATGGTTTTTCATGCTTAAGAAGAAGAAGAAGAGGATTTGACTT AAGCAATCCTCCTCCATTCAATATTGGTC | 6933 |
| | GACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTCTTC TTCTTCTTCTTCTTAAGCATGAAAACCATTAACGCCATTTAGAATTG GGGTGTCTTTGTACTGTTGCTGCTTCAT | 6934 |
| | TTCATGCTTAAGAAGAA | 6935 |
| | TTCTTCTTAAGCATGAA | 6936 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu22Term GAA-TAA | AAGCAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATG GTTTTTCATGCTAAATAAGAAGAAGAAGAAGAGGATTTGACTTAAG CAATCCTCCTCCATTCAATATTGGTCAGA | 6937 |
| | TCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATCCTC TTCTTCTTCTTCTTAATTAGCATGAAAACCATTAACGCCATTTAGAA TTGGGGTGTCTTTGTACTGTTGCTGCTT | 6938 |
| | ATGCTAAATAAGAAGAA | 6939 |
| | TTCTTCTTAATTAGCAT | 6940 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu23Term GAA-TAA | CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCTAAAGAATAAGAAGAAGAAGAGGATTTGACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC | 6941 |
| | GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTTAATTCTTTAGCATGAAAACCATTAACGCCATTTA GAATTGGGGTGTCTTTGTACTGTTGCTG | 6942 |
| | CTAAAGAATAAGAAGAA | 6943 |
| | TTCTTCTTAATTCTTTAG | 6944 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Vernicia fordii</i> Glu24Term GAA-TAA | CAGCAACAGTACAAAGACACCCCAATTCTAAATGGCGTTAATGGTT TTCATGCTAAAGAATAAGAAGAAGAAGAGGATTTGACTTAAGCAA TCCTCCTCCATTCAATATTGGTCAGATCC | 6945 |
| | GGATCTGACCAATATTGAATGGAGGAGGATTGCTTAAGTCGAAATC CTCTTCTTCTTCTTAATTCTTTAGCATGAAAACCATTAACGCCATTTA GAATTGGGGTGTCTTTGTACTGTTGCTG | 6946 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|------------|
| | CTAAAGAATAAGAAGAA | 6947 |
| | TTCTTCTTATTCTTTAG | 6948 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Tyr21Term TAT-TAG | GGTCCAAGCACAGCCTCTACAACATGTTGGTAATGGTGCAGGGAA AGAAGATCAAGCTTAGTTTGATCCAAGTGCTCCACCACCCTTCAAG ATTGCAAATATCAGAGCAGCAATTCCAAAA | 6949 |
| | TTTTGGAATTGCTGCTCTGATATTTGCAATCTTGAAGGGTGGTGGGA GCACTTGGATCAAACTAAGCTTGATCTTCTTCCCTGCACCATTAC CAACATGTTGTAGAGGCTGTGCTTGGACC | 6950 |
| | CAAGCTTAGTTTGATCC | 6951 |
| | GGATCAAACTAAGCTTG | 6952 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Lys31Term AAG-TAG | GGTAATGGTGCAGGGAAAGAAGATCAAGCTTATTTTGATCCAAGT GCTCCACCACCCTTCTAGATTGCAAATATCAGAGCAGCAATTCCAA AACATTGCTGGGAGAAGAACACATTGAGAT | 6953 |
| | ATCTCAATGTGTTCTTCTCCCAGCAATGTTTTGGAATTGCTGCTCT GATATTTGCAATCTAGAAGGGTGGTGGAGCACTTGGATCAAATAA GCTTGATCTTCTTCCCTGCACCATTACC | 6954 |
| | CACCCTTCTAGATTGCA | 6955 |
| | TGCAATCTAGAAGGGTG | 6956 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Arg36Term AGA-TGA | AAAGAAGATCAAGCTTATTTTGATCCAAGTGCTCCACCACCCTTCA AGATTGCAAATATCTGAGCAGCAATTCCAAAACATTGCTGGGAGAA GAACACATTGAGATCTCTGAGTTATGTTT | 6957 |
| | GAACATAACTCAGAGATCTCAATGTGTTCTTCTCCCAGCAATGTTTT GGAATTGCTGCTCAGATATTTGCAATCTTGAAGGGTGGTGGAGCA CTTGATCAAAATAAGCTTGATCTTCTTT | 6958 |
| | CAAATATCTGAGCAGCA | 6959 |
| | TGCTGCTCAGATATTTG | 6960 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Glycine max</i> Leu41Term AAA-TAA | TATTTTGATCCAAGTGCTCCACCACCCTTCAAGATTGCAAATATCA GAGCAGCAATTCCAATAACATTGCTGGGAGAAGAACACATTGAGAT CTCTGAGTTATGTTCTGAGGGATGTGTTGG | 6961 |
| | CCAACACATCCCTCAGAACATAACTCAGAGATCTCAATGTGTTCTT CTCCCAGCAATGTTATGGAATTGCTGCTCTGATATTTGCAATCTTG AAGGGTGGTGGAGCACTTGGATCAAAATA | 6962 |
| | CAATTCCATAACATTGC | 6963 |
| | GCAATGTTATGGAATTG | 6964 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|---|---------------|
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Glu8Term GAG-TAG | CATCCACCCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGC CCGGCTCGTGCTCTCCTAGTGCTCGGGCCTCGCGCCCGTCCGCC GCCTGCGCGCCGGCCGGGGCGCCATTGCGGCGC | 6965 |
| | GCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGGACGG GCGCGAGGCCCGAGCACTAGGAGAGCACGAGCCGGGCCATTGC CGCCGTCAGCGGGGCGGGTGCGGGTGCGGGTGGATG | 6966 |
| | TGCTCTCCTAGTGCTCG | 6967 |
| | CGAGCACTAGGAGAGCA | 6968 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Cys9Term TGC-TGA | ACCCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGG CTCGTGCTCTCCGAGTGATCGGGCCTCGCGCCCGTCCGCCGCCT GCGCGCCGGCCGGGGCGCCATTGCGGCGCGGTCA | 6969 |
| | TGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGCGG ACGGGCGCGAGGCCCGATCACTCGGAGAGCACGAGCCGGGCCA TTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGGGT | 6970 |
| | TCCGAGTGATCGGGCCT | 6971 |
| | AGGCCCGATCACTCGGA | 6972 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Ser10Term TCG-TAG | CCGCACCCGCACCCGCCCCGCTGACGGCGGCAATGGCCCGGCT CGTGCTCTCCGAGTGCTAGGGCCTCGCGCCCGTCCGCCGCCTGC GCGCCGGCCGGGGCGCCATTGCGGCGCGGTCA | 6973 |
| | GGTGACCGCGCCGCAATGGCGCCCCGGCCGGCGCGCAGGCGGC GGACGGGCGCGAGGCCCTAGCACTCGGAGAGCACGAGCCGGGC CATTGCCGCCGTCAGCGGGGCGGGTGCGGGTGCGG | 6974 |
| | CGAGTGCTAGGGCCTCG | 6975 |
| | CGAGGCCCTAGCACTCG | 6976 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Zea mays</i> Ser29Term TCA-TGA | GCTCGGGCCTCGCGCCCGTCCGCCGCCTGCGCGCCGGCCGGGG CGCCATTGCGGCGCGGTGACCCCCCGCGCTCTCCGCGGCGCCG CGCCGTCGTCCCGCGTCCGCGTCCATCCACCGCGA | 6977 |
| | TCGCGGTGGATGGACGCGGACGCGGGACGACGGCGCGGCGCCG CGGAGAGCGCGGGGGGTACCGCGCCGCAATGGCGCCCCGGCC GGCGCGCAGGCGGCGGACGGGCGCGAGGCCCGAGC | 6978 |
| | GGCGCGGTGACCCCCG | 6979 |
| | CGGGGGGTACCGCGCC | 6980 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Glu8Term GAG-TAG | CCCCCTCCCCACGCACACGCACAGATCCATCCGCGGCCATGGC CCCCGCAATGAGGCCGTAGCAGGAGGCGAGCTGCAAGGCCACCG AGGACCACCGCTCCGAGTTCGACGCCGCCAAGC | 6981 |
| | GCTTGGCGGCGTCAACTCGGAGCGGTGGTCCTCGGTGGCCTTG CAGCTCGCCTCCTGCTACGGCCTCATTGCGGGGGCCATGGCCGC GGATGGATCTGTGCGTGTGCGTGGGGGAGGGGG | 6982 |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|--|--|------------|
| | TGAGGCCG <u>T</u> AGCAGGAG | 6983 |
| | CTCCTGCT <u>A</u> CGGCCTCA | 6984 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Gln9Term CAG-TAG | CCTCCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCGGAG <u>T</u> AGGAGGCGAGCTGCAAGGCCACCGAGGACCACCGCTCCGAGTTCGACGCCGCCAAGCCGC | 6985 |
| | GCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCC | 6986 |
| | TTGCAGCTCGCCTCCT <u>A</u> CTCCGGCCTCATTGCGGGGGCCATGGCCGCGGATGGATCTGTGCGTGTGCGTGGGGGAGG | 6987 |
| | GGCCGGAG <u>T</u> AGGAGGCG | 6988 |
| | CGCCTCCT <u>A</u> CTCCGGCC | 6989 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Glu10Term GAG-TAG | CCCCACGCACACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCGGAGCAG <u>T</u> AGGCCGAGCTGCAAGGCCACCGAGGACCACCGCTCCGAGTTCGACGCCGCCAAGCCGCCGC | 6990 |
| | GCGGCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCCTTGCAGCTCGCCT <u>A</u> CTGCTCCGGCCTCATTGCGGGGGCCA | 6991 |
| | TGGCCGCGGATGGATCTGTGCGTGTGCGTGGGGG | 6992 |
| | CGGAGCAG <u>T</u> AGGCGAGC | 6993 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Triticum aestivum</i> Cys13Term TGC-TGA | GCTCGCCT <u>A</u> CTGCTCCG | 6994 |
| | ACGCACAGATCCATCCGCGGCCATGGCCCCCGCAATGAGGCCGGAGCAGGAGGCGAGCTG <u>A</u> AAGGCCACCGAGGACCACCGCTCCGAGTTCGACGCCGCCAAGCCGCCGCCCTTCCGCATC | 6995 |
| | GATGCGGAAGGGCGGCGGCTTGGCGGCGTCGAACTCGGAGCGGTGGTCCTCGGTGGCCTT <u>T</u> CAGCTCGCCTCCTGCTCCGGCCTCATTGCGGGGGCCATGGCCCGGATGGATCTGTGCGT | 6996 |
| | GCGAGCTG <u>A</u> AAGGCCAC | 6997 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Ser4Term TCG-TAG | GTGGCCTT <u>T</u> CAGCTCGC | 6998 |
| | CTTCACAAATCACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATGGCGGCGT <u>A</u> GGCGACCCAGGAGGCCGACTGCAAGGCTTCGAGGACGCCCGTCTCTTCTTCGACGCCGC | 6999 |
| | GCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGCCTTGAGTCGGCCTCCTGGGTGCGCT <u>T</u> ACGCCGCCATTGCCGCCGGGGTGTGCTGGTGGATCTGATTCCGATTTGTGATTTGTGAAG | 7000 |
| | GGCGGCGT <u>A</u> GGCGACCC | |
| | GGGTCGCC <u>T</u> ACGCCGCC | |

| Phenotype, Gene, Plant & Targeted Alteration | Altering Oligos | SEQ ID NO: |
|---|--|---------------|
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Gln7Term CAG-TAG | ATCACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATG GCGGCGTCGGCGACCTAGGAGGCCGACTGCAAGGCTTCCGAGGA CGCCCGTCTCTTCTTCGACGCCGCCAAGCCCC | 7001 |
| | GGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGAAGC CTTGCAAGTCGGCCTCCTAGGTCGCCGACGCCGCCATTGCCGCCG GGGTGTCGTGGTGGATCTGATTCCGATTTGTGAT | 7002 |
| | CGGCGACCTAGGAGGCC | 7003 |
| | GGCCTCCTAGGTCGCCG | 7004 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Glu8Term GAG-TAG | ACAAATCGGAATCAGATCCACCACGACACCCCGGCGGCAATGGC GGCGTCGGCGACCCAGTAGGCCGACTGCAAGGCTTCCGAGGACG CCCGTCTCTTCTTCGACGCCGCCAAGCCCCCGC | 7005 |
| | GCGGGGGCTTGGCGGCGTCGAAGAAGAGACGGGCGTCCTCGGA AGCCTTGCAAGTCGGCCTACTGGGTCGCCGACGCCGCCATTGCCG CCGGGGTGTCTGGTGGATCTGATTCCGATTTGT | 7006 |
| | CGACCCAGTAGGCCGAC | 7007 |
| | GTCGGCCTACTGGGTCG | 7008 |
| Reduced linolenic acid omega-3 fatty acid desaturase <i>Oryza sativa</i> Cys10Term TGC-TGA | TCAGATCCACCACGACACCCCGGCGGCAATGGCGGCGTCGGCGA CCCAGGAGGCCGACTGAAGGCTTCCGAGGACGCCCGTCTCTTC TTCGACGCCGCCAAGCCCCCGCCCTTCCGCATC | 7009 |
| | GATGCGGAAGGGCGGGGGCTTGGCGGCGTCGAAGAAGAGACGG GCGTCCTCGGAAGCCTTICAGTCGGCCTCCTGGGTGCCGACGC CGCCATTGCCGCCGGGGTGTCTGGTGGATCTGA | 7010 |
| | GCCGACTGAAGGCTTC | 7011 |
| | GAAGCCTTICAGTCGGC | 7012 |

[267] Although a number of embodiments and features are described herein, it will be understood by those skilled in the art that modification and variations of the described embodiments and features may be made without departing from either the spirit of the invention or the scope of the
5 appended claims. All publications and patents cited herein are incorporated by reference in their entireties.